

606

AACACGGTTC	CTGTGAAATT	TTTCAAAGAA	CAGGCTAGGA	TGATGTCTAT	GTCCGACCGA	9240
CGTGAGCAAT	TTCAATACGC	ATTTTGGAT	TCAGGTATAG	GAGGATTGCC	CTACGCACAC	9300
GCCTTACGCG	TGCGTGTGCC	TGAGGCCTCA	CTGGTGTACG	TGGCGGACCG	TGTATACTTT	9360
CCTTATGGGA	ATAAAAGTTC	TGCACAGATT	ATTGCGCGTG	CGTCTGCAGT	TTTGCAGAAA	9420
GTGCAGACGA	ATTTTTCACC	ACACATAGTG	GTACTCGCGT	GTAACAGCAT	GTCTGTCAAT	9480
GCACTTGAGT	TTTTGCGTGC	GCAGGTTTCG	GTTCCAGTGG	TGGGGGTGGT	GCCTGCAATT	9540
AAGCAGGCGG	TGGCGTGCAG	TCATAAAAAG	CACATTGGTG	TCTTAGCTAC	ACAATGCACG	9600
ATTACGCATC	CGTACACAGC	GTGTTTGAGA	GCACAGTTTG	GTGCaGGGTG	TGTGTTTCAG	9660
AATgcTGC GG	ATGCACGCCT	TATTGAGTGT	CTTGAGCGCG	GGTTAATTTT	TGAAGTCgAA	9720
GACATGCaGC	GGGAGGCAGT	GGCGCGCTCA	GTTATGCCCT	TCCAGGAAGC	GGGGTGGAT	9780
GTGCTCGTGC	TCGCGTGCAC	CCATTTTGTG	CACGTGCGTC	ATCTTTTTCa	GGACTGTGTT	9840
GGTACCTCGT	GTACGGTGGT	AGATTCGCTA	GAAGGTGTGG	TACGCAGGAC	GTTACGTCTG	9900
TGTCCACCGC	AATCTCAATT	GCGTGGGAAC	GCCGCCTGTT	ACGTAAC TGG	TGCGCGCGAT	9960
GCAGTGTGCG	CGGCACGATA	CGCACGGTAT	GCGCAGCACT	TTGGATTGCG	CTGGGCGGGT	10020
TTTTTGGaCk	TATGAACACG	GCACTGGATA	TCGGGTGCGT	GCACTGTGTG	TGTTTGTGTG	10080
GAGGCGGTAG	ATAAgAgAgG	CTGATAgACA	GCGCGGTGCT	GCGTGC GTAC	AATGGGCCAT	10140
GGGGAAGCCG	AGgTtTCGTG	CAGTGGCCTT	TGACATtGAT	GGGACAcTGT	ACCcTGGATG	10200
GCGCCTTGaT	GCGTGTtATg	CCCTTtATGA	TTCGCAATGC	GCGCTTGATG	CGTGC GTTCC	10260
GTGCGGTGCG	TCAGGAGCTA	CGTCGTGAGC	AACGTACGGC	ACTTATTCCT	TTGAAGACT	10320
TTTTTTTTGc	GcAAStACgC	GCATCGCGCC	GcGCGTGGGT	TTATCTGCAG	AAGAAGTGGC	10380
AGCCTTCCTC	GACACAGCGC	TGTATCGGGG	GTGGAGGCGT	CACTTTTTTAC	ATATAAAGCC	10440
ATTTCCCTCAC	GTGCTTTCCT	CGGTGT TGA	GCTGAGGCGG	CATGGGCTGA	AGATAGCGCT	10500
TTTGTGCGAT	TTTCCTCCGA	GTCAGAAAGG	CTGTC TATGG	GGGGTGC GCG	CGTTGTGCGA	10560
TGTAACGTTG	GGCACAGAGG	AGATTGGGTC	CCTCAAGCCT	TCTCCCCGGG	CCTTTTACGC	10620
GcTGGCGCAG	AGACTGAATC	TGcGCTGTGA	AGAAATCTTT	TACGTGGGGA	ACAGTGT TCA	10680
TGACGTGGAA	GGCGCGCACG	CAGCAGGTAT	GAGGATTGCC	TGTGTGCGCA	GgCCCTTTAC	10740
GAGTCTTCGC	GTTCGGCGCA	cGCGGaCTGG	CTCTTTTCCG	ACTATCGCAC	ATTGTGcGCA	10800
TATGTGATAG	CATGAGCGCC	GGCGCAGGGT	AGTCTGCCGA	ACCCACACG	TCCAGCGTGG	10860
CGCCCGCGGG	TACCCGCTGT	GCGTCGCGTG	AAGACGAAGt	GAGTGGAGCA	TGGAGTACTT	10920

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TCTGACGGTT GTCATTGCCT GCGCGATTTC CCTCGTGATG GTTGC GTTCT CCCGCCAGCT 10980  
 GGACAAAGGT AACCGTTCTC TTGAAAAGGT CAAGCGCTAC GCGKACTACA TAAAGGAAGA 11040  
 TCTTGAGTCA TcAGCGCAGA GAAGATTGCG ATGCTCAAGG ATGCGGCCAT CGAGTTAAAT 11100  
 GTAAAGCAAG AGCAGGCGAT TGCCTCAGTG AAAAAATGG ATCACCTCTA CGACCAGTTT 11160  
 ATGAagaAGT CTACTGCGCT TGCGGTGCAA A 11191

## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GGAAAAAACC TTAAATTCC CGGTACAATT GTGCAGAGAG CGTTTATTA TGACTGATGA 60  
 CAAGnGTCGG TTTTTCAnG CGTGCAATAA CGTTTGCAAC TGTAACGTT TTCCCCGAAC 120  
 nGGTAACACC CTTGAGCGTT TGAAAACGCG CCCCCGCATG CAAGCCACGC ACGAGTGCGT 180  
 CGATTGCGGC AATCTGATCG CCTGCAGGTT GGAAAGAAGC GTGTAATTTA AATTCTTTCA 240  
 TGTGCTTCGC AGTATCGGTT ATTACCATAG GATTTAAAAA ATCTGTAGTA CATGCTGTGC 300  
 CTTTCCCTTT GATTTTGCTC TCTTAGAACC TCTGGTTGAC AAACCACACC CATGGTGAAT 360  
 AGAGTGGACC CCGCTTAAGA GGAGGCACGT TATGGTCAAG TTGCTTAGCA TTGGTGGATC 420  
 GGATGCTTCA GGTGGTGCGG GCATCGAGGC GGATCTGAAA ACTTTCCAAG AGTATGGAGC 480  
 GTTCGGTGTG GcTACGCTCA CCGCATCGT TACTATGGAC CCATCCCGGA ACTGGTCGCA 540  
 TCGTGACAT TCACTTGAGG AAGACTGTGT GCGCGATCAG CTTGAAACCG CATTTGCAGG 600  
 CGTGGGGGTC AGCGCGGTGA AAAGCGGTAT GCTTGCTCT GTCCATGCAA TCGAATGTGT 660  
 CGCGGAGTAT CTCGAACGTT TTGCAGTTGC TGCATACGTC TTTGATCCTG TCATGGTATG 720  
 CAAAGGATCG GGAGATGCAT TGCACCGTGA GTTGAACGAA TTGATGATCC AGAAACTTTT 780  
 GCCACGCGCG ACAGTTGTTA CTCCCAATCT TTTTGAAACC GCCCAGATTG CCGGTATCAG 840  
 CGTACCACGG ACAGTGGACG AAATGAAGGA GGTGTCACGT TTGATTCACG AGCGCGGCGC 900  
 GTCGCACGTG TTCGTCAAAG GCGGCGGAAG ACTCCCCGGT TGCAAGCACG CTCTGGATGT 960  
 TTTCTACGAC GGCAAGACGT TTCACCTCGT TGAAGATGAA CTTGTGCAGA GTGGATGGAA 1020  
 TCACGGCGCG GGCTGCACCG TATCTGCGGC TATTACTGCA GGACTGGGCC GAGGACTCAC 1080

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CGCCTACGAC GCGATACTGA GTGCTAAGAG ATTCTGTGACT ACAGGCCTCC GCCACGGATT 1140  
 CCAAGTCAAC CAGTGGGTTG GAACAGGAAA CCTCAGCAA TGGCGCGACC GCTTCCACTG 1200  
 ACTCAGGCGG TACATACGTG GGCGATCAGT GCTGGTATAG GTGCTTGAAG TATTCCAAGT 1260  
 CGGTTGAGAG GATCTTCTCC GTGTCGGGGA GCGATTTCTT GTACACCTCC AAGCTTTTCC 1320  
 AGAAGCCGTA GAACTCAGGA GATTTCCCGT ACGACTGCGC GTACACGGCC GCGGCGCGGG 1380  
 CGTcTGCTTC ACCcTTGATA CGCTCTGCCT CCTCGTACGC TTTTGAAAGT AAAcTGC GTT 1440  
 TTTCTGTGTC GAGCTTTCCA aGCCACTCTG CCTTCTTTCC TTCGCCTGTG GAGCGGAACA 1500  
 TTTGCGCGAT CTGGTTGCGC TCTTTTACCA TCCGATTGAA CACAGATGCT TGCAGCTCAT 1560  
 CTGAGTACTT AATCCCCTTG AAGATCACAT CGACAACGAC AATACCGAAA TCTTTTAACT 1620  
 GATCATTCGC CGCCTGTGAG ATCTCCCGCG CAAGAGACTC TCGCCCCTTT TCTATCGTCA 1680  
 TATGCGCAGT TTTCTCCGCA CCCCTATCAA AGGCAAGCTG CGACACCGGG ACGTCAAAC 1740  
 GCTCGGAGTG ATTGGACTCG TTGATAGCGn TTn 1773

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CAGCACATGC ACATGCATAT TCTTCCTTTT CGTTCATGAG CGGTATCCGT TTCAGGTCAT 60  
 TCAAATATGC CGTGAGAGTA TTCTCATCGT GCGGGAAGT CATTGTGCTC ACAGAGTACT 120  
 CCTTTTGTTT GAAAGGTACG TACCATATAC TCAGCAAATA TCATGCCATT TACGATAAAC 180  
 CAGAGGAGAT CTGTTTCGGT TCCCTATCAC GCCACTGGAC CCTCTGTGCA TACCTCCCTT 240  
 TCCCACGGCG CGCTACAGTT CTCTTGATTC TTCAAAAGGA AATGTATAGA ATGCGCCCCG 300  
 CGcGGTGCGT GTAGGCATAC GCGGCAAACG TGAAGATATG ACTCGTTATG AGGAGGAACG 360  
 CATGAAAATT ATACCGCTCG CGGACCGTGT CCTGGTAAAA ACTGATAAAT CGGAAACTAA 420  
 GACTGCTTCT GGAATCATCA TCCCGGACAC TGCGCAGGAG AAGATGCAAA GCGGTACCGT 480  
 CATTGCTGTT GGTTCGACT CGGAAAAGAT AAAAGTTTCG GTGGGTCAGC GTGTATGCA 540  
 CGATAAATAT GCCGGAAC CAGTAAAGAT TGATGGAGAG GAGCACCTGC TGCTCAAGGG 600  
 TGCTGATATC CTAGCTGTCA TCGAGTAGTT TCATCTCTTT AACGGGcTGC GCGCGCTGGA 660

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GCAGTGCACG CGCGGCCACC GTCTTTCCCT GTTGCTGCAA AAGTTGTCCT GCACGCTGGT	720
ACCATTCTCT CCAGCGCTGT GCTTTCCCCG CCGCCGGGcG CkCTCGAGGA TGTTCTTCGG	780
CCTCCCCCTC TCCCCGnTCC TTTTGAAGTT GTCGTA CTGA TTCgCGCGTT GCTTCGTCTG	840
CCGCAAGCAC AAAGTGTTCCT GCAGCCGCGG TTTTCTTGCC CATCCGCTCA AGCACTATCG	900
CTATGTTTGC GgArCGnCTG tGCGCGCTTC CACAGCGCGT GTCGCTTCCA CCAAGCCCCC	960
GAGGATACTC TCCACCCTCC CCGTACGAGA AGCTGcAGCA AGTGCCCGAT AGAAAGCATC	1020
CTCAGGACCA CCTCCTGCAT CACTGAGACC AAACGCTGAC TCATATTCCC CAATTCGAAA	1080
AAAGAACCAA CGTGCATACC GACGCACtGT GTGTCCACAG GgAAGACTTC AAGCAACTGC	1140
CACAGCGCGC CCCGACTGCC CTGTAGTCTC TTTTGTGCAG GATAACAAAA ACGAAAGTAT	1200
TCCAATGCAA AACGCACATC TGCCCGCCCA TGcATCGCCT CTGTGCTAA TTCCGCCAGC	1260
AATGACCGAG CCTCCACAGG AAAATGGGGA GACAAAAAGT GTCCTGTTC CATCTGCACA	1320
GAATACACCC CCCTTTCAGA GAGCAATTCC GTAACAGAAT CGCGCTGTCT GTGTGCTGCA	1380
CGAAAGGCAA TGCTCTCTCG CGCATAGCAC GCAACGGCAG GATAGTACGT TTTATCCCCC	1440
TCAACACACT GCGCGAGCAT CCGAACACGC TCCTGTGCAT GAGGAGCAGT GAGTGCTAGA	1500
TTGTAGAGTG CATGTGTGGA TGTTCCAGGA AAACGGTCAA CGTACGCGTA CCAAAAAGCA	1560
CGTGCACGCG CTCTATCCCC TCCATCGAAA GCGGCATCTG CCGcTAACAG CAAGTGAGTA	1620
CGGGCGTGCG TCGAGGCGGC AGAGTACGTA CCGAACAAAT CTGCACGTGC AAGACTTATG	1680
GGGAGCAACT CAAAGACCAA AGAAAACTGT CCTGCGTCAT AGGCGACTGT GGCCCAGAAT	1740
GCCGTATTCT CCGGTGCCTC AGTACCCAGT ATACGGGAGT ACAGACGGAA CGCAGCATGC	1800
AACTCCCCCA CGCGGGCGTA CGCACACGCG GCATTCTGGA GAAAGGCATG CATACCAAGT	1860
ACACCAAAGG CTGCAAGCaA AGCGCAGGAG CAATGCGGGC AAGTGCGATG CCAGTTGTAT	1920
GCCGTATTGG CGGCGACGGT TCTACACGAA ACTGCTCTTC TCCCCGGTCA AGAGGGAACG	1980
CCGTCACGTG CGCTTGATCT CTACCCCCCT GAACCTGAGA AACTCAACA GGCTCCTCTG	2040
GCACGTGCTC GGCTCTCTCA CTGTGAAAAG AGCCCCGAGA TGGAGAGTCA CCTCCTGTGC	2100
GCGAACCTAT GAGAGCAGCC TTTATCAGTG CCTCTGCGCC AATACTCTCA TATCCCTTGT	2160
GCACCACCCG GGGGACATAG GAGATTGCTT CCTCGAAACG AGCCTCCCGC AGGAGAAGAT	2220
GTATACCAA TGCAGCAAGC CTGCCATCAT CTGCACTTCT TCGTATGCCA CGCTGGAGTG	2280
TACGCAtGCC GCAGCGGAGG CTGAGAGTTC CATCTGACGC TTGGCAATAC TCAGATACTG	2340
CGACGACTCT CGCGCGTGTC CCACCATACG CGCAAGACCG CGCAAGGCTG CGCCTTTGCG	2400



CtTCCTGAGC AATCAGACTA TCTGCACGCG CAAGTCTCTC CAAAAAGGGC CGACTCCCCC	2460
AAACGGAGCG ATAGATGCAT AGCCCAGCAA TACCCACCCC AACTACTCCA AGGTAAGAGA	2520
GGAGGTGGCG CTTACTACGC ACTTTTAGCA ATGTTATCGA GCACACCATT TACAAAGCGG	2580
AAGGAGTCGT CcGTACCGAA ATCCCGAGCG ATACTGACCG CCTCGTGTAT AACGACGACG	2640
GGGGGAATGT CTTTTTGAAA GAGTAGCGAA TACGCACTTA GGCGCAGGAT GGCCTTGTC	2700
ACCTTGTTCA AACGCACAAA ATCCAGTGT TCCAACCGTG AACTCACACA ACCGTCAATT	2760
TCCCGCAGGT GCTCGAGCGT ACCGAGAAAG AGGAGTCGGG AAAACCCCAA ATCCTGGGTA	2820
GAAGGAGGCG GGTTCCTCCG CAACCAAGTA AACTGAGTTA ACGTCTCCGG CGTGATGCCC	2880
GCCGCGTCCC AGGCAAAGAG AGCCTGAAAA GCCAGAATCC GAGCGCGCCT CCTCCCTATC	2940
TTTGGGAATA CTTCACTCAC CAGTCGAGCA CCTTGCCGAG CTCTGCGTCA GCCAAGAATA	3000
CCTTATAGGT ACCAGACTTC CTCAGcTCCG CCGACACTTC CCGGATAGCG TCCTCGAGCG	3060
CTTTTGTGTTG GATTGGGAA GTAAGAAGAT TCTTGATAAA CTCGTAAAGC GAGACGGTCT	3120
TGTCAGGCTC CACCAAATCG CTGAGCGTTA GGATCTTCGC TTCCTCTTTC TTCAAAATA	3180
TGAAGCACTG ATAGTCATTA GCCGTTTCAT TCACGTCCGA AACAGCACCA ACTCCCATGC	3240
CAAAAATTTC AAGCAACGCC TCCATCGTCA GACCAAGCTG CGTGGCAGTA ACCGCAGTCT	3300
TCCCCAGGTA TATTTCCCCG GCAGAGTAAC CCGCCTGTGC ACCATTTGCC TTACTCTTAA	3360
TGTCAGCCGT GGCTTTGACA CCGGAACCTT TAAGTTTCTT AACAACTCT TGCGCTTTCG	3420
CCTTTCGAGC AGCAGGACCT GAAAcTCGG GACAGAAATA AGAAACAACT TAACCGTGTC	3480
AGGGCGGAAA AAGGCCTGTT TATTAAGCTC GTAGTAGGAA CGGATTTGAG AGTCCTCAGG	3540
TCCCTTCAAA TTCCGAAACT CGTCTGCCTT CTTTGTGACC ACGTAGCGCT GCGTGCTCAC	3600
CTGCGTCTTT AGAAACTTTT TGTATTCTGC CATAGTCATG CCGTTTGTCT GCTTCATGAA	3660
CTGATCGAGC GAGATATTCT GCTTCTCCTT GACGTAATTG GCGAACTCAG CCTCCGTTAC	3720
CGCACGTCCA ATCTGTTGAG AAAGCATTCC ATTAAAATAC TGATTCACTT CAGCATCCGT	3780
TACCTGGATA CCCGCCTTTT CTGCCGCTTG AGCAAAAAGC TTTTCGTCAA TAAGACTGTC	3840
CATGAATTGT CTACGCTCAG CAGTGCTGAG CTTCTTTCCC ATCTCTTTCT CAATCGCAGA	3900
AATTCTTGCC TTAATCTGTC CGAGCGTCAc CGGCTCACGC CGGAATAAAT TCACTTCGGC	3960
GATAGGCTGC AGCGCCGACT GCGCGTGCGC AAACCCCATC CCCGCCACGC ACAACAGAGC	4020
GGGAACTATG TATCTGCCCA TGAGAACTCC CCGTAACAAC CGCGACTcAG TCACCAGCAC	4080
ACACGCCGGA GAAACTATAC GCAGCAGGGC AAGTTACGAC TTTTCCCCGC TTTTCTCAAG	4140

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AATCGCGCGA	ATACGCCGCA	CCCCCGCCGC	ACTCGACTGT	TCCTTTTGAA	TAGAAAACCG	4200
CCCGAGCTGC	CCGGTACGTG	CTACATGTGG	ACCGCCACAC	ACTTCCCGAG	AAAAAGTTCC	4260
TATGGAGTAC	ACCTTTACAG	TTGATTGTA	TTTCTACCA	AACAACGCCA	CGGCACCAGA	4320
ATTCATCGCA	TCTTCGAGCG	ACATCACTTC	ACAGCACACC	GGCAAGTCTG	CCCGGATCTG	4380
CTCATTCACC	AACTGTTCCA	CCTGCACCTT	CTCCTGCGCA	CTCATCGGTC	TTGGGTGAGA	4440
AAAGTCGAAA	CGCAGGCGTT	CTGCCGTAAT	ATTTGAGCCT	TTTTGCTGCA	CGTGCGTACC	4500
AAGAACCACT	CGCAATGCCT	GGTGCAGCAG	ATGCGTCGCC	GTGTGGTACG	CTGTGCTTTC	4560
CGCTGAATGA	TCAGCCAACC	CACCCTTAAA	TACTCGCTGT	GCACCGATCC	GAGAGCACGC	4620
CTGGTGCGCC	TGAAACGCGG	TGTCAAACCC	TGCACGGTCC	ACCCGTAAAC	CCGATTCACG	4680
CGCAAGTTCC	TCGGTCAGCT	CAAGGGGGAA	TCCATACGTA	TCGTATAGCC	GAAAGGCAAC	4740
TGACCCAGGT	ATTTCTCGCT	CTGTCCCTTG	TAAAACTTG	GGTATCATCC	TCTCGTACTC	4800
TGCCTACCCC	TTCTGAGGG	CGTCGAGGAA	CTTACGTTC	TCGTTTGCAA	GCTCCTGCGC	4860
AATACACGTA	GCTTTCTCTT	CCAGTTCCGG	GTATACCGCA	GCGTATTGCC	CAATCACCAC	4920
GC GCGGAGG	GAGGACAGGA	ACTCCCCATC	GATACCGAGC	TTCTTCCGT	GGCGGACTGA	4980
ACGGCGAATG	ATTCTGCGCA	GTACGTAGCC	TGCACCCACG	TTAGATGGGC	GTACAGGGAC	5040
AGGATCGCCG	AGGATAAAAG	TGGCCGCACG	GATATGATCG	CATACAATCC	GCATGGATAC	5100
GTCGTGCGCT	CCCTGACACC	CATACCTCTT	CCCACATAAC	TGACCTATCC	GCTCCAGGAG	5160
CGGGGTAAAG	ATCTCCGTAT	CATACACTGA	CCGCTTGCCC	TGCAAAACCG	CGACGGTGCG	5220
TTCAATACCC	ATACCGGTGT	CCACACAATA	ACGTTCAGC	GGCCGGTACC	TGCCGTCTGC	5280
GTCTTACGA	TACTGCATGA	ACACGTCATT	CCAAATCTCT	ACGTACTTGC	CGCAAGAACA	5340
TCCCGGACGA	CAGCTCACAC	TGCAAGGAGG	AACTCCAGTA	TCAAAGAATA	TCTCGGTATC	5400
CGGACCACAT	GGCCCTGTTT	CCCCCGTAGG	TCCCCACCAG	TTATCCGCAC	GTGGTAAAAA	5460
ATGAATATGG	GTGCGCGCGA	TACCAAGTCG	TTCCCAGATA	GCGGCAGATT	CCTCATCACG	5520
CGCAACAGCC	TCATCCCTTG	CAAAAACAGT	CACCGAAAGC	CGGTCAGGGG	ATATGCCGAG	5580
CCATGGAGCA	CCAGTAAGAA	ATTCAAAGCT	GAACGCGATT	GCCTCCTCCT	TGAAGTAATC	5640
GCCCAACGAC	CAGTTACCCA	ACATCTCGAA	AAAGGTCAGA	TGCGAGTTAT	CGCCCACCGC	5700
ATCGATGTCA	CCGGTGCGCA	GACACTTTTG	CGCATTGACC	AAGCGGGTAC	CAGCCGGATG	5760
TGGCTCACCC	ATAAGATAGG	GAACCAACGG	ATGCATGCCA	GCAGTAGTAA	AAAGCACGGT	5820
AGGATCGTGC	TCGGGCACAA	GGGACTTACC	CGAGATAACC	ACATGAGCCT	TCTGGCTAAA	5880

GAAGGCGAGA TAACGCGAGC GTAgCTGATC GGCGGAATA GGAATGCTCA TGGAGGGTAT	5940
TATCGCCTTT TCCCTGCTGC GGTCAACATC TGACCCATAA CGGGAAAAAG AAACGGGGAC	6000
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CAAGACAGTT TCGCACCCCTT AAAAAATATA AGGAGCACAC ACATGACCAC GTCATTTGTG	6120
ATCGGTGTTG TCCTTGTTAC TGTCGGTTTA AcCTTCGGAT GGACCATTCTG CTGGCTCTAC	6180
GCCAGATTTT ACTTATCCGC CTGTGAGCAA CGTGCAGAAC GTATCCTCCA GGAGGCACAA	6240
AAAGAAGCTG AATCCAAAA GAAAAGCATT CTCTTGAAG CAAAAGAATA TGTCTTTCGC	6300
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CGACGCCTTC TTCAAAAAGA GGAAGCCCTC TCTACGCGCG CGGGGGAGCT TGATTCTCGA	6420
GAACGATCGC TAAAACAGCG GGATCAGTCC CTCTGTCAAG AAGAGGCCCG CTATCGCCAG	6480
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GCTTTGAACG CTGAGCGTCG CGCGCGCGAC ATCCTCGTTA CTACCATGCA GCGTATTACT	6660
GCTGATGTCA CCGGTGATGT GACCGTCTCT ACGGTGAATC TACCCAGTGA AGAAATGAAA	6720
GGACGCATCA TTGGGCGCGA GGGACGTAAT ATCCGCGCGT TAGAGACACT CACTGGTGCT	6780
GACGTTGTCTG TAGATGACAC ACCTGAAGCT GTCGTCATTT CCTGTTTCGA CCCGGTACGC	6840
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CGCATTGAGG AAATTGTGCA GAAGGTGACG CAGGAAGTTT CTCAAAAAAT CTATGAGGAA	6960
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GCAGAAATTG GTATGGAGAT GGCTCGCAA ATGAATGAGG ACCCGCGAGT GGTAACGCC	7260
GTGGTTCTC ACCACAACGA CATAGAGCCG TGTGTGTTG AGTCTTGGCT CGTTCAGGTA	7320
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AAGCGTCTAG AAAACCTCGA GCGATTGCT GAGGGGTTCT CGGGTGTAGA GAAAGCCTAC	7440
GCTATTCAGG CCGGGCGCGA GTTGCCTGTT TTAGTGAACA ACGATAAAAT CCCCACAGG	7500
GACGTGAAGG CACTTGACG TGACATCGCA AAGAAAATAG AGAGCGACTT GAAGTATCCT	7560
GGCGTATCC GGGTCACTCT TATTCGAGAA ACGCGCGTCG TGGAGTATGC CCGCTGAGCC	7620

TCAGGGAGAG GGGAGAGAGT GCACGGGCGT CCGTGCAGGT TTGCATCGGC TGCAGTGACT	7680
CTCCTACCTC CCTATTCTAG TCCGGCGATA TTGGTCAACA AGGCACATGG GAGTATCATG	7740
GCACAACAGC GTATTACGTC TGATATCTTT GCTCAGCTGC TCACCCCTTC TCACCTCGAA	7800
AGCAGCGAGT GTGCAGTAGG ACTTGCAACA CAGATCGAGG ACATTATCCA GTATTTTCC	7860
GTTGTAGAAC AGTTCGACCC CGGTCCACGC GACGATCCTG ACACGGATAA CGCACAAGGC	7920
CGTTGCTCCC AGGGGAATAA AATTGACGTG GACTGCTGCC CGGACTGGGT ACGCAAGGAT	7980
GTGCGATTAC CTGGTCTTTC CGTTCACGAT CTCAAGCGGT TGTCCACAGA GTTTGCTGAC	8040
GGTTAcTtTy kCGCAcCGCG CGCGCTCGAT GGTAGCGCAT AAATGGACGC GCATGCTATT	8100
ACCTGTGCAA GCTGGAATAT GTTAAAGGCT CAGCTTGAAG CCGGTGCAAT CAGCTCTTTG	8160
CAGATTGTGC GTGCGTTTCG CAACGTATAC GAGGAAGACA CACGCAGCGC GTCCCCGCTT	8220
GGGGCTTTGG TCGAGTTTTC CTCTGATGCG GAGGAGCAGC CGCGTACGGC AGACAATCTC	8280
CGTGCCTCGT GTGCCCAGAG TACTAAAACA GCTGGAGCAA ACGGGGGGAG TGTCTCAGGT	8340
AAGCCTTTGT TAGGTCTACC CTTTGCTGTC AAGGACAATA TTTCAGTGAA AGGAAAGCAC	8400
TGCACGTGTG GCAGTAAACT CCTTGACAGC TATAGGCTC CGTACGATGC CACCGTTGhT	8460
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ATGGGCTCTT CCACCGAGTA TTCTGTTTAT GGGCCGACGC GTAATCctCG GGATCGGAGC	8580
CGCACCAGCG GGGAAAGTTCC GCGGTTTCGG CTGCCGCCGT nCGCAGGCGG TnCAGGCACC	8640
GTTTGCACTC GGTACCGAAA CGGGAGGCTC GGTACGCTG cCAGCTGsTT aCTGCGGCCT	8700
cTATGGcTGA AgCCGACcTA TGGTCTCTTG AGTCGATATG GGGTGGTTGC CTTTGGCTCC	8760
TCTCTAGACC AAATCGGCTT TTTTGCTACC TGCATTGACG ATATTGCCCT CGCCCTCTCC	8820
GTCACCTCAG GGAAAGACCT GTACGACAGC ACGAGCACTT GCCCCCTCC TGCACGGGG	8880
CGACACGCTG TGCTCACCA TCTTGCCCCCT TTTTCTGCCC ACGAGTGCTC TATCCTGCGT	8940
GCTGCTGTTT CCCGCGAATT AGTAGATGCT CCTGGCGTGC ATCCTGACGT GTCTGCGCAA	9000
TTTCAACGCT TCCTCACCTG GCTGCGTGCC CAAAACGTAC AGGTAGAAGA AGTGACGCTT	9060
CCTGCACTAC AGGCGGCAGT GCCTGTATAT TATCTTGTCG CGACAsctGA AGCCGCCAGC	9120
AATCTTGCGC GTTTTGACGG TATTCGCTAC GGGCAGAGGG GAGACACTGA TGCTCTTTTG	9180
GAAAATTACT ACCGCGCCGT CCGTACCTCA GGCTTTGGAC CCGAAGTACA GCGAAGGATC	9240
ATTGTGGGGA ATTATGTTCT TTCACGCCAT TTCTCCGGTG ATTATTACCG AACGAGTGTG	9300
CGCGTACGTT CGCGTATAGA ACAAGAATGT ACGCAGCTCC TCTGTTCTTA CCACTTTATT	9360

GTTTGTCCCTA CTGCCGCTAC CGGTGCCTTC CCGCTTGGAG AACGCATACA TGACCCGCTG	9420
GCCATGTATT GCTCGGATTT ATTCACCACC TTCGTTAACC TTGCCCCGCT ACCGGCGCTA	9480
TCAGTACCAG TGGGAACATC AGGCACTGGC CTACCCATCG GAATACAGAT TATCGGTTCT	9540
CAGTGGCAGG AGTGTGCCGT TCTCCGGCTA GCAAAACGTT GGGAGGAGGC ACCTCATGTC	9600
TGACCTCCAA ACAGGCACAG TTCCCTCCAT TGCAGGCGCC ACAGATGACA CACATGCCGC	9660
ACCCTTTTTT TACGAGGTAA TTATTGGCTG TGAAATTCAT TGTCAGCTTC TAACAAAGAC	9720
CAAAGCTTTC TGTGCTGTGC AAATCGCTCA GGAGGAATGC CGAATAGCCG TGTGTGTCCT	9780
GTGTGTCTTG GGTGCCAGG AGCGTTGCCC GTTGTGAGTG AAGAGTACGT GCGGCTCGGG	9840
GTGCGCGCCG GACTTGCGTT GGGGTGCACT ATCCAGCTTT GGTCCGCTTT TGATCGCAAG	9900
CACTATTTTT ATCCAGATCT CCCAAAGGGT TATCAAATTA CCCAGTACGA CGCTCCCTTG	9960
TGTACGGATG GTGCAGTGGA TGTACAGGGA GTTGACATGC CCGTGCAGCG cGTGTCCGTA	10020
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GCTATATTGA TTTCAATCGT TGTGGGGTGC CGCTCATTGA AATTGTATCT AGGCCGGATC	10140
TGCGCTCTGC AGAGGAGGCC GCATGTTTTA TGCAGACGAT CCGCGAGATT CTCACCTTTA	10200
TCGAGGTAAC GGATGGTAAT TTAGAAGAAG GCGCACTGCG ATGCGACGCG AATGTTAATG	10260
TGAGGATTCT GTACAAAGGG CAAGAACACC AACTCCCAT TTCTGAAATC AAAAATATGA	10320
ACTCGTATCG TATGGTGCGG GACGCGTGTA CGTATGAGGT ACAGCGTCAA TTGCAGGAGT	10380
TTTGCAAAA GGGTCTGCG AGCAAAGAAG AGATGCAGAG AAAACGCACG ATGGGCTGGG	10440
ATCCGGTCGA AGGGGTTACG CTTTACAGC GTACAAAGCA CTCACTGCGC GATTATCGTT	10500
TCATGCGCGA TCCAGACTTA CCTGACCTGC ACTTGACCCC TGCATATGTC CAGCATCTCT	10560
CTTACACAGT CGGGGAACCT CCGGCAGCGC GGCGTGACG TTTCAAACCT GACCTTGGCT	10620
TGTCGGCGTT TGCAGCCCAA ACGCTTACCG GCAGCCGCAT GCTCGCAGAC TGGTTTGAGA	10680
AGGCAGCGCA TGCGTCTAAG AATGCGCGAC GAGTGGCAA CTGGATTCTG TCGGAGGTTT	10740
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ATCCAAAGGc nCTGCGTGAT TGGCAACACG GTAAGACAAA CGTGGCTGCC TGGCTCATGG	11040
GGCAAGTAAT GAAGCGTTCC CGCGGGCGCG CACACCCTGC GCGAGTGGCG ACGCTCGTCC	11100

ACCAAGCACT CTCTCAGCTG TAACAGCTGG AAAAAGCTCCA CGGAAGAGCG GCGGTCTCTC 11160  
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AATACAAGGC CATTGCCAAC GCCACATCCA CCGCAGGCTC ATATAACCGG ATACCCCTG 11520  
CCACATTAC GTAGATATCC TGATCTGAGA ATTTCAAACC CACACGTTTC TCAATTACCG 11580  
CTGCAACACG ACTGACGCGG GCCGAGTCGA TACGATCAGA AAAACGCGC GTAACACTAC 11640  
TTTTTGCAGG AACGGTCAAT GCCTGTATTT CTACCATAAA AACACGGCTC CCCTCACACA 11700  
CGGGCACAGT TGCAGACCCA ACAGGAAACA TTCCCTGCCT GGTACTAATA AAAATCCTG 11760  
CAGTGTCTCTG CACAGCGGAA AGTCCATTTT CACCCATGGT AAAAATACCC AGCTCATCAA 11820  
CAGAACCAA TCGATTTTTT AATGCACGTA AAAACGAAT ATCTCTTCA TTCCGTTCOA 11880  
AAGAAATCAC AGTGTCCACC ATATGTTCCA CTACTTTTGG CCCGGCAATA TTCCCATCTT 11940  
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CGACATCCTC GACCCGCGTC GCACAAAGCA ACTCGATGTT CTGAATTGGA ATATTCAGCC 12180  
GATCCGCACG CCCACGAATT TGCCCCGAG ATTCTTCACC CGAAACATAG AGAACCGATT 12240  
TCCCGCAGgC TGCAGCGATT TGTAACAGTA ATGTAGATTT ACCAATGCCC GGTTCCTCCG 12300  
CAATCATGAT CGCGGAGyGT CTTACGGCGC CTCCGCCGAG GACACGATCG AACTCTGCGA 12360  
TACCACAACCT AATACgCTGc gCATCCTGCG CGCGCACAGC ACACAGCGGG AACGCCTGTA 12420  
CAGGAGAAGA AGATGCCTTT TTTACAGCAC GAACATCGCC GGAGGACAAC GAGGGTGTCT 12480  
CTTCGAAGGA ATTCCACTCC CCGCACTCAG GGCAACGCCC AAGCCACTTA GGATGAACGT 12540  
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GGCCCATATC CCCGcTTTCG CAGCTTCTCC AGCAACCTCA AGCAGAGCGT TTCTTCATCT 12780  
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GCAAAGCACA CCGCCCCGta CTGCTCATCA GTGGGACGAG TACCCACCAA CTCCTCTATC 13140  
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TGTTCGGATC CCAAGATTCT TCACGCTCTT TACCACTCCT TAACACGACA GCGGCACGGG 13680  
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CGCAGTGCAT CCTGCGCCCA CCCGAGACCA CAACCGTACT CCATAGGGGA AAGAAGAGCG 14280  
AAAACCGCG CTCCCATCAG CAGCACACCA ACCAAAACCG CGCCCACCAC CGCctCCCCG 14340  
GCAAAATCTC CCGATCGTCT CATAAAAATC ATTCTGTGTC AAGnTGCGCT AGcACAAAGA 14400  
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TGAAAGAAAT cAGCTAACTT GAACAAACGC TCAGTCCGCC TGATGATGGG CGCATAACGC 14520  
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GTCGACGCGG CTCATGGGGA GTTCGCGCAG GCCCCGTTGTG CACGCGATGC GTATGCGTCT	14640
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GGACTCAGTG AACTTCTCTT TTATGACGAG CCGTTGTACT TCCCTTCTGG AAATCCAGTT	15360
CCCCAGGGAG ATGCACCCTG GATATTGAAT CAGGCCGCTT GTATGTACCG CGAACTGTCC	15420
CCAGAAACAG ACCAGTTCTT TACCTTTATG CGCGAGTACC ACCTATTTGA TGTCTGTGCA	15480
CGTATTGCAA AAGCGAGCGG TGGATACTGC ACAACCTTGA GCACATATCG TGCGCCTTTT	15540
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CTGCACAACC CCTTTGAGGA AGACACGTTT GTTTCAACAC TCGCTTCCTG CCGTGCGTAT	16260
TTTCGCACGg TTGGTGACCG CCTTTCCTAG GTCTATGAAA AAAGGGTAAA AGATGCCTCG	16320



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CCAAAAAGAG	AACTACCTGT	CACCGTCCCC	CGTGGTCGGG	ATTCTTCGTG	ACTGGGGAGT	16380
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GGTGCGCCAC	GCGCTcGGTG	TGTTTCAGTG	TAAAGACAAC	TTCTACGGTC	AACACTCCCC	16920
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AGACATTCAA	GTTACAGACA	CCGAAAACGC	CATACGGGTT	GCAGTCGAAG	CGGTCAAATT	17160
ACTCATCACC	CAAGACTCCC	CGCGCTAGGC	GCACTGCAGT	GCTTTAGGCA	AAGTGTCGCG	17220
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CCCGCGTGCA	GGCAACGTAC	ATCAAACGCC	GCTCTTCTCTG	TATATCTGCT	TCGTCAACAC	17400
GCGGAAACAC	CCCGTTCTCT	AGTCCGGTCA	GAATCACCCG	TCGAAACTCC	AGCCCTTTTG	17460
TATTGTGAAT	GGTGATCAAG	TGCAtGCGTC	AGCCGcTCCT	CCCTCGTCGG	CCATATTTTG	17520
GTCCAATTGG	ATGTGTTCTA	GGAAACTCAC	TAACCCCTCA	TGCGAACATG	CATACAGTGA	17580
CGCTGCGTTC	ATTAACTCCT	GCACGTTGAC	CGCGCAtGCG	TCCCTTCTTC	CTCATCCTTC	17640
TGTCGATACC	ATTCTTCCAG	CCCCGTGTGT	TCCATTACCA	CAGAAACAAA	GCGCGCAAGT	17700
CctTCTGCat	CGTGGGTGCG	CTCctCTACC	GGCTCCTCAG	GCGGCGCACT	GGTGCGAGCT	17760
TCTTCTCCCG	CTGCGGGGGC	CTGTGGCATG	CGTGACGCA	GCGCACGTAA	CAGCGACAGA	17820
AAGCTACTGA	CCTTTTGCCg	CGCACGCGTG	CCAAGCGCGG	TCAGGTGGGT	GGACTGGAGT	17880
GTGGTAAAAT	CAGTTATGGC	TGCCTGCTGT	GCACAGACAA	ACAATGCGTC	TTGTGTCTTT	17940
TCTCCAATGC	CCCGAGGCGG	CTTATTACAG	ACCCGCCGGA	GGGCCAGTTC	ATCTGAGCCA	18000
TTGACTATGA	GCTGGAGAAA	CGCCAGCACG	TCTTTTACCT	CTGCGGCACT	GTAGAATTTG	18060

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AGCGTGCCGA CAATGCGATA CGGAATGCGA TTCCGCAAAA AACACTGTTC AAAACTCAGC 18120
GACTGTGCAT TTACCCGATA TAAAATCGCC CAATCCGCGT ATGGGATGCC gCGCGCACGC 18180
kcTTCTTGAA TGAGGTGCAC GCACAGCGCA gCTTCTTCAT CTTGATTATT CAGCAAGAAC 18240
AGGCGCGGCT TAGTACCTCC CGTGCGCTGG GCAATCAGCG CCTTTCCTAA GCGGTCTTGG 18300
TTTTTTTTCA CTACCGAATC AGCAACACGC AGAATTGCGT CTGTGGACCG GTAGTTGTAC 18360
TCCAGGCGGA TAATCTGGGT ATTTTGAAAG AACTCAGGGA AGGTCAAGAT ATTTTTTACC 18420
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CGCCGATGGT wrcACGCATA TGCGTGCGCA AACTGCCTGT CACCCAGAAC GGCTCTGGCA 18720
GCGCATGCAG GAGCGGAGAC ACGCGCGTGC ACTGACTCAA ACGAGGCGCA GTCGAGCCCA 18780
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CGCTTTATTG GTAAAGGTTA CTGCCAGAAT CTGCTCGGGG CGAACCTGCC GGGAACGGAT 19080
AAGATGGGCG ATTTTGGTGG TGATAACGCG CGTCTTTCCT GAGCCTGCGC CGGCAAGGAT 19140
AA 19142

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## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

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TATCTATTTC AGTTGGATTT TGGCGCCTGG AACTGGGGAT TTTTCGTGTG CCACTTTCTG 60
ACACGCTAGC TCTGTGGCGC ACATTGAAGG AGCGCCTcTC AgGGTTGTGCT CTTCACACGC 120
TTGCGgTGGA CTTGCCAGGG GGTGGAGGAA AGTTTCCGCT TGTGGCATTG GCCTTGACGC 180
AAGATGTCAC GTGGCATCAG GAACGCGAgG CGTTCCTCCG ACGCGGcATC GATGGCGCGT 240

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620

GGTACACGTA	cCCGTTCTGA	CCGTCAAAAC	ACCCCGCGCC	TCATCGAGTG	GAGAGTGCGC	300
CGCGTGGTAC	AsGGGGCAGC	GCGAAACACC	CCTGCGTGAA	GGTAGGCGGA	GGAGGGGGTA	360
CGGTGGTATG	CACCGAACCC	AGTGATGCAC	CGCCGCCCCC	CCCCGAGGGG	TCCTCTTCTG	420
CCCCGCGCGC	CCACGCAGCG	CCGCAGAACG	GTGAGAAAAG	AGGACGCGCT	CTCTACCGGC	480
TAACACATAT	CACGCGTGCA	CGCAGCCCCC	TCGCTGCCGT	TGATGCGAGC	TTCCAAAACC	540
TCGAGTGCAT	CGCGAAGCTG	CTGTGGCAGC	CGCGCGCCAA	ACTTTGGGTA	GTGATTCTCT	600
CGGATGTCTT	TAATTTCTCT	TTTCCATCCG	GCTATGTCCA	CCGACAAAAG	CTCTTTCACT	660
GCCTGCGTGC	TTACGTTTAA	CCCCTCTGTG	TTCAAGGCTC	CCTCTTTGGG	CATCCAACCG	720
ATCGCTGTTT	CCACCGCGTT	GTCCACACCA	TCACAGCGGT	CAAAGATCCA	CGCGAGTACT	780
CGGcTGTTAT	CGCCATATCC	GGGCCACAGG	aAGTtGCCct	CTGCATCTTT	ACGAAACCAG	840
TTAACGCAGA	AAATCTTTGG	CAGGTTTTTCG	GCACGTGCCT	GCGATCCGAG	CTTAATCCAG	900
TGCGAAAAGT	AGTCTGCCAT	ATGGTAGCCG	CAGAAGGGGA	GCATCGCGAA	cGGGTCTCGG	960
CGAATCTGAC	CTACCTGGTC	AGAGATAACT	GCTGCAGTTA	CCTCCGAGCC	GATGATGGAA	1020
CCTAGAAACA	CCCCGTGATT	CCAGTCCCAG	GCCTGATGCA	CCAGGGGAAC	CGTACTGGGG	1080
CGACGGCCGC	CAAACAGAAA	AGCGTCGATA	GGGACCctTC	GGGATCTTCC	CAGTTACTTG	1140
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TTGTTCCTTT	AGCGGGATAG	CCGATACCCT	CCCACCACAC	GTGCGCGTCT	TCGGTCAGAC	1320
CACAGTTGGT	GAAAATGGCG	TTTTCTTGA	TAGAGTCCAT	GGCATTCTTG	TTGAGAAAT	1380
CAGATGTCCC	TGGTGCTACG	CCGAAGAACC	CCGCTTCAGG	ATTGATAGCG	TACAGGCGGC	1440
CGTCCTTTCC	GAATTTTCATC	CACGCGATGT	CATCGCCTAC	GGTCTCGACC	TTCCATCCAG	1500
GAAGGGTAGG	GATCATCATA	GCCAGATTCG	TTTTTGCCACA	TGCAGAGGGA	AACGCCGCAC	1560
CAATGTACTT	GGTCTTTCCA	GCAGGGTTGG	TGATTTTAAG	GATGAGCATG	TGCTCTGCAA	1620
GCCACCCTTC	GTCTCGTGCG	AGTACTGAAG	CGATGCGTAA	TGCGAAACAC	TTTTTCCCCA	1680
ACAGGGCATT	CCCTCCGTAT	CCTGAACCGA	AAGACCAAAC	CAAGCGCTCT	TCAGGAAAGT	1740
GAGAGATGTA	TTTGCGCTCC	ATATCCGCGC	AGGGCCACTG	GCCTGCGTCA	GTTACGCCCG	1800
GTCCTAACGG	CTTCCCCACA	GAGTGCAAAC	AGGGGACGAA	CTCACCATCA	GTACCCAACG	1860
CCTCAAGCAC	GCGGGTACCC	ACGCGTGTCA	TGATGTGCAT	GTTGCAAACG	ACGTACTCAG	1920
AATCGGTGAT	TTGATGCCA	TTTTTAGAGA	TGGGTGAGCC	GACCGGTCCC	ATGGAAAAGG	1980

621

GAATGACGTA CATGGTACGG CCCTTCATGC ACTGGGAATA GAGACCGGTC ATAGTCTTTT	2040
TTAATTCTGC aGGATCGGTC CAATGGTTAG TGGGTCCTGC ATCATCCTCC CTTTTTGAGG	2100
CGATGAnAGT GTTCGCTTCG ACGCGCGCAA CGTCGGAGGG CTGTGAGCGA AAGAGGAAGC	2160
AGTTCTTACG TTTTTTTA	2178

(2) INFORMATION FOR SEQ ID NO: 83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TAAATATCTT GTAAGCTACG AGGAGCGAGA ATGTCTGCAT TGTTCCTT GGTGCGGTG	60
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GGCAGTGCGT GTGTCACTGT TCGGTTGTC TGTGCTGTGT GGAGCGGCGC AACCAAGGGG	180
AATTTTGGCG TCGTGTGCT TCTGCATCCG CTGACGAGTG CGAGTTTTTC CACCGCGATC	240
TTTACATTTG TGATGTGCGC GAGTGTGCTG AAGAACGGTT TGCTCAAGCA GCGTGTGATG	300
GGGTGCGTG CGGAACGGC CATCACCGCG GCGATTCTCA CTCTCGGGCA TAACATCGCG	360
CATGGAAGGG ACTACCTGGT GCGTCTGTGC GGGAGTACCG GGGATTGTG TACAGGGTTT	420
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TCTTTCAAG TAGTGCGCAG GCGCATGGGC GCAAAGACAT GGAAGCGTGT GCAACGCCTT	540
GCATATCTCT TTACGGGCT TACGTATGTG CACCTTTCCT TTATCCTCCT ACCGACCGCT	600
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TCCGCGGCGG TTGCTGTGTC CTCGTTGCG TTCGTCTTGG GCGCGTCTCA CATGGTCAGG	780
CACACGAGGC GTGCGCACAC GGAGAGGACT ACGCGTGCAA AGGCGCGGAA GTGTTCTCCT	840
GCAGAGATGA AGGACGGCGT CTATGAGGCT AGCGCGCAGG tCACAACGGA AAGCTAAGTT	900
TGAGGGTGAC AATCTCGCAG GGTAGGATTG AAGCTGTAC CGTCGTGGGG CACAGCGACG	960
ATGATCCTTA TGCTCCTGG GCGGTAgAGG GTGTCTCGGC GGCAATTGTA GGGGCTCAGT	1020
CTACCGATGT CGATGTGGTG AGTGAGGCAA CTCCACTAG CGAGGCAATA ATTGCGGCCG	1080
TGGAGAAAAT TCTCCAGCAA CCGCAACCGT AGATCTAAGA AGAGCGGCGG TGGGATGTGC	1140

622

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AAGGGGTACG CTCATTGGTG TGGGCGTCTC ATTGGCTTTC CTGTTGGTGG TATATCGCCT	1260
CTTCGCGGGG AGCTATAACC GTATGATCTC GCTTGATGAG GCTGTCAAAA GTGCCTGGAG	1320
TCAGGTAGAG GCGGTCTTGC AGAGGCGCTT AGATCTGATC CCCAACTTGG TCTCGACGGT	1380
CAAGGGTTAT GCAGAACATG AGTCGGATAC gCTGAAGCGT GTTGCGGAAn GCcGTTGCGg	1440
TGCCGGTGGC GTTATGCAGG TGGGTGAAAG CGCACTCTCT GATCCGAAA AGTTTGCTCG	1500
GTTCACGCGT GTCCAAGCAG AAATAGGCGG TGCACCTCGG CGTTTGTTC TGTTCAGCGA	1560
GCAGTATCCT GCCTTGCGCG CAAACGAGAG TTTTCTTTCG TTGCAAAGTC AGCTGAAGG	1620
AACTGAAAAT CGTATCTCTG TGGAGCGGAC GCGCTACAAT CGCGCCGTCC AGGAATACAA	1680
CGCCTATATC CGTCTTTTCC CACGCAGTGC GGTGGCGCGT TGGGGTAATT TCAGCTCCCG	1740
CCCGTACTTT ACGGCACATG AGGGGGCTGT TGcTGCGCCT CGCGTTCGGT TTTGAGTGTG	1800
TGCGTTGCCG CGCCAAGAGC GGTGTGGTTT TCTTTGCGTA GGATCGGTGA TCTTCTCTCA	1860
TGGCTCGTGG GGAGTAAGGG GGTTCGTGGG TCTTTTGTG CCGATCCTGT CCCTCGTGTG	1920
GATGGCGCGC ACGGTGGCGA TGACCCGAGG CGGGAGGAGG ACGCGTCGGG CGCTTTTCAT	1980
ATCCCCGTT TTGCTGCTCG GTTAGGACTG GACTCTGCAG GACTGCTGCG TATCCAACGT	2040
ACGGTGGCTC GTGTCAAGG ACACACTGAC GGAGAGGTGG CGCTCGCTCT TATCAAGGAA	2100
AGTGATTCTG ACTCGGTCTA TGAGCTGTTT TTCGCACTCG TACTTGCTGG CGCTGTTTT	2160
TGCGTTCAGC TGAGCATGGT GTCGGTGCTT GAACAAGCGT TTGCgCGTTT CTTTGGGCG	2220
CCGCCATCGT GGTATATGCC gCGGTTTATG GTAGCGTCGA GTGTGGCAGC GTGTGTAATT	2280
TTTTTCTTTA TCGCAAACAT TCCGTGGGTG GATCGCGCGC TGGTACCGGG ACCTCTCAAG	2340
CAGCAAAAGA GCTATGCgCg cCGGGTGC GCaCTTTGTGG AAAGTGGTGT GTGCAATACG	2400
CGCAATCGCA CGGGGATTCT CATCTTTATT TCTGTGTTGG AGCGGCGTGT GCTGGTGCTC	2460
GCAGACGTGG GGGTGAGCGC GTACGTGCCT GCCGgTGAAT GGAAGTGAAT GTGTCAAATA	2520
ATTACTGCGG GGTGCGCTC GCGTCGTGCA GCGGACGCCT TATGTGAGGC ACTTACCGT	2580
GTGGAACAGG TGCTCgctAC GCgGATGCCA CCTCAGaAAA AAAGTTCCAA CGAGTTACCG	2640
GATGGGTAG TGATTTTGAG TCACTAGAAT TGAATCGGTG TTCTGCGTAt GTGATTCCAC	2700
TAGGTAAGCG GCATGGGCAT TCTGCTGTGG CCGTGTGTTT GCGGGGTGTT TCTGTGTTCA	2760
GAGGAGAGAA GCGATGGAT GGGGTGCGGG GCGCCCTGAG TGCCCTGCGT TCGCTGATGC	2820
GTGCGCAAGG GGTAGATATT TGTTATATCT CCGGTGAGAA CGCGCATGGG CAGATAGATG	2880

GTGCGCGTGA ATATTTTCTT	GGATTTACAG GCTCTGCAGG	AATAGTGGTG GTGACcACA	2940
ACGTGyGTTT TgTGGACAGA	TGGACGGTAT TTTATCCAGG	CTGAGCGTGA gcTGTCCGCA	3000
TGTGAAGTGT GCCTTTTTCG	TACAGGGCAG GCGGGCGTAC	CTCGGGTAAC TGAGCTTTTG	3060
CGTACAGAAC TCCGTGCTTT	TTTCATCCGGG CCTGGGCACG	GAGGGGGAAC GCTCGCAGTG	3120
GATGGCCGTA CGATTTCTGC	GGCTGTATGG GAGCAGTTTC	AGCAGGAGCT TGTGGATGTA	3180
TCGctTCGCC TAGACTTTGA	TGGGgCsCTC CTGCTACCGC	AGaGCATCGC tTTCCGTAtT	3240
CCTTCCctGC GTTTTTGTG	GATGAGCGCT ACACGGGgTT	GAgTGCGGCG CAAAAGCTCA	3300
CCCAACTGCG CGCAGCGCTC	AgTGCACGCA GCTGTGATGC	AACGGTGTG TCCACATTGG	3360
ATGATGTGTG CTGGCTCACC	AATGTGCGCG CACACGATGT	GCCGTGTACA CCGCTGTTGG	3420
TGGCATACAT GGTGCTCAG	CACACCCGTG CCTTCTTTTA	TGTGGATATG CGCAAAATTT	3480
CTTCTGCATT GCATCAAGCT	TTGTATGCGC AGGCGTTGAG	TGTATGCCGT ACGATACTTT	3540
TTTTGATCAG GTGTGTGCGC	GCTGTGGGAT CAGGAACCGA	CGGTACATGC TGTGGGGAAA	3600
GGAAGAGCAG GAGTGCAGGA	AGTGGCAGGC AGAACGCCAG	TGcGTGTTGT TGGACTTTGA	3660
GCGTTTCGTGT GCTGCACTGG	TGGATCTCTT TCGTGATCG	CCGCAGtGTG TAGACCGCaG	3720
tGGAAcGATC CGCTCCTTCC	GGTTCGTTAT CTTCTGTGCT	GGGCATAGAA GAGGATGGTA	3780
CTGAGACCAG CAGAGGTGGG	AAAAGTGCAT GTGCGTTGCA	GTCTGCaCGC GACGCTCTGG	3840
CAGCAGGGAA AGAAAAGGAG	AACAAAGAGG AGCGGGGACA	GACCATGTGC TTCTCCGTTT	3900
GTCGTGGACT TTTGCCAACT	GTAGCGCTCA AAGCATTAAA	GAACGACACC GAGCGAGCCA	3960
ATGTGCACCA GGCAATGATA	CAGGATGGGA TTGCGCTGGT	AAAAACGCTG CAGTGGGTGT	4020
ACCAGCAGCT TGaCGTGGGT	GCAGACGTTG ATGAATGCGC	TGTAGCGGAG TTTGTACGTG	4080
CTGCCCCGGC GGTGTCTCCG	TCTTTCATTG AAGAAAGCTT	TCACACCATT GCAGGATACG	4140
GGGCGAACGC AGCAATGGTG	CATTACCGCC CCGTGCGTTT	TTCAGCTTTA CACCCTGCTG	4200
CGGGTCAAAC GGCAGCAcTg	cTTCGCGCGC GTGGTTTTTT	ATTATTGGAT TCTGGCGCGC	4260
ATTATCGTGA GGGTACCACC	GATGTGACGC GCACGCTGGC	TCTCGGTCCT TTGACAGATG	4320
TGCAGCGTGC AGACTACACG	CTGGTATTGC AGGCGCACAG	TGCgCTTGCC GTGCGcGCTT	4380
TCCTGCAGGG ACCAGTGGGG	CGGTGCTCGA CGGAATTGCC	CGGGCTCCGC TGTGGGCACA	4440
GGGACGAGAC TACCCACATG	GGACGGGGCA TGGGGTGGGT	TTTTGTCTTT CAGTGCATGA	4500
GGGTCCCTAT AGTATTTCTC	CGAGTGCTCC CGGGAGAGGA	GGAActGCAC GAGGCATTGG	4560
GGCAGAGCAC ACGGGAGATC	CTCCCTTTTT TTCTGAGGAG	GCGGCGTGGC AGCTGCGCCC	4620

GGGTATGCTC CTTTCCAATG AGCCTGGGGT GTATGTGGCT GGCTCTCATG GCGTGCGCAT	4680
AGAAAAATCTT ATGTGGGTGG TACAGGCGCA TGAGTCTGAC GCGCagTGTG TGTGGAAGGA	4740
AGGAGGGGAG GGAAAGGAGG AGAACGCGGC GGC CGTGAG TGTACGGGTG CAGATAGGAT	4800
GCAACCGTCA CGATGCCGAA GTTCTATGG ATTTCAAAC GCAACGCTGT GTCCAAAtGA	4860
CACGCGGCCG CTCGTGCGAG AACGATtGCA CGATGAAGAT ATTGCGTGGC TGAATGCCTA	4920
TCACTACGGG TGTATGTAAC CTCGCGCCGT TTTTAGAATc cGTACGCGCG CCTTTTTCG	4980
CACGTGCTGT CGTGCGCTAT AGCGTTTTC TGTGTATTGG TGTATACGC AGATCTTGAT	5040
TTTTGATCAT AAAGGACATT AGCTTAGGCG GGTGCACTGC ATGTGGTGTG TGAAAAGATG	5100
TCCGCGGGCA AGAGGAGGGA ATTGTGATTA CGATTTTCGA AGCGCTGAG CGTGTGCGCG	5160
TCATTCCGGT GGTGACGCTT GAGCGCGTGG AAGACGCagT GCCGCTTGCA CGCGCCTTGA	5220
TAACAGGTGG TATCAGGTGT ATGGAAGTAA CATTTCGAAC GTTGGTTGCT GCGGAGGCGA	5280
TTGCGGCAAT CCGTCAGgAA TGTGCTGATG TGTACTTTGG TGCAGGAACC GTACTGACGG	5340
TAGAGCAGGC GCagCAGGCG CAGGCAGCAG GTGCGCagTT TGTGGTCAGT CCCGGTTTTA	5400
ATCCGCGGGT TGTTCGCGAC TGTTCGGGGC ATGGCGTTCC GATCATACCG GGGATAGCAT	5460
CTGCAACAGA AATTGAGCGT GCGCTTGAGT TTGGTATTTT gGTAGTAAAG TTTTCCCCCG	5520
CTGAGCTTTT GGGAGGTACG GCAATGATGA GTGCGCTCGC AgTCCCTACA CGGCGGTGCG	5580
TTTTGTGCCT ACGGGGGGAA TTCATCTTAA TAATCTTGCT GAGTATGTGG CGCATCCTCG	5640
GGTGCTCGCC TGTGGGGGCA GTTGGATGGT ACCGGCGCAG TCAATAGCGG CAGGAGATTT	5700
CTCGCAGgTT ACTGCACTTT CTCAGCAGAC GTTACAGATT GTCGGGGTAA TGTAGGGGGT	5760
GGTGGCTCAA ACGTTGTCTT TCTCAGAGAG GGCACGTATA CTGCCGGCGG CACTCAGGTG	5820
CGGGAGGTAA CTGGTGCGCA GAAACTCGAG GACGATGGCA AAGATAGTGG CGcTGCTTGC	5880
GCTTATTCTT TTGCTCATAT TGGCAGGTTT TATTTGGTTT GATTATTTAG GAGTCCTCGA	5940
TGCAAAGCGG GCGATTTCTC CGTTGTACCG TCTTTTTGGA CGTTCGGTGC CGGAGGGACT	6000
TGTGTGCACT GCTGATCCGG ATTTGGATGC GGATCGTTAT GCCAAGCGTC TTGAGGCGCT	6060
CGGGGAGCGT GCAGAGGAAT TAGATAAAAA GGACCTGAG CTACAGGAAA AGGAAAAGGA	6120
TCACGAAAGG GTTCTCAGG AGTTGGATGA GCGTCTGCGC GCGCTTGAGG ATAAGGAGAA	6180
ATCCTACAAC TTGCTTGTTG CGGAGACAAA CGAGCGTCGC GGGAAATGTGC GTAAGATTGC	6240
AGAATACGTC AGTGGTATGC CTCCGGAGAG TGCGGTAAAG ATTCTGCTGA AACTGATGA	6300
TCAAGATGTG ATTGAAGTGT TTCGTATGGT GGATGCGGCC GCTCGGCAA GGGGTGTTAA	6360

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CTCTCTTG TG	CCGTATTGGC	TTTCTCTTAT	GCCTCCTGAC	AGGGCAGCTG	AGATTCAGCG	6420
GAAGATGGCA	AATAAACCTG	CTGACTTTCC	CTAGGCGGTT	TATACCAACT	TGATAAAGTG	6480
CTCTTATGTT	TTTTTCTCTC	CTTTCGCCGG	CTGCTTTTCT	GTTTATTTTT	TTTATCCTGT	6540
ATTGGTACGT	TTTCCGCACC	GCGACGCAGC	GGGTCGTTGT	GCTGCTTGTA	GCAAAC TTTC	6600
TTGCTATTGC	AGCTTTTGAT	ATTTCGCTTCT	GCATTCCGTA	TCTCGTTTTA	AGTGC GTTAc	6660
CTACAGCTGT	GGGTTGCTCA	TACTCATGCA	GAAAAGTTTC	TTATGGAGAA	AAGTCCTGCT	6720
CATTGCGGGT	ACCTTGTTGC	AGATACTTTT	CTTTTGTCTT	TTTAAACATT	TCTCTGATAT	6780
GCTCTCGCTC	GTGCGTGCAT	TTGCTCCTGC	ATATTTTGCG	CAGCACACAT	GGCACCAACA	6840
TGTAAAAGAC	TGGAATATAT	GGCACCCAGT	GGGTATTTTCG	TACTGTACAT	TCAAATGTAT	6900
GAGCTATGTG	TTTGACGTGT	ATCTGTGCAA	GATACGCAGA	AGAGAGCCgT	TTGCACGTGT	6960
GCTTTTGAT	GTGCTTTTTT	TTCTCAAAT	GATTTCAGGA	CTATTGCAA	ACGCATCGCA	7020
TTTTTTTACA	CGTCTGCCGC	ACAATTTGCG	CGCTGGTGAA	AGCCCCCTTAG	ATCGTCCTAT	7080
CCACTTTGAT	CGTGCGGTGG	TATTACTGTA	CACGGGGTTG	GTCAAGAAAG	TTATTTTTCG	7140
AGATTTTCTT	TCTATACTTG	TGACTGATAA	AAATTTTACG	CTTCCTTCCG	CATACAGTAG	7200
CACCGAGTTG	CTCTTTGGCC	TCATCAGTTA	CAGTGCGGTT	TTATACTGCG	ATTTTCTGCG	7260
GTACAGTGAC	CTGGCAATTG	CAGTTGGGTT	GCTTTTGGG	TTTGAAACAC	CGGCGAACTT	7320
CAAACGCCCT	TACATATCTC	AGTCAGTTAC	TGAATTTTGG	AGACGCTGGC	ATATTTCTCT	7380
TTCTCAATGG	TTGAAAGAGT	ATTTGTATTT	CTCACTTGGG	GGTTCACGTT	TTGGGATCAA	7440
AAGAACGGTG	TGTGCACTTT	TTTTTACCAT	GCTGATCGCA	GGTCTCTGGC	ATGGCGTACG	7500
CTTGACGTTT	CTGTGTGGG	GTATGGCGCA	GGGTGTGGCT	TTGGTAATTG	AGCGGGTGTA	7560
TAGGGAAAAA	AGACGGGTGA	ACGGTGCGAA	TGCCTTTGGA	TCAAGTAGTG	TGATGGGAAG	7620
ATGGAAAGCG	CGTGCTATGC	GGTGATACG	CGTCAGTGCA	TTGTTTCTTT	TTGTCaGTGT	7680
TGGATGGCTT	ATTTTTCGCG	CACCGTCTTT	TGCAGAAAGTG	TGGCGGTACG	TTACCTTGCT	7740
GTTCCGAGGA	AGTTGGCATG	GGCCATTCCA	AGTTATCACG	CCATTTACCG	CGTTGCTCGC	7800
GCTGTGTGCA	CTGTGTGTAC	AACTCCCTTC	AGATCGTACG	CGTGCGCGCG	CGTTTGCTTG	7860
CTACTGCGCA	GTGCCCTTAC	CCGTAAAGGC	TTGTGTGCG	GCGTCTTTT	TCTTTGTACT	7920
GTCGGTTATG	ACTCCATCAG	GTATTGCGCC	CTTTATTTAT	TATAGTTTTT	AGCGAAGGGG	7980
CTATGATGAC	AACAGTGCGT	GTTATATTGC	AAAGGTGTGC	ACGGGGAATA	TGTAGTAATA	8040
AGGGTCGGTA	CAGTGCGAAT	CAGGTACTGC	TTTTTGCAT	ACTTACGCTG	AGCCTGTGGA	8100



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CGCCATTCT	CGGTCCGGCG	TTGCGCCATC	CTGCCGTGTA	CATACGGCAC	AAGAGCGTGA	8160
AAAACATCTA	CCTTGCATTC	GTAGATCCGC	TCATGCACAC	TGCAGAACAG	TGGGGAATAG	8220
ATACGGTATT	TCCTCTTTTG	CGCGAGAGTT	TTTTGCATGC	GACAGGTTTG	ATACAGCATC	8280
CGGAGTGGGA	AGATACGTTT	TATCACTGCG	AGCAACGCTC	TTATGAGCCA	GCTGCTGCCC	8340
TGGCGGAGTC	TGTGCCTTCT	CCTGTCCTTAC	AGGAGGCCGT	GGCCGTTTyC	CCTCCGGGGG	8400
TGGCGGTTAA	CGATTCTGTT	GCGGAAAGAA	AAACAACGTC	TCCCGCACGT	GTCTTTTCGC	8460
GTACAGCGCT	TCGTATTTTG	ATGTGTGGAG	ATTCCCAAAT	GCGTTACCTT	ACCGGCGGTG	8520
CGTTGCAGGT	GCTAGGGACG	TCTTCGCACG	TGCAGATTCA	AGAAGTGACG	GTTAGTTCTT	8580
CTGGTTTTGT	GCGGACCGAT	TATTACCACT	GGCCACGAAA	ATTTCTCGCG	CTCCTGGATA	8640
CGCACACCCA	ACAAGAACCA	TATGCAGCGG	TAATTATGGC	ATTTGGTATG	AATGACTATC	8700
AAAATTTTFA	TGATGCGGAT	GGCTCTTTGT	GTGTGACGAA	AACTGCACGC	TGGGAACGCG	8760
CGTATGAGCA	AAAAATGCGC	GCCTGTTTGA	ATATTATTCT	GCACACAGTA	CCGAAGGTGT	8820
ATCTGTTGGG	TATGCCAGAG	ACACGTAACA	AACAGTTGAA	TGAGAAGCTT	GTGTACATCG	8880
AGCACGTACA	AAAGAAAGTA	GTGGCGCAAT	ACGATCCGcA	GCGGGTGCGC	TATTACTCCC	8940
TCAAACCAAT	TGTACCCGGT	GTACACGGAA	CATATGCAAG	CGCGATAAGG	GACACGCACG	9000
GCCGTTGGGT	ACACGTGATG	CACAAAGACG	GCATCCACTA	CACCATAGAG	GGTGGTGCCT	9060
ACGTTATGGA	AACTCTCTTA	CCCCTTATTC	TTGCAGATTT	GGAACGGTCT	CGTCACGGAT	9120
ACATGCGTTC	TTCTCTGGGG	TCGCATGAAC	TCCCTGCGAC	GAAGGGGATG	GAAAGAGCAC	9180
GTCACGCGTC	AACTCGAACA	TAGGGATAAA	CCGCACCGTT	GTATCCTGCA	TGACAGGGGG	9240
TGCGTCCTGT	CAGGGGGTTA	TCGTACGTCC	ACACCGTTGC	CTGCACTTGC	ATAGTGCTGT	9300
TTTGGTCACC	TGAGAATGTT	ACCGTAAAGG	GGAGTGGTGG	GCGCGCCTGC	GATATGAAnC	9360
GTACC						9365

## (2) INFORMATION FOR SEQ ID NO: 84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AGGGTGn	Cn	CCGCACGGAA	AATCTCn	TCT	ACAGCn	TCCC	GATTGGTGGG	ATCCTGCTCA	60
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ATGACGAGTA TATTGCTTTC GAGCTGCTCA ACCTGTGTGtC CGCCTCGCTG AAAAAATCCT	120
TCAGCAACTC TTCGTGCCCC GCGTCGAGGT AATCGCTCAT GGGCACAATC TTCCCGCATT	180
CTCAGCCTTT GGTCAAGGCA ACGTCCAAAA GACCCCGCCA CCCGCTGCAT CCCTTGACAC	240
TTCCATCAGC CGAGAATAGA CTCCGCCATG GCCCGCGCGC AGGTACGTTT GTCAGGTCCG	300
TTTCTCGCCC TCGGTGGTTA CTCCTTGATAT GCCCGGGGAC TGGTCTACT CCTCTACCGA	360
GCGGTGGGGG TCTACGTTTG GATCCACTTT TATCAAAACC AGACCTCTC GCAGCTTTCT	420
ACCCACGCGC GGTCGTCTTG GGTATCGATT GCGGACACG CaGCCTCTTC CTCGGCGCGG	480
TGCTCTTGAC CGTTCGGGAC GTGCGCACCT TCAGAGACGA CAGCACGATG TGGATAGCCC	540
CCGTCTTCT CTGGTCCGCG GCGACCTACT CCAGCATGGG aGmCTGCGGCTTCTCTCTCA	600
GGGCCGTAGC CAGCGGCGCA TCGGGCGTGC TTCTCTTCGC CGTTTGGTGC CTCGCGTcAG	660
AGCTTGGGCG CCGCCGCCCT TAGCGGCGCG TTCGCCCGmG GCTGAGCCTT TTTTATAAGA	720
GGGTGcTGC GTAGGCAGCG CGCGCAAATC CGCATGTTCA GCGCAGAGCC ATCTAcAACT	780
ACTcTCAtGC GAgCArGTTT GGTTCACACA CCCGCTTGCC AGTGGTGCAT CGATTTACTC	840
ACGGCGCACC CGCTGATCGT CCCCTTTCCA CACAGTCCAC ATCTTCTTGC caTCGkwmAT	900
GTCTCCGCCG CCGATGATAA AGAAAAGGTC CGCCAGAGTA AAGGCGgCAC GCGCGCTTTA	960
TGGCATAATG CTCCCCGTG CCGTGGTCAA CCAACGCAGA AGGAGCGCCC TCATGTGCGG	1020
AATTCTCTCC ATCGTCGTAA GTATCGCTGT TCTTGACCG CTGGCAGTTG CAAACACCCT	1080
cTGtACGCAC TGTACCGCCC GGGATGCAGA TGGGTTAATC ACGCGGTATC CACCTGGGGT	1140
GCACGGACTA TCTTTGCCGT TCTACATAct ACGGAAGACT TAAGTTTAC AGCGACTACA	1200
CCCACGCTGA GCACCTGCCC ACGCAgTACC TTGTAGTCTC AAATCATCAA AGTGTGCTAG	1260
ACACCCCTGc ACTCATGCGT TACTTTGGcT ATATtGATGC GCCGAGGTG CGCTTCGTAG	1320
CAAAGCGAGA GCTCGCGCGC TTCGTCCCCC TTGTGTCCAC CATGCTCAAA AGCGGTGCGG	1380
ACTGCCTGGT AGACCGGCAT CAGTCAGGAG CACAGGCGAT GCAAGCGCTC GAAACGTTTA	1440
CACACCACGT CATGCGAGAg CGATGGCTCC CTGTGATCTT CCCTGAAGGG ACACGATCAA	1500
GAAACGGCGC CCTGCgCATC TTCCACGCCG CAGTtTCCGT GCGCTCACGG CACGGCTCCC	1560
ACTCCCCGTA GTTGATGCG CGTTGGACGG AGGGTGGAAc cTACGCCCGT TGCTGAAAAT	1620
AGGACAGAAG CTTAAAGGAA GCGCTTACCG CGTCAAAGTG CTCGGCGTTT ACCCCGCACC	1680
CCACAACAAA GACGAACAGC TCTCCCTCCT ACGCGAGGCA AAAGCGCTCA TTCAAGCGCA	1740
gcTAGACGTC TGGCGCTCGG AGACCACCTG TCCTCAAGAC GAGTGCCCTCA CGCGCGCCTC	1800

CAAAGACTCC TAGTTAAAGT CACGCGGCCG ACCTCAACA CGCTGCACT TAGGACACTC	1860
AGCGATGTTT TTCACCTTTC CGTTATCAAC AATAGACCTC AGCACCACCT CTCCCCGCA	1920
CGGACAGTTA AAGCGCTGCG TCGCCGCCCG AGTACGCGAA TTTTGTCTGG CACCAGCCAT	1980
TTTCATACCT CCTAGTAGCT CGCTCGCCAG GCTGCATCAC ATTGTCTTTT TGGTCAAGCG	2040
TATGGCGAAT TCTAGGGGGA AGACACGACA CTCGCCCCGC CTACCGGCGg TACGTACTCT	2100
CTGCATCGCG ATATAGAACC GTGGAATGAG AAAAAATGGC CTCATATTGA CAGAGATTTT	2160
TCCTGTTCCC ATAATGGCAC CCTGGGTGGG GTAGGCGTGG CGCTCACTAA GTCGTTTTTG	2220
GAGTCAAGAT CAACCGGGGA GCTGTTTTCG CTTGCAGATG AGCTCGGTCT TTGCTTGCCT	2280
GAGGATCTTA ATCGAAGACT TGTCAATGGC GAGATCCTTG ATTGTTACCA CAGCGCTCTT	2340
GATTTGAACC CTCCGTGCGC TCCCCAGTCC CTTGAATCAA AGGGGACTTC GTGTGCCTAC	2400
AATACCACCG AAATCCATAT CCTTGCCCCG GACCCGCTTT GGTCTTTTGT CTTTTGGGAT	2460
ATCCACGAGC AACTCTTTTG CACACTCACC CAGAGTCCTC AATTTAGGTC GTTCTTTCTG	2520
CGCGTGCACT CCCTCGGTGG TCATGGCTGG CACACCTCGC TCGACCACTT CGATATTGAT	2580
GTACCCCTCA AAGACAGAAA GCGTTACGTG CACCTGTCTT TGGCCGACGA TGCTAATCGC	2640
ATAGATCTTT GCTGCAAAAT GCTCCAACGC GAACGCATCC TTGCTCAATC CAGAgTTGTC	2700
ACGCTCCAGC GCAGcKTCAT AGAACGGAGT CTTwACCCCG AGGATCCAAC CGGCGCAGAA	2760
GTTCTCAGCC TCTGTGGGCT TCCCCTGCTT GAGGAAACCT ACCCAAGCAC GTCTCTTCCT	2820
GTGTGCTCAT AAGTGGGACC TTCATGAAGA AAATGCCaGT GCACTCTCTT GCATTTGTTC	2880
TCGATTGTAA TCTTCCcTTC GTCCGAGGGG CCGGCGCATC TTCTCTCCTC GCTGAATCCC	2940
GTTTTTTTCT CGAGATTTC TATACCTACC TCCCCCTACT CCGCTTATGC GAAACACTCG	3000
AACGTGAGCG TGTTCCTTTT AACATCTCCC TCGCTATCGG GCCCGTTCTG TCGGAAATGC	3060
TCGCTAACCG CGTGCTTATG GACCGATACC GCGTGCACT CGACGCACTC ATCGAATTCG	3120
GAGAACGGGA AGCCATTTCG CTGAGGAACA GTCTCCAAGA GCGCGTGCAA GCTGAAGCAG	3180
TGCTTCGGTC TCTTCGCTCT CACCGGGATT ATTTTgATCA CTGmGATGGG GCACTCCTTG	3240
AACGcATCAA TCACTTTTTT CGcACAGGTT CCATTGAATT ACTCGcAACA ACGGCAGTTA	3300
ATTGTTTCTT ACCCTTCTAC CAAGaCATGc CCGAATCTAT ATCCGcCCAA ATCGAAATGG	3360
GGCTTATTAA TTACCGcAAA CATTTTTCTT CAATTCCCCG CGGTTTTTAT TTACCTGAAC	3420
TTGGCTATGC ACCAGCGCTT GAGCGCACTA TAAATCATA CGGATTCTCG TACACCATAT	3480
TGGAAACACA TAGTTTCCgT TTGGcACTCG CGTACCCCGA CGTGGcATCT TgAGCCkGCA	3540

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CAGACGTCCA AgGCTTGTGG TGCTTAGGAA AGGAsCGTGT CGCCACkGCA GAAGTGCAtG 3600  
GCGCCACgCA TTCCTTCTGT ACACAGGCGG TGTACGAAA TACAGAACAA GATGCTGGGT 3660  
TTATACTGCC TGAGGAGGCT CTGTACCCTT TATTTGAACC ACACAAGGAA CGCATGGCTA 3720  
CTGGGTATCT GTACCAGGCC CGTTCAGGCA CGCCGTATGA GCAAGAAAA GCGCAACGCA 3780  
CGTGTGTGCG TGATGCGCGG GCGTTCGTGC GTAATCGGAC AGAAATATTT GAAAAAGTAG 3840  
TCCACGCAAC CGCTCCCTTC GAGGCTATGT CGGTGTGCGT ATTCCTTGCA TCACTATTTG 3900  
GAGTTGCATG GGCAGAGGGG ATGGATTGGC TTGAAGCCGT ATTCGCACC GTTGCAGAAA 3960  
GCGCGCAAAT GCGnGTgTCC TGTACGCGG CGCTCACCTG CCCCgCAgTG GGGGTGTCAA 4020  
TCATTGAACC CTTTTTTGGA TCTTCACTGG GGGGAGGTTA TCGGATGAG CTTATTAATA 4080  
GCGCAAACGA CTGGATGCAT CCTGCAATAC AAAAAACCAC AGAACGCATG ATCGACCTCA 4140  
CAGAGCGCTT TGCACACGAC ACCGGCTTTC GCGAACGCCT ACTGAACATG GCAGCACGTG 4200  
ATGTGCTTTT GTGTCAGTCG CTGTTCTGGC CCCTTTTAGG GAACCATTGT CGCTACCCCG 4260  
AGTACGCCGC TAGCGAGTGC GCCGACCACC TCAAGGCCTT TACGAGGGTA TACGAGGCGC 4320  
TCGGCTCCGG AGAGGTAAGT GCACAGTGGC TAATGCGGCG CGAACGCGAG CTACCACTGT 4380  
TCTCTGAAAT TAACTTTCGC TTTTTCAGTA AAAAGAAATG ACACCTCACC AAAAGGCGAT 4440  
CTCCCCAGAG TAATACGATC GCATCGACCC AGCGCTATCT ATGCACAGCG CGCCGTCCGC 4500  
GGCCAATCCG ACAACACGAC CCAGAATCGG AGGACGTGTT CCCGCACATT CGCGGAAACA 4560  
GACGTACTCA CCCTGCTTCC ACAGACACGA CTCAAGCACG CCGATACTCG GcGGCGCCAT 4620  
GaCACAGGCA TACAGCCGAT CCAACAGCAC AGGAAGGAAA GCAAACGGAT CAGGGCACCG 4680  
CTCGCTCCG ACAATCTGCG CGAGAGAGCA GGCATGCGAC AACTCGGGCG GAAACTTCAC 4740  
CTGcAGGAGG TTACACCCAA TACCCACGAG AArCGCTCCC GCGCGcAcCT GGCAGAGCAC 4800  
CCCGGnGATC TTACGATCGC ACACCAGGAC GTCGTTGGGC CACTTAaTGc GCGGTGCGCA 4860  
CACACCTCCG AGGAAGGCCA TGTATGCAAG AGCGACCGCA TATCCAACAC AGAGCGAAAA 4920  
CGCAGGGAAA GCAACACGCC GCAAAACGAC AGTACACAAA AGATTCTTTC CCGGCTCCGA 4980  
TTGCCACTTT CTCTGGTCAC CACGAnCACG TCCAGCAA 5019

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GTGATCACTC AGGTACGCTA TCACGGTTCT TTAGATCCTA AGAACGTGGA AATTGACGAG	60
CACAGCTATG TGGGTACCCA CCAAGCGGGC AGTCGCGTGT TCTGGGCAGA GCGGCAAATT	120
CTTCTCTCCT CGGTTGACGC GCGCGCCTAC GTCCTGCAGC AGGATGCGCG TGTACGGTC	180
GACGGGGTCA GCATCCCCCTT GGTGCGAGGG GATAACGTGT ACGCTATTAT TTCTAAAATT	240
AATGATTTCAG GCGCGGCGAGT CCGTGCGTAC CTTGACCCGG TTACCAACGG TTTGAATATG	300
GAGACATCTG ACGCCAGGCA GTTGTGGTTG CAAGATGAGG ACGAGGCAAA CGTGTTTGCC	360
TCGTTGGGTT TGATTACCGA AGGcAGCGTC CGCCGTACAA TGTGTCAGCA GGTGCACGGG	420
TTTCAGGCGG GTCCATTTTT GACATGGCCA TTGCGGTGCG CAATGCCCTG CTTGCAGGTG	480
ATCAAGAGTC GCTCGGGGGT AAGATTTTAG GAAGTGCAGA TGGTGCAGTT GACAACCTTT	540
CAcTGCGTCT TGCCGAGACA GGAGCGCGGT ACgcACGTGC ACAGGCAACA CTTGCACGTT	600
TTAATAGCCA CATTCGGAAT GTGGTTGCAG CGGAGTCTCG TGAGTCTGAT ATTGATTGA	660
CGCAGGCGAT TACGGATTTG AAAATGTTTG AGTATACGCA CCAAGCAACG CTGAGTACGG	720
TGGGCTCTTT GTATAAGCAC ACGCTCTTGG ATTATTTCG GTAGGGGAAG GAGCCGCACG	780
CTATGGAGAT TCAGACGAAG ACGCTCGGTA CACAAACGGT TGAGGCACAC CAGATTATTA	840
CGTTGGAGCG TGGTCTCTAT GGTTTTGAGA AATATCATCG CTTTGCCTTA TTTGATGCAG	900
TGCAGGTTCC GTTTATTTCAT ATGCAGTCCT TAGACGATCC GCGGTTGTCC TTCATTGCTA	960
TTGATCCGTT TTTGTTTCGT CCGGACTACG AATTGGACAT TGACGATGTA TTGTTGCAGC	1020
CGCTCGATAT TTCTTCTCCT ACCGACGTCT TGGTGTTCGC GTTGGTGACC ATTCCTCCCG	1080
ATGGATCTGC GGTGACTGCA AATTTGCAAG GTCCCTTGAT TGTGAACAAG AAAAACCGCA	1140
AGGCGATGCA AGTGGCGATG GGTGGCGATC GGTGGAGAAC GAAGCACGAT ATCGTCGCCG	1200
AAATGGCAGA AAGAAGGGCG CAGGAACAAT GTTGATCCTT TCGCGCAAGA CAAATCAGAA	1260
AATCTTTATT GGGGACTCGA TTGAACTGAC TATTATTGAG ATTTCGGGCG ATCAGGTAAA	1320
AGTCGGTGTG GAAGCGCCGC GTTCGGTGAA AATATTCCGA CAAGAGGTAT ACGAAGAGAT	1380
CCAGAGAGAG AACCGCGCTG CGTCCGACTC CCCCTGGTCT CCTAACTCAT TGCCTCAGTT	1440
GCCTGTGTAG TTGCAGAGGA TACCCATCCC TCGGGGTGGG AGTGTTTTGC GCGGATGACT	1500
GAGTTCACCT AAATCGCACC GCGTTCCAGT GCGCATTGTA GTGTTTCGATT GCTGCCCCCA	1560
CATCTGTTTT TAGCGTTCCT CGCTCGAGGT CATGCTCGCT GTAGTATGGA GTCTTCTTCT	1620

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GATATGCTGC	CGCTTCCCGG	TGGATAGTTG	AAGGGAATCC	AAAGGTGTCC	AAAAACTCCG	1680
CGTAGTGTGC	AGGCTCTAGG	AAGAAGTTGA	TAAACGCATG	GGCAAGGTCG	CGATTGCGTG	1740
CCCCCTTGGG	AATGCAAAAG	CTGTCTACGT	ACACTGGGCT	GGCGACATCT	TGTGGTATAA	1800
AGAAGTCTAT	ATGTTTCGTGC	ATTGCCTCAG	GAGTCTCTGC	AAAGAAGGCC	TCTGCAAAGC	1860
CATGAGCTAC	AACAAAGTCT	CCCGATGCAA	ATGACTTTGC	GTATCCGTCC	GAATCAAAC	1920
TTACCAAGTT	TGGTTTCCAG	TGGTCGGTGA	CAAGTATTGC	TGCCTGCGCA	AgCTCTTGTT	1980
CGTTTTTTGT	GTTTACGTTG	TAGCCAAGTG	AAGCAAGTGC	AGCACCCATT	AcTTTCGCGCA	2040
TATCGTCCAT	CATGCTCATA	CGATACGCCA	GGTCTTTGCG	TGAGAAGATA	GACCACGTGC	2100
GCGCGTATGA	CGGAACTGCT	TTTTTGTTTA	CCGCAATGCC	TGCCGCTCCA	AGATAATACG	2160
GCACCGAATA	TTCCATTTTT	GGATCGTAGG	CTATGCGAGC	ACGGACACTC	TCTTTGATAA	2220
ACTGTACGTT	GGGAATCTTG	GATAGGTCAA	TTTTTTCCAA	CAGATGCTTG	CGTTTCATGA	2280
TGCTGACAAA	GTCACCCGAA	GnGCCACTAA	ATCATAACCA	CTTGACCAA	TGCTCAGTTT	2340
TGCAAAACATA	TCTTCATTTG	AAGCGTAATC	ATCATAGACT	ACCTGCACGT	TATACTGTTG	2400
TTCAAACCTT	TTAATGAGGG	ACGTCGGGGT	GTAGTACGTC	CAGTTATACA	GGTACAGGAC	2460
ATCCTGTCTG	GTCTGCAGGC	ATGATCCCAT	CCAGAGGGAG	AGAAAAAGGA	GAGAArGAAT	2520
GCgCGAACTG	CTCACACAAA	AACGTTTCAT	GCTTTGCTCC	TTACGAGATT	GTTTGCAGAA	2580
AAGTAGTTAC	TTnGAATGGA	CTATTGTTTT	TAnAGAATTG	CGCAGGAGGT	AGGCGACCCC	2640
TACAATCCCT	GCCATCATGA	TCAGGGAAAG	GGCATTGATG	ATaGGAGAGA	CCCCATAGCG	2700
GATCATTGAA	AACACATACA	GGGGGAGTGT	GGTGGAGCCC	GGTCCTGCAA	CGAAAAAGGT	2760
GATGACAAAA	TCTTCCAGAG	AAAGGGTTAC	TGAAAGTAAA	AAGCCAGACA	GTATGCCTGG	2820
CATGATGGCA	GGGATCACGA	TTTTTCCTAG	CGCTTGCCAC	TCGTTTGCAC	CTAAGTCTTG	2880
CGCCGCTCT	ATGAGAGAGA	GGTCAAAGGT	GTCGATGCGA	GTAAGGATGA	GCAGGAGCAC	2940
GAAGGGCAGA	CAAAAGGTGA	TATGAGCGGT	GATGnATGTT	GCGCGCCCCA	GCGGCAGGCG	3000
TACTAGGGAG	AAAAAAACGA	GCATTGCCAT	ACCTGTGATA	ACCTCAGGGA	GCAGCATGGG	3060
CAGAAGGCTC	ATTACCTGCG	CATATAGCCG	GCCTGAGAAA	CGATACCAAC	GAATTGCGAT	3120
GGCAGCGGCA	GTCCCCACAA	TTGTTGCTAC	AAGTGCAGAA	ACAGATGCTA	TAAGCACGCT	3180
ATTAAGAAAG	GAAGACCACA	GTTTTTCTGA	ATAAAAGAAT	AGCTCTGTGT	ACCAGCGCAG	3240
CGAGAAACCG	GTCCAGATAA	GGGATTTATC	CTTGTTGAAG	GAAAAAAGCG	CAATAACTGC	3300
AAGCGGCAGA	AATAGGAACG	AGACAACTGC	CGCCAGCAGC	ACAGCAGAGA	AGGAACACCG	3360

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TAGGGGAgTG CGTGCGCGCG TGTGGATCAG ACGGCAATTA GGCATATGAG CGGCGTCCTC	3420
CGCAAGGGGG AGGTGTTGTA TTGCAGGCAC CGCTTTCTGC AAGTATCCAG AGTACTCCTA	3480
CCCCCCTGC GAGGGTAACG AGCATCGCGA AGGCCGAAGC GAGTGGCCAA TTTCCCACGA	3540
TACGTACCTG GTCCACAATT GCGTTTCCGA TAAGGTAGGA ATCCTTTCCT CCCACCAGGA	3600
GGGGGACGGT GTAGGAACCG AAGACAGGAA TGAAGGTAAA GAACACGGCG GTGGCAATGC	3660
CGGTTTTGAT GTTGGGAAGC AACACGCGGA TAATGGCACC CGTGGGGGTA GAGCCTAGAT	3720
CGCATGCAGA TTCAAGGAGG GAGAAATCGA AGCGATCGAT AGCGGCGAAA ATAGGAAAGA	3780
TAGCGTAGGG CAGGAACATA TAGGTGAGCA CCACAATGAC TGCCCCGTTA TGGTACAGGA	3840
GCG	3843

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CnTCATCCGG CCCAGAGGG AAAAAACGCG CGCCGCGTTT CCCGTTGTTT CAGGCCACACC	60
AGCnCGGTGC TCCACGTTCC AGTGTACCGG GTAGTGCGCA CGTACTATGC GCGCATGAGA	120
GATTGGGTGA TCCGTGCTGT GCGCGCTCAT CTTTTTTGCC AGAAGGAGTG CGCATGGCCG	180
TGCACACCCG CCGGCACAGC ACCACGCAGG CGGAAAGCTC ACTGCAGCAG ATAAGGGGGG	240
AGCATGTTTG AGCAACTGAG CGCGAgcTTT AAACGTATCG TAGGAGCGCT GGGAGGACGC	300
GCAACTATCA GCGAACGGAA TATTCAAGAA GCAGTAGAAT CAATTAAGCG CGCACTGTTA	360
GACGCCGACG TGCACGTTTC CGTAGTGCGT CGCTTTGTGA ATCAGACCAT ACAACACGCG	420
CAGGaCAGAC GGTGCTTGCG TCGGTTAGCC CTGCGCgCA ATTCATAAAA ATTGTACACG	480
AAAGACTAAC TGCTTTCCTC GGTGAACATA CGCGGTCGCT GCATCTTAAG GGGCCCGATA	540
CGCAnTCGAT TATTCTCTTG CTTGGGCTCC AAGGATCGGG GAAACTACC AGCGCgCAA	600
AGCTTGCTGC GTACCTGAAG GATGCAGGTC GCTCCCTCTT CCTGGCCGCT TGCATCACG	660
TTCTGCGCGC AGCGAGTGCT CAGCTGGCCG TTCTCGGCAC GCACATTGGC GTTCCCGTGT	720
ACCAGCATGC GcTGCCGCAC GAACAGCAGC CGTGTGCTCT TGATACgGc CGCGGTGCGc	780
yTTCAGTACG CGCGCTCACA CGGCAATGAC GTACTTATCA TTGACACTGC TGGCCGTCTC	840

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CACGTGGATG CCGCGCTCAT GCAGGAGTTA ATCCTTCTCA AAGAAACACT GGTTCCTGTG 900  
GAAACACTCC TTGTTGCAGA CGCTCTAACC GGTCAGACTG TGGTGCGCAT TGCAGAAGAG 960  
TTCCATGCCG CGGTGGGTAT TTCAGGCGTT GTGCTCAGTA AGTTTGATTG AGACACCCGC 1020  
GGCGGAGCTG CACTGTCTTT GAAAAGTATT ACCGGTCAGC CACTGCTGTT TGTGGAACC 1080  
GGTGAACGAC CGCAGnACTT TGAACCGTTC CATCCCGAGC GAGCCGCCGG AAGAATTCTG 1140  
GGTATGGGGG ACATCGTTTC TCTCGTGGAA AAGGCGCAAA AAGCCTTTGA TGCACAGGAA 1200  
CATGCGCGTG CGCAGAAGAA AACGCAATCG CACGAGCGTT TCACGCTCAG CGATATGCTC 1260  
GACCACCTGC AAACATATAGA AAAAATGGGA CCGCTGCACT CGTTGGTGA GATGATTCCC 1320  
GGTTTAGCGG TAGCCGTTTC TGCCGATGCT CTTGACGCGC GCGCGTTCAA GCGTCAAAAG 1380  
GCGATTATTC AATCGATGAC CGTGCAAGAG CGTGACAATT TTCTCATTAT CGGCCCTCA 1440  
AGGAGGCGGC GCATCGCGGC AGGGTCAGGC ACTTCGGTGG CTGATGTTAA CCGTTTAATT 1500  
AAGAATTTTC AGAGGATGCG CACGCTCATG CGCAAGACTG CATGGCAGTC ACGCCGGGCA 1560  
CACCTAAAG GAGATACACC CTATGGATGG CCACATCGCT AGATACGCCG CCTGCGCCCT 1620  
TTTCGCACTC AGTGCGCTGT GCsCCCCgcT TCGCGCGCAG AAGACGCGGA CCACTCCTGG 1680  
TCCCCCGTAC ATACCCACCC CTACGATCCT AACTTTTCC AGTCGGACGC GCAGcGTGCC 1740  
GCCTTCCACA CCTTGGCGGC GGAACACCTT TCCTTCCTTA CCGGTCACAT GTGCTTCTTC 1800  
CGTCCTATCC CTACCCGCGA TCCTTTCCTC ACCCGTGCCT ACGAAATCTC CCCACATCCC 1860  
CGCACACAGA AACCACCGT GCTGCTCGCC TTTGACTCGG ATATCATCTA CCTTCTTTTC 1920  
TAGATCACC GACCAACAGA TTTCCCCGCC CTCCGCTTCT TTCAAAACGC ACCTACTTTC 1980  
CAAGAACTTC CGAGCACCTT CTACCCCTAC ATTGCCATGC ACAGCGACGC CGTTCTCGTG 2040  
CGACATCCAA CGCCGCGCCC CCCTACCCTT CC 2072

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

ATGnTATGAT CACATTCATC ACATCTCCTA CATTTTCTTG CGCACACGAA AGCTCCACGC 60  
TCATGATAGG CTCAAGCACG TATGGCTCAG CGGCTACACA CGCCTCACCA AATGCTTGCA 120



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CCGCTGCAGC TTCAAATATA AAAGGCGAAG ACGTCAGTTC CTGATACTCC ACCGACAGGA	180
GATGCACCCC CACGTCTACA CACGGATACC CACTCTGAAT ACCTCCATCC CACGCGCCGc	240
GGATAGCATG CTCTACCGCT CCGATAATTT CTGCCGGAGC AGTATGCGCC GTGCACACTG	300
TGCCCCGCAA CTCTTTTACC TGACAAAAAA ACTCATTTC CGACCAcgC TTCCGCGCCT	360
CCACACGCAA GgTTAACCCCT GCCATATATT CTTTGCCACC GATTACTCGC TGTACTCGCA	420
GCGTACGCTC AACTGTTTTTA CGAATAGATT CACGGTACGT CACGTGCGGC TTACCAACAC	480
GTACCTGCAC ATTAAAATCC TCGCGCATCC GGGTGGTGAG CACATCAAGA TGCAACTCCC	540
CCATACCGGA AATTAAAAGC TGCCCTGTCT CTGCATCTTC CCGAACCGAG AAAGTTGGAT	600
CCTCTCGCGA AAGAATACCA AGTGTCTCCT GTAACCTATC GCGCGATGAT GCGTCCATTG	660
GCTCAAGCGA CACAGAAATA ACCGGTTTCAG GAAAATGCAT AGACTCCAGC ACTACCGGAC	720
ACGAACCATC CCCCACGCTG TCCCCTGTTT GTGCAGATTT TAGTCCCACA ATTACCGCAA	780
TATCCCCCGC CTGTATGCAT TCAACGGTTT CAGACTTATT CGAATGCATA CGCAAAATGC	840
GATACACCCG TTCACGTTTC TTTTTCCTAA TGTTAACGAT ACTGTCCCCC GTACGCAGTT	900
TTCCCGAATA CATGCGCACG TAGCAGAGTA AACCcGCTTC ACGTTCGTAC TGAATTTTAA	960
ATACAAGTGC CAGCAACGGT CCTTCAGCAG TAGGAGCGAT AAAACAGGC TCCTTTTCT	1020
GTACGTGAAA ACCTTCTACT GCTTTacGCT cgCGGCGCAG GCAAtACTCT AmCACTGCAT	1080
CGAGCaGTGG TtGCACACCC AAGTTATGAC GAGAAGAACC GCACAAAAAA GGAACATATC	1140
GwCCGtCGCG CACAGCCTTT CTAATTTCTG msTGCagTAA CTGCACTGGA ACGTGCTCCC	1200
CTGCAAGCAC AACTCGGTT ACCTCATCCG AATATATGGA AATGACATCA AGCATTTTTT	1260
CTcGCGcttc gGcCTGGGCA ATACGTGCGC TTTGAATAGG CCGGTACTCC ATCTGTTCGC	1320
CACTACTTGC CGCATCCCAG AAAATCTCTT TCATGGTGAT CAAATCAATT ACCCCCTCAA	1380
AAGAGGTACC AGAACCAATG GGTATCTGCA ACGCGACTGC ATCTATACCG AATTTATTGT	1440
GGACTTGGTC CAATACTGAG AAAAAGTCAG CACCGATCCG ATCCATTTTG TTAACAAAAC	1500
AAACACGCGG GATATCATAA CGATCTGCCT GGATACCATA CGGTTTCTGT CTGTGGGCTG	1560
TACTCTTCCT ACCGGCACAC AATACCACCA CTACCCCATC TAACACGGGG CAACGCAnTT	1620
CGACTTCTGC AGTAAAATCT ACATGtCCCG GcGTAcAATA AtGGTAATGT CTACTTCACG	1680
CCACCGCACC GTCGTTGCAG CACTCTGAAT GGTGATACCG CGTTCCTGTT CCTGTACCAT	1740
CCAATCCATC GTTGTGCGAC CATCATCAAT TTCCCCCATG CCGTGGATCT TGCCCGTGTA	1800
AAAAAGCATA CGTTCAGTGG TAGTAGTCTT ACCAGCGTCA ACATGTGCCA TAATGCCAAT	1860

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ATTCTCATC TGCTGTTGTC TCATATCTTC CTCTTTATCA CGTACCTGTA CGGATAAAAA	1920
ACAGTGCACA GGACTACTCC CCACCATCAT AGCAGCGGGA AAGAGAATAC CTA AACGTA	1980
AAACAGTGCA CGCTACACCG CACGCGCAT CAGTGACAAA TCACAAATCG TCTGTGAAAA	2040
CAAAATCTGc AATTAAATGG GGTGGTACCG AATCTTTCAG TTTCCTTACA ATAGACTGCA	2100
GCACACGCAC ATCTTCGGCT TCACTTAACA GAGACTTTTT TTGACGCAA AATTCAACCG	2160
CCTGAATATA TTTTTTCGCG TGCACCAATA CGTTTGCATA CTCAAGAATA CGTTGAGTAT	2220
TTTTCTGATC ACGCTCATA AACTGTTGAT AAAGAAGTAG CGCGCGAGCT GTTTCACCAA	2280
AAGAAAGCa cCATAnCGTA CGCGGCAGCA ATGGTTGCAT TGGCAGAATC CGCATCGTAT	2340
AACGGTTGCA GTGCATGAAC AGCaGTTTT CAATCATTCT GCAATCCACA CACACGCGCA	2400
AAATTATACT GCGCTGCATG ATAGTACGCA GGGTCACGCG CTGCACGCAT ATAATAATCA	2460
CGCGCCTCGT CATAACGATG CAGCTGCACA TACGCATGGG CAAGATCAAA ATACTCTGGC	2520
GCAAGAGACG ACTCAGGCTT TCCGCATGCA AATAGTCCTG TATAAACAG GTGAAACAAA	2580
AAAAAGCAAA AACACTGCTT ACCGTTTCATC AGTCAGCGAG AACCTAATAC CGTTTCCTCT	2640
ATCTTGCGGA GCTGGGACCG GTACAGGCCA GAAATATTTG AACCATAGTC TGCCAAAAGC	2700
TGGATAATAT TCCGCGGATA GTCTTCAACA TCAACCCCGT TAACTCGATC ACCAGCATCG	2760
CCAAGACCAG GCATAATATA CGCACGCGCG TTGAGTACGG GATCCATCCA CAGCGTATAC	2820
ACCGTGCAAT TCTCTAGGGA ACGCACTACA CGAATCGCAC CTTTCAGTGC AGAAATCATG	2880
TGAAAACAGC TGATAGATTT TGGTTTCACA CCGAGATCTT GCAAATAACG CACTATGGTA	2940
ACCAAACACTAC CACCGGTGGC GTTCATGGGA TCGGCGAAAA CCAGATCCTT ACCATCCAAC	3000
TCTCGTGCAG AAAAGTATGA TTTATCCAGA TCAAACACAT ACTGcATATC GCGCTCATCA	3060
CGGAGaTCAT CTCGCTTGaT TTTAAAAAGC GCAAACGGcG TTACGTACCC ATGcGAAGAA	3120
TATTCTTCTA TCTCCTTAGA AACATCATC GAaGGTAACA GCGCTCCTCG TAACATGACA	3180
CACATCACCG TGTTCCTCAAT TTTATAATCC ACGTTTGCAA TTTTATGTAC TGCATAGTTT	3240
TGTACAGGAA AAGCAACCGG TGTTTTTGTA ATAAGATATG TTTTATGC	3288

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AGCCGTTGCG TCCGnTGGGA GTGGATTcAG ACTGTGGCGn CAGTGGAGGT GGTGGAGCAC	60
GGGGAGCATC CGTGgTTTTT CGGCGTGCCA GTTCCACCCG GAATTTTGTT CTCGACCGAA	120
CCGGGCTCAC CCTTTGTTCC GGGCGCTGGT GGGCGCGGGC TTGGAGCGAA AAGACAGTCG	180
TTCTTGACGC GCGCAGGTAT TTTTCTAGA CTCCTCTGTC CTTCCTAGCC GGTGAAAGA	240
GCTTTGTGTG GCGGTGCGGG TTTGTgTTC GCGCGCTCCG ATGCGGTGTC AGGTTTGAGG	300
GAGTGGATAT CCGTTTTGTG GGGAGGGATG CGGCATGCAG GGAGTTATGC GATGGCAGTG	360
AAGCGGGCAC GGGGAAAGAT TGTACGTCGG CTGGGGATTA ACATTTTTGG GAATCCAAAG	420
TACACGCGGC TTTTGGGCAA GAAGCCCGCG CCTCCAGGCA AGGAGCATGG GGTGAAGCAG	480
CGGGCAAAGG TGTCTGTGTA CGGGGAGCAG CTAAAGGAAA AGCAGAAGTT TCGCTTTGcg	540
TATGGAATGT CCGAGCGACA ATTCCGTAAT CTTTTTGCTC AGGCACATCG GATGAAGGGC	600
GTGACGGGTA ACAATATGcT GTCGCTAATG GAGCGGCGGC TGGATAACAC GGTGTTcAGG	660
ATGGGCTTTG CGATCAGTCG TGTGCAGGCG CGGCAGATGG TGTCACATCG TTACTTCCTT	720
ATCAATGGGA AGACGGCCAA TATCCCTTcC ATGCGCATTA GCGCGCATGA TGTCATCACT	780
ACTAAGAACC GGAAAGGTAT TCATAGCATC ATTGCTCACA ACCTGACCCT TTCTCAGGGG	840
CAGCGCGGTT CCTGGCTAAA CGTGGATGAG GAGCAGCTTT CGGCAACTGT CTCTGAGCTG	900
CCGCGTGCGC AGGATATCCA TCCGGTGGGG AATATCCAAC ATATCGTGGA GTACTACTCG	960
CGGTAGGATC CTTTGCCACT TTAGCTGGCG TTGCTCAATT ATCTCCCAAG TCTTACCAGG	1020
GACTTTGGGG CGTGGAAGGA TGGCGGCGGT GTATGGATGA TGGTCCCTTG AGGGTTGTgT	1080
TGCTTACCTC ATTTGTcATA CTCGTAGTAG TCTGTGCCGT TCGCTGTGT ACTTTTTTTG	1140
TGTTCTCAA AAGCCCTGAT CAGGTGATGA CTCCCCATAT CGTGGGCAAG GACTTTGTGT	1200
CTGCTGCTAT AGAGATGCAG GCAAAGGAGC TGTATCCCCG CGTTCAGTTG CGGTTTTCTA	1260
CCCGTGAGAA GCCTGGTgTT GTTCTTGAAC AGAACCcACC TCGGGGGGCC ATCGTCAAGG	1320
CTGGGCGCTA CGTGGACCTC GTAGTGAGCC AACAAGCAGT GACTACGCAC GTTGAGGACT	1380
ATCGGGGATT GCAGGTGAA GAAGCGGTGG CGCGCATCGC TGCTGCTGAA GTTGAGCGCC	1440
GCATCTCAGT GAAAACACCC CACTTATATC GGTTCAGCAC TGGCGCAgCT GGcACCATTT	1500
TGGAGCAGGA CCCTGCTCCT GGGCGGgTTC TGTCTGCGGA TGTAAGTTG CGTTTTGTcG	1560
TCAGTAAGGG GTCTGAGCGC GAGCAGACTA CAGTCCCCCT ATTGGTAGGA TATAGTTTGC	1620
CTGAGCTGTA CCGTGTtATG GCGCAGACGG CGCTCACCTT GCAGTTTACC GTATCTCCCC	1680

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CGTCTCCTTC TGGGGAGAGA AAAGACGGAG AAGCACGTGG AAGAACGCGT GCCAATGCGC	1740
AGGACTACGC GCGGGTTTCA GCACAGGATC ATGACCCTGG TTCGCGCGTT GAAGCCTTTC	1800
GCGCCATGCA GGTGCAGGTG CTCTTTCCAG AGCGTGGAGA GGCTCACGAA ATATACGGTA	1860
TCTTAGCTCT CGATCTGCCG CGTTATCCGT ATCCTATGTC CTGTGTGTG GATGTACAGT	1920
ATCCAGGGGG GGTGCGTACC GCGCTTGCAA TGTTTCAGCA TCCGGGGGGA CGTTTCACCA	1980
TCCCTATGG ATTGCCTGCA GGGGCGACGC TCTTCCTAAC GGTGGGGGGG AAGGAATTGT	2040
TTTCTGGAGA GGTGGGTGCA TTGCCTCATG CAGGTTCCCTA GCAGACGTGA TGGAGCACTG	2100
CGGGTGCAAA GGTGCGATGG CTGCGTGGTC TGGCGCAGcG TGTGTTGTGC ACTGCTGGTG	2160
GCGCTTTTGT GTCTTGCCGT CGGCTGCGAT TCCCTTGATT TGCTCGTAGA TAGCGATCTG	2220
TCTCTTTTCG CCGTGCGCgT GGCAAAAACG CTGGTTATGG GAGTGAGCGA TCGTACGCCG	2280
CCGATGTGTT TTCGCTATCC GAATGGGGAG AtTGTGTGGTT TTGATGTTGA TCTTGCGCGC	2340
GCGGTCTGTC GTGTATTGGG GGTACGCCCTT ATCATTCGTC CCATAAAGTG GACGCTGAAA	2400
AGGAATgcGC TGCCTGTGG TCTTGTGAT TCGCTTTGGa CGGCGTTTGC CGTAaCGcTC	2460
GGCGCCGCAC TGAGTTTMTA CTTTCCGAGC CATATCTGCG TACTGCGCAG GTACTCCTTG	2520
TGCGTGAgGG CAGGTTGCAT CCGATTGTTG CACACGTGGA ACGGGAATTG GGGCAGCGTA	2580
TGACAGGTGT TTCGGCTGTG CATACGCGCG GTGATATTTT GCCTATGCGC TCGTCGCATA	2640
GACAGGCTCG CATCGCCGTG TTGCGCGGTG GTcCGGTACC GGGAAATGAG AAGTGGCAGT	2700
TTGGATTGTA ACCACACGGG AAGGTTGTGT GGTACCGACA CCGGAGTGCC ATGCTTGrAG	2760
GChTGCAC CCGGCGGTG GACGCGGCAC TTGTGGATCT GGTGAGGCT CATGACGCAG	2820
TGCATCGTCA GGGTGCGCCT CTGAGGGTGA TCGGGGTACC GCTTGGGTG AGCCAGTATG	2880
CGGTGCAATT TCGGCGTGAG GATCGTGCGT TCGGTGACGA AATTCAGCGA ATCTTGTATC	2940
GTATTGCTGC CTCCGGTGAG GCATACCGTA TTGCAGAAAA ATGGTTTGGT GTTGSTCAGT	3000
CGGTATTG GATAGAATAA AGGTGCAAGG CAGCGGTGCG TTTTGTGCAC TGCGCTTTTT	3060
TTGCGTGTGT GCAGGGGTGG GGGGATGCT CTGGTCGTGT ACTCCTCGTG CAAGGGTGTT	3120
TCACGCGCAG GATGCGTCGT TCGATGAGGC GCGCGTGCGG GGTACACTTG TGGTGGGCGT	3180
CGGTCGGGGC TTGGCACCCCT TGGTGGATGC TGCCACTTTC TCTGCCTTCT CTCTTCCTTC	3240
TTGCGTTGTT CCTCCTCCTG CGCGGTGTTT GTTGCTTTTG CAGGAGGCGC GCGGCTACGA	3300
TGTTGAGCTG TTAGCTCAAG TGGCACGTCG TCTCCATATG GACGTGCAGG TGAAAGTCGT	3360
TCATTGGGAT GAAAAGGAGC GCGCCCTCCA TCGGGGGGTA ATTGACTGTA TCGCAGACGG	3420

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ATTCACCTAT ACTGCAGATC ACGCGCGCAG ATTTGCACTG ACGCAGCCGT ACGTACGCGA	3480
TGTGCGCGTC TTTGCGGTGT TGCGCCAAGC CCCGTACGCA ACGGTTGCAG ACCTGCATGG	3540
AAAGCGGCTC GGGGTCCACG CATgACCGAT GTGGAAGAAA ATGATGCATA CCACGCGTTG	3600
TTTGGGCAGG TGAAAACGTA TGCCCACTAT GTTCAGGCAC TCACTGCTTT GTCGCGAGCG	3660
GAAGTAGATG TGGTGGCGCT GAATTTGGTG ACGCTCTGCG CAGTGACGCC GCACCTGCGG	3720
gCTTGATATCG AATTTTGGAT GAACCGATAG ACACGTGTGA ATACGTGTTT GCGTTTCGTG	3780
CGGATGCGCG TGCTTTGCGC GACATGGTTG TGCGCACTCT GTCGCAGCTG CAGCGAGAGG	3840
GTTTGTGTGTC AGCGCTCTCA AAGCGGTGGT TTGGCAGCGA TATGTCCATC ATCGACCGCT	3900
AAGGCGGGTG GAGGGGGAAT ATCGGTGGAT CCGTTGAATG CCGTTATTGT GGAGGGAAAT	3960
GTCGTTCCAT CTGCTTCCGC GCGCGTGCCG GAGGgGCCGT GTGTGCGTTT TGCATTCAAA	4020
CGCAACGGCG CGTGCAAGGG GAGGGGAGGG TGCACACAGA GGTTCGTAT TTTGAAGTTG	4080
AGGCATGGGA TGCATTGCG CGCGTGTGTG CGCAACAGGT GCGGCCAGGA GTGGGGTTGC	4140
GGGTGGTTCG CCGTCTCAAG CArGATCGTT GGCAGCAGGA GGACGGGGTG CGAGTCAGC	4200
GGGTAAAGAT TGTCGCTGAG CATGTAGAGT TTCAGACT	4238

## (2) INFORMATION FOR SEQ ID NO: 89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TTCCGTTTCG GGATTGAAGA TTTCAATAGG TTTTCCTGAA TCGTTACCGG ACCACAGTGC	60
CTTTTCCTTG CGTTGTGTAT TGTGTGCGAT AACGCCATTT GCGGCAGCCA AAATAGTTCC	120
GGTGAACGG TAATTTTGCT CTAAGGTAAT TTCTGTGGCG TAGGGGAAGT CTTTTTCAAA	180
AGAGAGAATA TTGTCGTGGT GTGCTCCACG CCAAGAATAA ATTGATTGAT CATCGTCCCC	240
TACTACACAG ATATTTTGTG TAGCGAGCAT TTTCATTAAA CGGTACTGCT GTGCACTGGT	300
GTCTtGGAAT TCATCCACTA AAATGTAATG ATAGCGACTC TTATATGAAG CAAGGATATC	360
AGGATATTCA CTGAAGATCT GGATtGGCAG TACGATCAAA TCGTCAAAGT CTACCGCATT	420
AAATAATTTC AACGCAGtAT GATATTCGTG CCAAAGAGCA CGTTCCTTGT GCTGTAGCTC	480
TTTTAAGTTC TTACGCTGCA TTTTAATAGC GGAAAAGAGC GTgcTCACGC AGTTTGTGTC	540

AAGAACTTCT GGCAGGAGAT GTACTTCCTT TGcTGcTTCG CGAATGAGAG CACGTTTATC 600  
ATTTTCATCA TAAATGCTAA AGTTCTTCCT CCAGCCGAGA ACATGGATAT GTTCTCGCAA 660  
AATCGTAACG CCAAAAGCGT GAAAAGTACT GACGGTCGTG TTGCGTAAAG GTTTGCCCCGT 720  
GAGAGCTTTA ATACGTTTCA ACATCTCGTG TCGCGCCTTG TTAGTGAAGG TCAGTGCAAG 780  
AATGCGCGAT TGCAGAATAC CGCATTTCGAG CATATACGCG ATGCGCGCCG TGATTACGCG 840  
CGTTTTCCCT GAGCCTGCGC CGGCGATAAT GAGAAGCGGT CCCTCaAGTG TGGTAACGGc 900  
TCGACGTTGC TCAGGATTAA GTGTAGAGAG CATAGACGCA CAAGCGTAgm AnAATAGGGC 960  
GGAAAAAAGA ATATCCGTAT GTGGAAGGGc ATAGACTGTG GGTAATACTT CAGATTGGGT 1020  
AGAGATGGAT GGATTGCGCT ATGTGTATGC CGCGCAnGGT GCGGCCCCCA TGCCTGCTCC 1080  
TACGGATAAT CCTGCTTGTG ATGCGCACAT GTCGCATGAC GTCATAGCGC GTACTGCCCA 1140  
AGCAGTTTTT GGTATTCTGTG CGCTGTTTTCC TTGGCAGCGC TTGTAATTG CTAACATACT 1200  
GGATGCGGCG CATGCGTGTA CACATACAAC TCCGTTTCGCT GCGGCAGGTT CTTCTCAAAC 1260  
CGATGCTACG AGGGTGACTC ATGTGGATGA CGCGCACCTG AGGATAATTT CGTCGGTGCC 1320  
ATGCAAGACA CACGTTTTGA TCAGGATGGC GTGTCACGCG CACATCAAGT GGTGCTATTG 1380  
CCGACAGgTG CAGGAAAATC GCTGTGTTTT CAAGTACCTG CCCTCTTTTT AGAGGGGCCG 1440  
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TATGCGCatT GGATAgTGTG CTGAgGCGTA TGGCCGGATG CGAGgCGTTA cGCcTCctGc 1620  
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TGATGACGTG AGTACCTTCT CGAAGGTGGT ACATGTGGAT GAACGTCTTG CTCAGAAAAG 1740  
GACAGAAAGT CGAAGAGGTG TATGCATCAT CGCAAGTCCA GAGATACTCA CACAAcCgck 1800  
CTGCGCCACG CGTGCGTGCA TGTGCGGTTG CGCATTGGT TATTGATGAA GCGCACTGTG 1860  
TGTCCGAGTG GGGAGATTCG TTTCGTCTG ATTACGTGCG ACTAGGCGAA TTGGTGCAAG 1920  
ATCTTGCGCC TCAAGTGGTG ACTGCATTTA CGGCGACTGC AAGTCAAACA GTGCTTGCGC 1980  
GCATCATGGA AGTGCTGTTT GGCGGTCGTG CGCACGTGTT GCAGGGAACA GTAGATCGCC 2040  
CGAACATTCG ATACACCGTA CGCACGGTGC TGTGTAAGCA GACGGCACTG ACTCAACTTG 2100  
TAGCGCGTTG TGTGCGCCCT GCAGTTATTT TTTGTGCTCG TCGGGTACAG GTGGAGCGTG 2160  
TAGCCCACCA TTTGCGCACG TGTCTTTCTG ACACACAGAT ACGTTTTTAT CACGCAGGtT 2220  
GCAGAGGGAA GAAAAAGAAA CAGTGGAGCG ATGGTTTCAT ACCCATGATT CTGCCGTTTT 2280

GGTAACTACT TGC GCGTGGG GAATGGGAGT TGATAAGCCG AATGTACGTA CGGTCAATTCA	2340
CGTGGATGCG CCACTGACTG TGGAGGCGTA CGTACAGGAG GTTGAAGAG CAGGACGGGA	2400
CGGAATGCGT GCAGACGCAT TTTTATTGTG GTCACCTCGA GATGCTCGCT CGATAGAAAC	2460
ACTGCCGCAT GCACAACGGG TGC GTGCGCA CGTGTGCGC CACTTTGCTG AAAGCGGACG	2520
TTGTGCGCCG GCAGTTTAC TTGAGTCTTT GGGGGAACAG AATGTGTGTG CCGGATGTGA	2580
TGTGTGTGCA GGC ACTGCAC GTTTTGTATG TGAGGATGTA GAAGCGCTCT TACAGTTTTT	2640
GAAAAAGAAT GCGCGCAGAT TCACTGTATC ATCGTTGGTG CAGCACCTCG CGCTACATCA	2700
GAAAGTGCTC AGTGTGGCGG ATGTACGTGC CTTGCTATAT TACGCGCTCG AAACAGGACG	2760
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CTGCGAGCAA ATCGTATCTG CAGGAAAGCA AGAAGGATGG CGAGAACATA CAGTTGCCTT	2880
GTATATTCCG CGAGTTACGC GCATTTTAT GGCCGAGTGG TTAGCATTAC TTCTACAGGT	2940
TTTTTATGCA ATTTTATATA CTGAGCCGTC GTTCATGTGT CTCCGATACG GTGTGGTCTA	3000
GGTCCGTAC GTGCGGGCAC GGAACACATC GAGCGGACGC GTCTGTTCTG GGAGGATATT	3060
ATGAAAAGGT TTATTCCCA TCGGGTGATT CACGCGGTGT GTATCGGGCT TGCACTTGTA	3120
GGTTGTAGGA AACTCGATTG TCGTGCGGG GATTTTGAGT TAACGATTAT ACATATCAAC	3180
GATCATCATT CGCATTTGGA ACCAGAACCC TTAGAGCTTG CAGTGGCAGG GGAAAGACTC	3240
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TCGAAGAACG CATTGGTACT GCATGCAGGA GATGCACTCA TAGGTACGCT GTATTCTACC	3360
CTCTTTAGAG GCGGTGCGGA CGCGGTGCTG ATGAACCATG CAGGATTTGA TTTTTTTACC	3420
CTTGGAATC ACGAATTTGA TAATGGGAAT GAGGGACTCA AAGAATTTCT GCACTATTTG	3480
GAAGTGCCAG TTCTCTCTGC AAATGTGGTT CTAATGCTG CCAGCACGTT GCATGGCTTG	3540
TGGAAGCCGA GCGCTATTGT GGAGCGTGCA GGTGAGCGTA TTGGGGTTAT CGGACTTGAT	3600
ACGGTAAAGA AAACCGTGGA GTCATCCAGT CCCGGTAAGG ATATCAATTT TATTGATGAG	3660
ATAGAGGCGG TGCGTCGTGC AACTGTTGAA ATGCAGCaG AAGGAGTAAA TAAAATAATC	3720
CTCCTTTCTC ATGCAGGTTT TGAGAAGAAC TGTGAAATTG CTCAGAACAT TTCTGGTATT	3780
GACGTCATCG TGT CAGGTGA TACCCACTAC CTTTTGGGG ATGAATCACT CGGACGGCTA	3840
GGTCTTCCGG TAGTTGGTGA ATATCCAGA AAGATTATGT CCCCTGCAGG GGAGCCTGTG	3900
TATGTGGTAG AGGCGTGGGA GTATGGTAAG TGTCTGGGCG AGCTGAACGT AGTCTTTGAC	3960
CGAACAGGAG TAATAACGAG TGCAGTAGGC ATGCCGCGTT TTTTGTTACA TACGAATACA	4020

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ATATCTGTGT	TGGAAGAATT	TAAAAAGGAA	AAGGAGGCGC	TTGGTGC GCA	GGCAATTGGC	4200
GTAATTACCG	GTGCC'TCAAT	GCGAGGkGGn	TCTGTGCATC	GAGT'TCCCGA	TGCACAGAmT	4260
CCACAGGGTT	CGGTTGCAAC	GCGGTTTGTA	GCAGAGACGA	TGCTCTCAGA	CATTCAAAGT	4320
TTTGGTGC GG	GGAAGgTAGA	TTGCGTAATT	CAAAATGCAG	GCGGTGCGCG	GTCAAATATT	4380
CAGCCTGGTG	AGATTACGTA	TAATGACGCA	TACACGCTCC	TCCCCTTTAG	TAACACGCTG	4440
GTGTTGGTGG	ACGTCAGCGG	TGCAGAGTTG	AAACAAATTA	TAGAGGATGC	ATTGCAGTTT	4500
GCACTTGGTG	ATGGTTCCAC	GGGAGCCTTC	CCCTATGGGG	CGGGTGTCCG	GTATGAAGCG	4560
CGCCAAGAAC	CAGATGAACA	TGGCAAAACGA	GTGATAAAGC	TTGAGGTGCA	AAAAAAAGAT	4620
GGAGCGTGGG	TGCCAGTAGA	TGAGCGCGCG	CCGTATCGGT	TGGGTGTGAA	CTCGTACATT	4680
GCGCGGGGAA	AAGACGGATA	TAAAACGCTC	GGAGAGATTG	TCAGTACGCG	CGGAcTGAGG	4740
ATACGTATCT	GCGTGATGCG	GAGTCTTTGA	TTAAGTTTTT	GCGTGC GCAT	AAAAATTTTC	4800
GTGCATACAC	AGATTCCAAT	GTGATATTCC	GTCTTAAATA	GTAGGAAGTA	ACTTACATTA	4860
GAGGcCTGTA	AAGAACTACG	TTCTTTACAG	GCTGTGCCAA	TCTGCTTTTC	CGGGAAAGAC	4920
AAAGGGTATG	CCACGTTAGG	AGCGGAAAGA	AGGGTGCTGC	ACATAACCTT	ATCTTTGCGA	4980
TTGACCGTGG	TATACTCCTT	GCACCTTATG	CAAGAGAAAA	AAACGCTTTA	CCTTCTTGAT	5040
GCCTACGGAC	TTATTTATCG	GAGTTACCac	GCGTTCGCGC	GTGCGCCGTT	GATTAACGAC	5100
AGCGGTGCGA	ATGTTTCTGC	CGTATATGGT	TTTTTTTCGGA	GTTTGACACAC	GCTCCTGTGT	5160
CACTATCGAC	CCCGTTATTT	TGTTGCTGTT	TTTGATTCTC	TCACGCCTAC	CTTTCGGCAC	5220
GTACAGTACC	CAGCCTATAA	GGCAAAAAGG	GATAAGACTT	CTGCAGAGCT	TTATGCGCAA	5280
ATTCCCTTTA	TCGAAGAAAT	CCTGTGTGCA	CTGGGCATTA	CAGTTT'TGCG	TCATGACGGC	5340
TTTGAAGCTG	ACGACCTCAT	TGCAACCCTA	GCAAAACGAG	TTGCGGCTGA	GCACTGTCAT	5400
GTTGTGATTA	TCTCCTCAGA	TAAAGATGTA	CTTCAGCTTG	TGTGTGATAC	GGTGCAAGTG	5460
CTCAGACTTG	ACATAGATCA	TAAGTGGACA	TGTTGCGACG	CTGCGTACGT	ACAGCAACGG	5520
TGGACGGTCA	TGCCAACACA	ATTACTTGAT	TTGTTCTCTC	TCATGGGAGA	TTCCTCCGAC	5580
AATGTGCCTG	GTGTGAGAGG	GATTGGTCCT	AAGACGGCTG	CACATCTTCT	CCACTGTTTT	5640
GGCACACTTG	ATGGTATTTA	TCGTCATACC	TATTCCTTAA	AAGAAaGCGc	TGCGCACGAA	5700
GATAGTGTGT	GGGAAGAAAG	ATGCATTTTT	TTCTCGTTCA	CTCATTGAGT	TGCGTGACGA	5760



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TGCACGTATT	TTTGTGCGAG	AAGGATTGCA	TGCGCTTGCA	CAACAATATC	GTGCTTGTGT	5880
GCAAGAAATA	GATACAGAAG	CAACAAACGA	TACATTACAA	ATGACAGAGT	CTTCTGTGCT	5940
CACGTCTGGT	CGATGTGCAA	ATGAGTGTTT	CTTATCTCAG	GTAAGAGGA	GGGCTAGTAC	6000
ACCGGAGGTG	AaCTCCGTAT	TGAAGTCGGA	GTTGAAGACG	AGTGCTGTGT	CTGGCGCCAT	6060
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TCGTGGTGTT	ACTGACCCTG	TAGAACTTAA	ACGTATTATT	GATTGCGCGT	GTGCGAATGG	6180
TGTGGTCGCG	TTTGATTGTG	AAACGGATGG	ATTGCATCCG	CACGATACAC	GTCTGGTCGG	6240
ATTTTCGATC	TGCTTTCAGG	AAGCAGAGGC	TTTTTATGTT	CCTCTTATTG	TTCCGGACGT	6300
TTCTCTTCAT	ACCGAGTCAA	CTCAGTGATC	ATGTGCACGT	AGCACTAATG	TCGAGACTGA	6360
AAAGGAGTGC	ACAGAACAGC	ATGGGGTATC	TGCATCTGCT	GTGCAGGATC	CGGCATATGT	6420
CCAAGCTGTC	ATGCACCAGC	TTGACGTCT	TTGGAATGAT	GAGACGCTCA	CACTTGTTAT	6480
GCATAATGGA	AAGTTTGATT	ATCACGTTAT	GCATCGTGCA	GGCGTTTTTG	AGCACTGTGC	6540
ATGTAATATT	TTGATACGA	TGGTTGCAGC	TTGGTTGCTG	GATCCCGATC	GCGGTACATA	6600
CGGTATGGAT	GTACTTGCCG	CATCATTCTT	TCAGATCAGA	ACGATTACAT	TTGAAGAAGT	6660
GGTAGCAAAA	GGGCAAACCT	TTGCGCACGT	CCCTTATGAG	TGTGcAGTCC	GCTATGCAGC	6720
GGAGGATGCA	GATATTACTT	TTGTTTTATA	CCATTATTTA	AAACTCCGCT	TGGAACAGC	6780
AGGATTGCTT	TCTGTGTTTG	AGACCATAGA	AATGCCGCTT	TTGCCTATCC	TAGCACGTAT	6840
GGAAGAAGTG	GGGATTTTTT	TACGTAAGGA	TGTTGTGCAG	CAGCTCACTC	GATCTTTTTT	6900
AGATTTGATC	CAGCAGTACG	AGCACGATAT	TTTTTCTCTT	GCCGGTCATG	AATTTAATAT	6960
TGGTTCTCCG	AAGCAACTGC	AGACAGTCCT	TTTTCAAGAA	TTACATTTAC	CGCCCGGTAA	7020
AAAGAATACT	CAAGGTTATT	CTACTGATCA	TTCTGTATTG	AAGAACTTG	CACGTAAGCA	7080
TCCCATTGCA	GAAAAAATAT	TGCTCTTTAG	AGATCTTTCA	AAGTTACGTT	CGACGTATAC	7140
CGAATCGCTT	GCAAAACTTG	CTGATCAAAC	AGGGCGTGTA	CATACTAGCT	TTGTGCAAAT	7200
TGGTACCGCA	ACTGGAAGGC	TTTCGAGTAG	AAATCCAAAT	TTACAAAACA	TTCCCATTA	7260
AAGCACAGAA	GGAAGAAAAA	TAAGGCAGGC	GTTTCAAGCT	ACTGTTGGGC	ATGAGTTAAT	7320
TTCCGCAGAC	TATACACAAA	TAGAGCTGGT	CGTGTGGCC	CATCTATCTC	AAGATAGAAA	7380
TCTTCTCAAT	GCATTTTCGAC	AGCACATTGA	TATTCATGCA	TTGACTGCTG	CATATATTTT	7440
CAATGTGTCT	ATAGACGATG	TACAACCTGC	AaTGAGAAGA	ATCGCAAAAA	CTATTAACCT	7500

TGGAATCGTG	TATGGAATGA	GCGCTTTTAG	ATTGAGTGAC	GAACCTAAAA	TTTCTCAGAA	7560
GGAAGCGCAG	AGCTTCATTT	ACCGTTATTT	TGAAACGTAC	CCGGGGGTGT	ATGCTTTTAG	7620
TACACAGGTT	GCAGAGCAGA	CACGTAAAAC	CGGCTATGTG	ACTAGCTTGG	CTGGAAGACG	7680
ACGCTACATC	CGTACTATCG	ATAGTCGCAA	TACGCTTGAG	CGCGCGCGTG	CCGAACGTAT	7740
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TGAATTGATT	TTTGAGGCGC	CAGCTGCTGA	GACAGCGATA	GTGAAAGAAA	TTCTCTTTGC	7920
TGAGATGGAA	CATGCTGTTG	AGCTCTCGAT	CCCCTGCGT	ATACACGTGG	AGTCTGAAA	7980
TAGTTGGGGT	GATTTTCATT	AGCATACCCA	TCTGAGGGAT	GCAACAGGGC	ACGTTATGAG	8040
GTTACCTCGG	CGCGTAGTTC	CTTAAAAAAT	GATGCTACCA	CGCACAACAT	AATCAGCGCT	8100
AAAGGAAATG	CCGCAATGAT	GGCTAAACTT	TTCAGGTGCA	TGAGTGTGGA	CTGGGAGAAT	8160
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TCAAAAGTAC	TTGCATAAAA	GGCGATCATG	GTAGCTGCCA	ACAGCGCCAT	AACGATGTAC	8340
GCGCAGGcAG	TGTCTGAATA	ATTGCGATAA	TCACCTCAGC	GGGTGTATTTC	CCCGCGCGCA	8400
naAGGTACGC	GGCAGGAAGG	AGGTGGTGCG	TTTGTAATA	GAGCCCGTAG	TTCCCTAAGA	8460
CGATGAAGGA	GCCGTACGTA	CCTGCGATAC	CCCAGCAGAG	CCCTCCGACG	ATGGTATTCC	8520
GGATGGTTCT	CCCTTCGGAT	ATCGCGCCGA	TGAAGAATGG	GGTTGCAACA	GACCACGTGA	8580
TCCAATACGC	CCAGTAAAAG	ATAGTCCACC	GCTGTGGAAA	TCCAAGCGTC	CCATCCGTTT	8640
CCTGTAATGA	AATACGAGAA	GGATCCATCC	ACGTTGCCAT	AAGAAAGAAG	TTTTGTAGCA	8700
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GGGTACCCAG	CAGTACTGCT	GTGGTGTA	CCAACGCAAT	AACGCAGAGC	AACGCTAAAG	8880
CGAGCAGCTG	GGTGTTAGAA	ATACCGAACA	AGAGAGAAAC	CATGAGCGAA	AGGAGGGGCG	8940
TTGCTAAGGA	AAACGTGGTT	GCAACGCCTA	GAAGCAATCC	CACTACAGAA	CAGATATCGA	9000
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TAAAAAGACC	AAGGTATGAT	GCCCCAATGG	AAAAGGGGAT	ACGTGCGCGC	CCATTCTTGT	9180
CTTCCCGTGG	GAGGGGAGTG	TTCTGCTATA	AACGGAGCTT	GAGTGAAGTA	GTGCGCCCAT	9240

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TCGATGAGCG	ACCAATACAA	AATATCCGCC	GCCATGGTGG	ACGTAAAAAT	CATGGAGCCC	9300
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CCCAGTTTGT	TTACCAGTAT	ATTCAAGAGG	GTACCGATTA	CCCGATGAGA	AATGTCAGGA	9480
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TTCGTAATAT	TCTTTTGCAT	ATCGGTACAT	TTTCAGTCCA	TAATCTCCAA	ACGAGATACC	9660
AAGCGCTGT	TTGTAGCTCG	TCCACAAAGA	CCACAAAAAT	CCCCAAGAG	CAATATAGCA	9720
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TTCTATCTGG	GCGGTGTAA	AGTGGGCATA	CAAAGAGAAC	ATCGCGATAT	CCACAAGCGG	9840
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CTGGTCGAGG	GCAAGCTTTT	CGTAATACGC	AATACGCGAT	CTGAAGTCGA	ACCTATGGGC	10080
AACACAAATA	CCTGATTGAT	GGAGTTTGCG	CGCAATCCTC	ATGCACAAGT	CAAGGTCTGC	10140
CGGATCACTA	GGGTTTGCAC	TGCGGCAGTC	TTTGTGGAAG	ACGGTGATTT	TAATACCACG	10200
GGCAGGCTCA	AGGTGAACGA	GAGTGTCAAC	AATATTAAGG	GGCTTAATTG	CTTCATACAC	10260
GGCAGCTTCT	TGGAAGCGAT	TGACAAGGAG	TTCGGTACCC	TCTCCAGGAA	TTCTGAATAG	10320
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CTCGTTATCG	CTCGAAACCA	TGTACGCAAA	ATCAAACCTG	CGCAGCTCAT	CGAGCGACTC	10500
AAATTCGTAG	ATAAGGTTGT	CAGCCTGTTT	GTTGGCAAAC	ATGGTAAGGG	ATTTTGTATT	10560
GCGCATAAAG	ACGTCTTCCC	AGAACCACGC	GCGGTTTTCT	GGGCGCATGT	AGGCAGCTTC	10620
GATGAGGGGG	ATGATCTTTT	TAGAAAACGA	TGCAGAAAAG	TAAGCTGGAC	CGTACATGAT	10680
CCACCCACTT	CTGCCACCAA	TTTTCACGGC	GGTAATTTTG	TCGTACAATC	CGGTTTTTAA	10740
CACCCATTCC	TTTGTTTTCC	CTTGTGTCTT	GACAGCCGTA	TACCAGGAAT	CCCACTCATG	10800
GGAGTGATAA	ATGTTTTCGC	GTAGCCAGTT	ATCGCTTGAG	AGTATGTAGG	TATTTCGAAG	10860
TAAATGACGG	GCGTGGTAGA	GGGTGGATAG	GTTGTTGGCA	GTTTCATAGT	CAGGGTTATA	10920
GGTGAGCGTC	ACGTCATGCT	TGTCGACGAG	GTA CTCAAAG	GCCTCTTTGA	GGTAGCCgAC	10980

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GACGACCGTG ATGTCAGTAA TGCCGACTTC GTGTAAGTGA CGAATTTGAC GCTCAATCAT 11040  
GGGCTCACCA AAGACTTTCA GCAGGCCCTT TGGAGTAGCG TATGTAAGAG GCACGCAACG 11100  
GGAGCCAAAG CCTGCAGCCA TTATTACCGC ATTATGAACC CGGCAAGACT GATACTGACT 11160  
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TCCTGCAGAC TCCATAGCGT GTAGAAGGCG ATTGGTGTA GCAAGGACA GGCGCAACGC 11280  
CTTGCGGATG TCACGCTGGC AAAGCCGAg CGCATCGCGC AAAAGCTGAA AAATCTGGAA 11340  
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AAAACAGGGG AAAAAGCACC CCCCCCTG CTCGCTTCCT GCACACAGCT GTGAGGAGCG 11460  
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GCGTCGCGCC ACAACGATCC TTCAGGATTT ACGTGTTTGC GTTGGCACAC CACCACATCG 11580  
ATTGGGAGGT GTACAACTT ATTGTGCACC AAGCCAATGA TCATTTTCGT TTTACCGCAC 11640  
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gcAACCGCGG aACGAATCAA GTAGCTCGGA TCGATGTA TTAATTGAT GTGTATACGC 11760  
TTTTCTTTGA AATAGACTCC AATCTTTTCT TTTAAGAACA AACC GATATC CGCAAGGCGC 11820  
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GAGGGCACAC CGTCCGCATT TACCATTAGG TCTTGCCCCG CACCTTCTGC TACAACGAGC 11940  
ACCGCATGCT TACGTAGCGC GATTGCTTC TCTAGGTGAG CCAAAGCCC ATTTGGACCG 12000  
TCAAGGTCAA AGCTCACTTC AGGGATGAGT ACGAAgTTTG TCTCATGGCT CGCAATCGCC 12060  
GTGTACGTAG CGATGAATCC AGACTCACGC CCCATGAGTT TGACCAGTCC AATGCCGTTA 12120  
ATCTGTGAAC GAGCCTCCAT GTGCGCTGCG GCAACTGCCT CTGTTGCTTT GACAATAGCA 12180  
GTATCGAAGC CAAATGACTT TTGAACAAA GAGATGTCGT TGTCACCGT TTTGGGAATG 12240  
CCGATGATGG AAATCtTAAG GTTGCGGtGT TTTATTTTCGT CGGCAATCTC TTTTGCTCCC 12300  
TTCTGACTCC CATCCCCCCC AATGaTAAAG AGAATGTGCA gGTTGAGCCG CTCGATACCA 12360  
TCGAAGATGT CAAnCAnAAG GTTCCCCCA ACGCGnGAnG TGCCTAAGCA G 12411

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ACCACCGCAA CAATCGGGAT ACCAACTCGC CTCGCTTCAC GGATAGCGAT AGTCTCCTTA	60
CGCGTATCAA TGATAAACAC TACACCCGGC AGCTCCTTCA TTTCCTTTAT GCCGCCAAA	120
TTCTTTTCTA GTTCGCGTGC TCCTTGCGTA AAGACGCCAC CTCCTTCTTA GAGAGATGCT	180
CGAAmGTACC GTCTATCTCC ATGCGTTCTA TCTTCTTGAG ACGCGAAAGA CTCTTCCTTA	240
TGGTGGAAAA GTTAGTGAGC ATGCCGCCGA GCCAACGGTT AGTCACATAA AACATCCCAC	300
nAGCgcTGCG CTTCCTTGGC AATGGTTTGC TGC GACTGCT TCTTTGTGCC CACAAACAAA	360
ACGGACTTGC CTGAGGAAAC AGTCCTGCGC ACCATGTCGT ACGCCTCGCG GATGGCCGTA	420
ATCGTCTTTT GCAGATCAAT GATGTGAATG CCGTtACGCT CCGCGAAAAT ATACTTTTTC	480
ATCCGCGGAT CCCACCGCCT GACCTGATGG CCAAAATGAA CCCCAGATTC AAGCAGATTT	540
TTGATAGTCA CCACTGCCAT ACCATTCTCT CACAGAGAGC GCCGAGGCTC TCATCCTTCT	600
CTCTTTCACC ACACGCACAC GCGCCGGGGA TATTCTCGAG AGGACAGAAA AACGCGTCCC	660
CTCACACACG GTCACCTTGA CTAAAATCAG ACGTATGGAA TACGGTTGCC CGCCTCTTCT	720
GTGGACCTTC CCAGGCCCGC AGCAGGTTAC AGAGCAGGGA AGATTAGCTC ATTCGGATAG	780
AGCGTTGGCC TCCGGAGCCA AAGGCGnTGG GTTCAAATCC CGCATCTTCC ATCCTCTTAC	840
CCACGTAAAC GGGCGCCCCG CGmTrACGC TCCTTCCAGT CAAGCTGGCA ACTCAGGGGc	900
CGTCCGCCCG CTCTCCTTCA GCAGGTCACT TGCCGCCAGA AACGACTCCC TTCAnCACTT	960
CGAGCGCGCG A	971

## (2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AGTGCCGACG CGCGAGAACG TATTTTGGCC CATCTTGAAA TGCGTGCGC AGGTGCACGG	60
CGCGTCACCT ATCGCCTACG C GACTGGGTG TTCAGCCGTC AGCGCTATTG GGGAGAACCC	120
ATCCCTCTTG TGCACTGTCC TTCtTGCGGT GTTGTA CCTC TCCCTGAGAG TtGCCTGCCG	180
CTTTTGTTAC CCGAAACCGC CGATTTCACT CCCACGGAAG ATGGGCAGGG CCCCCTTGCA	240
CGAGCGCGCA CGTggTGCGC GTTCCCTGTC CGCAGTGTGC ATCTGACGCA GTGCGAGAAA	300

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CAAAACACAAT	GCCCCAGTGG	GCAGGATCCT	GCTGGTATTA	CCTCCGTTAT	ATGGACCCCC	360
GCAATAAGAC	TGCCTTTTGT	GCACCCGAGA	AGGAGCGTTA	CTGGGCgCCA	GTGGCGTTAT	420
ATGTAGGTGG	TGCAGAGCAC	GCCGTACTGC	ATTTACTGTA	TGCACGCTTT	TGGCACAAGG	480
TATTGTACGA	CTTAGGTCTT	GTAAGCACGA	AAGAGCCCTT	TGCGCGGTTG	GTGAACCAAG	540
GCATGATTAC	GTCGTATGCA	TATCGCAGGA	AAAATGGCGC	GCTTGTACCT	CACGACGAGG	600
TGCACACTAA	TGCTCAAGGT	ACCTACGTGC	ATGCTCGTAC	GGGGGAAAAA	CTCGAGTGCG	660
TTGTGGCAAA	AATGTCAAAA	GCGTTAAAGA	ATGTCGTCAA	TCCTGATGAC	ATGATTGCAG	720
CGTACGGTGc	tGACGCGTGC	CGGGTATACG	AGATGTTTCAT	GGGACCTCTT	GAGGCTTCCA	780
AACCGTGGAA	TACGCAGGGG	TTAGTGGGGG	TTTTTCGGTT	TTTAGAAAAA	ATTTGGGTAC	840
TTGCGGGGCG	CGTGGCGGCC	GCAAACGGTA	TTCCACAAGA	CTCTCGTGCA	GAGCCGCCAG	900
GTGACCTGCA	CGCACAGAAA	AAGTCTTGCA	GCATGTACGC	CCTCGAAACG	CTGTTACACC	960
GGACTATTCA	AAAAGTgaCg	ACGATACGTC	GGCGCTTAGT	TTTAACACGG	CAATCAGTCA	1020
GATGATGATA	TTTGTAATG	AwGgTACGCG	GGTGGCGCGG	AGGATGCCTC	TTCCCTCTAA	1080
AATGTGGGAG	ATGTTTGTA	AAATCCTCTC	TCCCTATGCA	CCACATTTGG	CAGAAGAACT	1140
CTGGGAAATG	TGTGGGCACA	CGCACACTAT	CGCATATGAG	CCTTGCCAC	AGGTGGACCC	1200
TGCGCGTGTG	GCGCCGCATG	TGTGCTCCGT	AGTGGTGCAG	GTGAACGGTA	AAGTGCGCGA	1260
CACCTTCTCC	GTAGCGCCGA	ACGCTCCAAA	TGAGGAACTC	GAGCAAAAGG	CGCGGGAAAC	1320
CGCCGGTGCG	CGTAAGTTTC	TTGGTACGCA	GCAGCCAAAG	CGCGTAGTGA	TAGTTCCCAA	1380
TAAATTAGTA	AATTTTCGTT	TGTAGTCCGC	ACTGCTCCTG	CAGCGTTGTG	CAGTACCTGT	1440
GTGGTGCCCT	ACCCGCGTGC	ACTACAATCG	CGTAAAGGCA	CAGCTGCATC	AGCGGCCCTT	1500
GGAGAGGCGT	CCCACCTGAG	CGGATCATTG	CGTCTGTCTG	GAACAATCTA	TCCAAAATAG	1560
CATGCGTATC	GCTCAGGGTC	CAAAGAGACG	CAGCGCGCTG	GTATTGCGCA	ATCATACGCC	1620
GAGAAGTGAA	CCCATAGCGC	TTTAGCGTTG	CAGGGTGCGT	TTTGTCTCTC	GGTATATGGT	1680
GCCAATGCGC	AAGGCGACGG	AACGCGTAAG	naGtCCTGCA	AGGATTTGTA	CAGGGGCAAC	1740
GTCTTTTCGAA	CAAAGCAGCG	TGTTGAGAAT	CATAAGTGAA	TGCTCAAGAT	CTCGTTTGGA	1800
CAGCGCATCG	AATAAGGTAA	ACGATGTCTC	TTCTTTTGTG	TGCACCAGCA	ACGAACTAAT	1860
GTCGTGCGCA	gTGATGCGGc	GTCCTTTTTc	AAAAAAAAGA	GAAAGCTGCG	TACAAAACAGT	1920
TTTGAGCGCA	CGAGTGTTGT	TCTCCACCAA	CTCAAGAAGA	GATTCGATAG	CCTCCCTGTC	1980
AATGC						1985

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## (2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AGGGAGTGGC TTATGGGATA CGGTTTCATCA GCTGAGGAAA CGTCTTCTAC ACCGCATGCG	60
TCAGGCCAAA GGAAGGTTGG TTTTCTGTCC CTGCGCACCA AGCTCGCGCT GGTGTTTGGG	120
CTGCTTGCCT TCGTGTCTGG TCTGGTCCAG GCGGTATAT TGGTCGTTT TCGCGTAAC	180
TCCATAGTTG GGGAGATTTC TAGTCACCTT GCTGGCCGTG CTCGGGATAC CTCCTCCATC	240
GTGGAAGGGC GGATCGGCGC GCTGTTCCAG TTTTGGGAAG GTTTGGCACG TCTTGAAGTT	300
TTGCAAGGCT CGTCCGACAG GCGCCGTGCC CAGGTGGACA GGCTAAAGAA GGAAGCGTTT	360
TTTAACCGGG ATATCGCGCG TCTTGGCGTG GTAGATCTCG cAGGCGTGTT GTACGGGGAG	420
GACGGGCGCA CGCATTACGT ACAAGATCGA AAGTACTTTC AGCGGGCGGT TAAAGGCCGT	480
TGTTACGTCT CTGCGCCCTA TCCCTCGCGT TCGTCGGATG ACATGGTCAT TACCTTTTCC	540
ATCCCGGTAT ATGACGAAaT CGGCGGGTTA TgCCGTGCTC GTAGCGGaTG TGATTtGGAC	600
GTGGCTGTGT GATATCACAG GGGATTTTTT TGTAgGgGGG TGGGGAGAAT CGCCGTTATT	660
GACGAGGTTG GTACCGTTGT CGCGCACCCA CGTCACGAGG TAGTGGCGCA CAGACAAATT	720
ATATCCGCCT GGCAAAGGAA GACCCGGCCA CGTACGCGTC CGTCGAGAG TTCGTTGAGA	780
AGGTTATCAA GTCAGACTCT ACTGCCTCTC ACGTGTtCTC GTATGAAGGC TTAGAGAAAA	840
TCGGTTCATC TGCCAAGATG AAGAGCACAG GATGGACCGT CGTGGTGTtT GTGCCTGTCT	900
CCGAGTTTAT GGGGCCTGTG TACACCCTGG CAGAACTACC TGCTTGCGGT GGGTATCATG	960
TGGTACTCTT CTCCCTCATG TGGTGTATGC CGTTGCGCGC AAGATTGTGC GCCCGCTACG	1020
CTCTACCGTC AGGTGTTAGA AGA	1043

## (2) INFORMATION FOR SEQ ID NO: 93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CnTCTnTTAT TTATTTTGAA AAAGACACGT TGCTTTTCCT GCGCGAATGC GTCAGAATGG	60
CGCGGTCCCT ATGATATCGT GTTCGGTGCG CAGGAGGCCG AGATGGGAGC CTCAGGTCGG	120
CGCTGCGTTT CTTCGCTTTG CGCTCTTACC GGTCCTGGCG AGCGGACGTG GTATGCAGGC	180
GGCAGTGGCC ACAGCCGAG GGTCCAGTGG TTCCGGCAGT GATGGCAAGC ACCCCGGCAA	240
GGAACAGTTT CTCCAGTTCC TCATTCCATC TGGCGGTGCG TACGAATACC TCGGGGTGAG	300
CTTTACAGCG CTGGCAGATG ACGCCAGCTT CTTTGAAGCT AACCCTGnCG GCAGCGCCGG	360
GCTCAGCCGC GGGGAAGTTG CTCTGTTCCA CCACTCGCAG ATCCATGACT CACACACCGA	420
AACGGTTTCG TTTGCGCGAC GTACGCAGAA CACCGGCTAC GcGCCTCCGT GCGCGCCTTC	480
TCTTCTGAGT CAGATCTCAA GTCCTTCTTC GGGGGCAACA GTGGTGGCAA TAAGAACGGC	540
GGACACCAGG GCAAACAGGG AAAAGGCTTC GTGGCAATAG CCAATGCGTC TCACACCTTC	600
TGTGGCCAGT ATCGCTTTAA GGGCGTAACT TTGGCTGCAA TTTCAAGATG GGATTCCGCA	660
AGGtAAAAC TACAGCCACG TGACCGTCGC GGGTGACTTG GGCCTGCGCG CTGCCTTTTC	720
TGTGGCAAAG AACTTTGGCT CAAATGAGCC GAACATGCAC GTGGGGTTGG TGCTCAAAAA	780
TGCCGGGATC TCGGTAAAAA CAAACAGTTG CCAAGTCGAA CACCTCAATC CGGCCATTGC	840
CGTCGGCTTT GCCTACCGGC CGGTGTATGC GTTTTGTTC AGTCTCGGGC TGCAGCAAAC	900
CCTCACCAAA AGGGAGTCGC CGGTGTGCAG TGTGGGTTC ATGTTTTTTT GTACCCAACA	960
CGTTACCCTC CTCGCTCTG CTGCGTGTGA AGGAGGGGCC TACGCCCTCT CAGGCGGCGC	1020
AGAAATCCGC ATTGGCTCCT TCCACCTCGA CATGGGGTAC CGGTACGACC AGATTTTCCA	1080
AGCCGCCCAC CCACACCACG TGTCAGTAGG GCTGAAGTGG CTCATACCCA ACGGCGGCAC	1140
CCAGGCGGAT CAGGCCCTCT TGGTCAAAGA GTCCTATCTA GTGGGGCTGC GCTTTTATGA	1200
CCAGCGGCGC TACCAAGAAG CAATTACTGC GTGGCAGCTG ACGCTGCGCC AGGATCCGGG	1260
CTTTGAACCG GCTGCTGAa GCATCGAgCG CGCACGACGC TTTTAAAAAC TACACGAAAA	1320
ACTTTCTCTC TTTGATATTC TCAACTAGCC TGCCGTG	1357

## (2) INFORMATION FOR SEQ ID NO: 94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CACCGaCCCT GrAATaAAGC GTTACAAAAC CTACTCCTAC CATAAGGGCG ACAAGCAGTA	60
TGAATACAAA ACTGTAAACGC TCTTGATGTA CATTTTCTCTC GATGGAAATC ATCGGTCTCA	120
TCGCTCTTTC CTCAAAGAG GTTCAAGCCG CTCGAGCGcA AcACTGCGTG AACCTTTCAC	180
CAGAACAAAA TCACCCCGCC GTAATTGCGC GTCTAACGTT TCTTGACGCG CAGACAGTTC	240
CTCTAGTGCA AAGGCGTACA CGCGCTTCCT CCCCCAGGAA ACTTTTCTTA CCGCACGACA	300
AAATTCGGGA CCAAACACAT AACTGCACG CGCGTCAGAA GCGGCTGCCA AAACACACAC	360
CCGATAGTGA GCTTCGGCAG CGGTAACCTC TAGCTCTCCC ATGTCACCGA GCACATATAC	420
TTTGTACT GCAGAAATAT GCGCACACAA ATGAAGCGCC GCAGCCATTG AATCAGGATT	480
CGCATGTAA CAATCGAGCA AAAAGGTCAG CGACGCACAC ACCACATGAG AGCGGCCAAA	540
GGGCGGTTTT ACCCGCTCCA TCCCCGCTG AATTTCTCA GCAGGAAGTC CTACCTGTGC	600
GGCAAGCGCA ATCACTGCAA GCGCATTCTT TGC GTTATGC ACCCCAGGTA GTGGCACGCG	660
AATCCATCGT CTTGATATA ACACGCGAGA ACCACGTAAA CCTCATCTA TCACCTCAGT	720
TGCTAGACCA CGCCCCCCT GATCGTAAAC TACAACCTA CCGTACGGGA TATTAGACAG	780
GAATACagAT ATGCATCGTC GGGGACAAAA CCCACGCTGT GTTCAGTAAA TTGAGAAAAA	840
ATCTCTTTTT TCTCTTCCGC AATGcCTGC TGC GTGCCA GAATGcTAC GTGCGCACAA	900
CcTACGTTGG TAATGATCGC GTAATGAGGA ACAAGTATCT GAGCGAGCGT ACGCATCTCC	960
CCCCGACGAT TCATCCCCAG CTCAAAGATT CCTACCTCAT GTTCTGCACG CACAAAAAAC	1020
AGCGACTGCG GtAAACCTAt CTCTGAATTT AAATTTCTG GCGTCGCAAC CACCCGATAC	1080
CGTTCACTGA ACACCGCGCG AGCcATTTCT TTTACGGTTG TCTTTCCGCT TGATCCGGTA	1140
ATGCCAATCC TAATAAGCGC AGGAACTTT TTGCAGTAAA AGGAGGCAAG ATCTTGCAGC	1200
GGCTGAGCG TGTCGTGCAC CGCAATACAG GCAGCTCAA AGCGAGTGCA CCAAGCAACA	1260
TATTCCCCAG CATGGGGGtA CCTTTGATCT ATAAGCGTTG CAACTGCGCC CTTCTGCAGC	1320
GCTTCTTCAA CAAACGTATG TCCATCTACG TGCGCACCAC GGAGCGGAAT AAACAAATCA	1380
CGCGGCACAA CCGCACGACT GTCAAAGGAA ACCCCGTCAA AACC GCGCGC CCCTCGTGCA	1440
TCGCACACGC GAGCCCCTTG CACTGCCGCA CATACCTCAT CAAAACCTCAG AAGCATGAGG	1500
GGAGGAGTCC TTGTGCGCAG GACGCAGCTT AATGCGCACA ATTTGCGCGT GCGACGCCCG	1560
GTGTAAGTGC AGTTTCTCTA CCGCGAGCTT TTCAATACGA TCCGCTTAG ACAGGATCGC	1620
GATCCCAGAA ATCTTACGCT TATTTTCTGC GATAATACGG TGTGCTCTG CGTCGTACTC	1680

ACGCACCACA CGCTCAACCG CCTGATAGCG CGAAGCCTGC CACACCCCCG CACACAGCAA 1740  
CACGGGGATA CTCACCGTAA AGAACAACGC GCTCACCTTT TGCACCGTCA TCCCTCTTTG 1800  
CCGGCGAGGT ATTCCCcTTC GCTGCTTTTC TCTCATCGCC CCTTTCTCAC GCATCAGCCC 1860  
AGTCTCTTAC CGTTTCTCAA TGACGCGTAA CGTAGCACTC CgcGAAGCGG CATTCGCAGC 1920  
ACGCTCCACA CACGAAGGTA CAAGCGGCTT CTTGGTAATC AGCGATGCAC GCGCCACACC 1980  
GCCGCAGCTG CATATCGGCA CACGAGCCGG ACAGCTGCAG CGTTTCGCCC AGTGCCGAAA 2040  
ATGTACCTTA ACAATCTAT CCTCACGCGA GTGAAACTA ATAACCGCAA GTCGACCCCC 2100  
AGgCGCAAGC GCCGTAAACG CTGCCGTAAG AAGGCGTGGC AAACGCTCAA GCTCCCTGTT 2160  
CAyCGCAATG CGCAATGCTT GAAACGCCTT GGTGCGCGGA TGGAGCTTCG GCAAAACCCC 2220  
AAGAACACgC GCCGCTTCCC AAAmCGCGCC GTyCGCATCG GCGGCaCCAC GCGCGCAACG 2280  
ACTTCTGCAA ATGCGCGCGC AGAGcAAAAG GGCGCCTGCC cGaaCTGCGc GCACACCGCC 2340  
TGCGCAATCC GACGCGCGTA ACGTTCCTCT CCCCCTTCAA AAAACAATTG TGCCAAAnCG 2400  
TCTGCGGCAG CCGATTcAGG AGGTCTGCAG CGGTCTGGGA GG 2442

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCGGGATG CGCGGCCCCC TGGGGGAAAC GGAAATTGAA ATTGCGGCCG GGGCAGCCCC 60  
GGTGTGCCGC TCGCCgTGCG CGAACGGCAC kTGCACTCGCG CACCCGCCGG TGCAGCGGGT 120  
GGGGGAGTGG AACGCCTGTC TACCGAACGG CGTCTTTCTG TACTGCACGG CACgACGCGG 180  
CTGAACCcGA AGCAGACGCC GTGCAGTAAC GCGCCGGcgC GCCCGCGCGC GTGCCGGCAG 240  
ACGGCGCTGG TGGGACAGTC CGCAGGCGGC GCCCGCTAC CACGCGATTT TAAGGCCGCA 300  
CACAAAGGTG CCAAAGTGCT TATCTGAGGA AATATCTTCG GTAATTAGCA TGTACGGCGC 360  
GGTGGCCAGC CGCCCCTGCT CCCACCGGGC GTCAAATCC ACTTTTTCTA TTGGGCTAAC 420  
GGTGAACCCC ACGTGGTACT GCATTGCCTT TTCGCGTAgc AGATTGTTAG CTTTGTGCGT 480  
GTTGAAACGG TTAGTGTTTC CGTACACCAC CGCGTACGGC TTGAGCCAGG CGTGGGAGCC 540  
GAGCGCAATC TGATAGCTCA GCCACGTTTT GCCCACGACC GGCAGgTTGA TAGGCCCCCT 600

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CATTGTAGTC TTCTTGTAAT CGATGCCCCC GTTGTTTACG TAGGAGGTGT AGGTGAAGGG 660  
AATGTACAGG CGCGCCTCCA CCCCCGCGTT CAAGCCGGTG AGCAGGTGCG TGTAGGGGTC 720  
GCCGGACTTT GTTTCTAATT TTAAGAATGC GCGCGAGTCC AAGTAGTCTG TAAGCTGCCT 780  
GGAAAAGACG CGCTTGCCAA ACATATTGGC GCCGGCGGTG GCAAAAATACG CGCCGGAAGA 840  
AAGCCACTTC CACTGCATGC TCAGCAAGGC GTCAGcGcCC AACTCGTGCA CGTGCAGGCG 900  
GTGCAGCCAC GCAAAGAACG TGACGAGCGC AATGGCCGGG TCCGGCTTTT TAAGGAGCTC 960  
GGCGAATCCC TGGGTGAGCT GGTTTACCAC CGCTCCCAGG CCCAGTGTGC TCTGAAGTAG 1020  
ATTGGAGAGT TTTCCTTCCA AATGGGAAAC CACcAGTGCC AcTTGCGCTA TGAaGGCAGC 1080  
GCCCGcAcTT TTTTGACAAA AAAcTCTCCG ACGCCACCGT TGGCCATaTC TGGGCCATTG 1140  
TGCCCAAAAT cGGTTAACGy TGCAtTmAGG CTTcTGCCGm CTTGGsCTGC AgTTTACCGT 1200  
CTTCCCTATA TCCGCGTCGC TCCGGTGAAT GTTTCCCACA TCAAGCGCCA GCACGAGCCG 1260  
AAACCCGTAC CCCGGGGTCA GCGTCAGCCG TCCGCCGGCG CTCCACAGCA GGCGGTTTTT 1320  
CTGCTCATTG TTTTTTCCCT GCTCAGTCCC CGTGGTGTAT TGGGGCTCCA GCGTGGCGTT 1380  
CCCCGCCAGC TCCATCTTGA TGCGCTCAGC GCGGTGGTGC GTGTACGTAA GCGTGGCGTC 1440  
TGCTCCAAAG CCGTACTTGC TGTGCGCAGT ACCACTATCC CACATACCGT TTGACGCAAA 1500  
CGAGAGCAAG CCCACGTCCA ACCCAATGCC AtGCCGCCGA TATCCTGCGC ACGGTAGCCG 1560  
AGCTTGCCCC CATAGCCGCC AAAGCCGGGs CATAGCGCAC GTCCTCCTGC TTGTAGTCGC 1620  
TGGTCACGAA CGGGTCCCAC aGtGCGCAAA GTTAATAAAG CAGTTCGGGT CCTTGCCAAT 1680  
GGTCAGGTAC GCGTTGTAGC AGTGGAGCGT TGCTTCAAAA GACGCTTTGG GTTTTTTGAG 1740  
CGTAAAGGCC TGCCCCGCC TGGGGGATTC AAAATCAACG GTCAGGTCCT TGAGCCGCAG 1800  
TCCGCCACA CGCCTGAGCG CGCCCCGCCG CGACGCAGGT GCGTGGCCTT GGGCACGAGG 1860  
GGGAGCGAGA TTTTCAAATC ATTGGTGGTG CGAAACCCGT GCGTGACTC GTTmnTTGCA 1920  
C 1921

## (2) INFORMATION FOR SEQ ID NO: 96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

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GTCAATTGCA TTAAGGTTAT CACGCGCGCC CACACCCTCG GCTATTGCGG CGGGGTGCGT	60
ATGGCGGTGC GCATGGCAGA ACACGCCCGC GCCCACCACC GCGGGAGtTC TACACGCTCG	120
GTCCGCTCGT CCACAATCCC GTGACGCTCG CCCGTTTGCG CGCGCGTGGC ATTGAGTGTC	180
TGGATCCTGC TCATCTATCT TTTGCGCTGC ACGCTCCTGC GGcACCGGGC GCACGCCGCA	240
TGCAGTGGA GAAAAGACGG CCGGTACCGT GGTGATTAGA GCGCATGGCG TGGCACCTGA	300
GGTGTATGAG GCCCTCGAGC GTTCCGGAGC GCAGGTGGTG GACGCCACCT GCCCGGAGT	360
TAAGGAAAGT CAGCGGCGTG CTCAGGGTTT TGCCGCGCAG GGACTGCACG TTATTCTCGC	420
CGGGGACCGC AATCATGGGG AAATCGTTGG CATCGAGGGG TATGTGCGCG CGGGAGCTGC	480
GCAGGCGTGC ArCCAATTGC CAGGCGGCGC ACCAGACGGC ATGCTGCCAC AGGTGCAGTG	540
CTTTGTGGTG CAAAACGCGC GTGAgGCTGC CGCGTTGCCG TGTtTagCGC GTGCAGctTC	600
CTTgCCCCAA cTACCATTAC ACAGGGTGAA TAmGACGCGA TyGCCGCTGC GGgCGTAA	658

## (2) INFORMATION FOR SEQ ID NO: 97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TTCTGCAGTG TACGTAAAT CGGACGCATA CTATGGGAGG TGAGCATTGA TAAGGCGTAG	60
ATATCGTGGT TGTACGCAGG AGCGTGGATA GTAAGTGTG GTATGCTATT TGCATCGTGC	120
ACTTCAGGGG CGTGGAAGGC ATCAGTAGAT CCGTTGGGGG TTGTGGGATC TGGTGCAGAT	180
GTGTACCTGT ATTTCCCTGT AGCGGGGAAC GAGAATTTGA TTTCTCGTAT TATCGAGAAC	240
CATGAGTCAA AGGCAGATAT TAAAAAATA GTGGACAGGA CTACCGCGGT ATACGGTGCT	300
TTTTTTGCCC GATCAAAAGA GTTTCGTTTG TTCGGAAGCG GTTCGTATCC ATACGCCTTT	360
ACTAATTTGA TTTTTTCTCG ATCCGATGGC TGGGCATCTA CGAAAACGGA ACACGGAATC	420
ACGTACTATG AAAGTGAACA TACGGACGTT TCGATTCTCG CGCCGCATTT TTCTGTGTG	480
ATTTTGGTT CCTCCAAAAG GGAGCGGATG AGCAAAATGC TGTCTCGGCT CGTTAACCCC	540
GATCGACCGC AGTTACCGCC TCGCTTTGAA AAAGAATGTA CGTCGGAAGG TACGAGCCAG	600
ACTGTTGCAC TCTATATAAA AAACGGGGGA CACTTTATTA CCAAACTGTT GAATTTTCCG	660
CAGCTTAATT TACCACTTGG GGCAATGGAA CTGTACTTGA CCGCGCGGAG GAATGAGTAT	720

CTTTACACGT TGAGCTTGCA GCTGGGGAAT GCAAAGATAA ATT

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## (2) INFORMATION FOR SEQ ID NO: 98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

GGCCCCAATC CCATAAAATA CTCTGGTTGT GTTTGCTGCG TATGACGTGA TAGTCAGCTC	60
TTCCACCGTA AATGAGATCG CAAATACGGG GCGGGGTGCG ATATACAATG AGCATACAAG	120
GATCATGCAT TCGTATCGTA AACGGTACAG TTTGATCTGC GCTCGATTCTG AGTACGGACT	180
TTCTACTACT CACAACCTTC AAACCTACGGG AATCGCTTTT GTCGACAATT AAAAGTTGAT	240
ACATAACGGA GTGAAATACT TCACCAACCG ACAGTATAAC CCCATTGTGT TTTCTAGTTG	300
TGTGAGATTC AAATCCCAAG GATGGCACGG AACTGAGTAC GCGCCAATAC ACCTGcCTTA	360
ATCGTATAAA GCTTGCAGGT ACCACCACGT CGCTAAAAAC AAATACAAA AGCGCACTGC	420
ACAAACCAAT CGACAAAAGA GGAATATCA AAAACCGCGG CGAAACGCCC AGCACTTGCA	480
GCGCAAgcAG TTCAAGGTTG TTACGCAGCC GCCCCAACCC CAAGAGGGAA CCGAcCAACA	540
CGGCAAAAGG AGTAACGTAA ATCAACGCAG CGGGAATGGA ATACAGCAAC AGCCGACCA	600
CGTCCGCAGC GCTCACGTGC TTGGTAAGTA ATGTCTGCGC AAAAAGCAGT ACGTTGTTCA	660
CAAAAAAAC CAAGAAAAG CACAGCACGC CCACCAGGAT GTGTTTGAAC ACTACCTCGC	720
ACACGTACAC AAAAAGCACT CTTCTCCACA TCTAGGTAAC TACAGAACCC CTGTGGATCC	780
GTACCCTCCT TTTCCCCGTT CAGTCAGCGA GATACTACCG GAGCGCACAT ATTCAACACG	840
GAGCACAGAA GAAATCACCG CCTGCGCGAT ACGATCTCCA TGGGAGACTA CGAAAGCAGC	900
TAGCCCAAGG TTGACAAGCA ACACGCGTAT TTCCCCCGG TAGTcAGCGT CTATCGTTCC	960
CGGGGAATTT AAAACCGTCA CTCCGTATTG GAGTGCTAAC CCAGAGCGGG GACGAATTTG	1020
CATCTCCAAC CCCACAGGAA GCTCCACACA AACACCCGTG GGGACGAGAA CCCGGCCCAG	1080
GGGATGAACC TCAAGCGGTC CTCCGGGAAG AAAGGCCCGC AAATCGGCTC CACTTGAGCC	1140
TAACGTCTGG TACTCGGGAA AAGAAGCTCC CGGATACAG ACAGCTCGCA CACGGATCAT	1200
TTCGTCGTGT CCAGACCTCC AGACTTCCCC TCAAGAGCAT CGATATAGGA AAGATTCAAA	1260
CGACCCATCC TGTGATATC AATCAACTTC ACACATATCC GCTGACCCTC TTGCAGCACA	1320

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TCGCTGACTT	TGGACACGCG	GCTGCGCGAC	AGctTTGAAA	CGTGGCAGAG	TCCTTCCTTC	1380
CCTGGAAAGA	TCTCCACAAA	AGCACCGAAC	TCTACGATTC	GTTTCACTAC	ACCCTGATAC	1440
ACCCTCCCTA	CCCGAGGATC	TTCAGTAAGG	CCCACCACGG	CGACCTTTGC	GTCGAAAACG	1500
GACTGCGCAT	CCCTTCCGGA	GACGGTTACG	GTACCGTCAC	TATCAGTGTT	GATAGTCACC	1560
CGATACGGT	CAGAAAGCGA	CTTAACGGTT	TTCCCCCAG	GACCGATGAG	CGCGCCGATT	1620
TTTTCAACCG	CTATTTTAAA	ACTCTCAATA	TGCGGCGCAT	AGCGAGAAAT	GTGcACGCTC	1680
GGTGCCTGa	TTGTCTGATT	CATGACAGAA	AGAATATGGA	GCCTACCTAC	ACGAGCTTGC	1740
TGCAAAGCCT	CCTTCATCAG	AGACGCAGAC	ACCGCCTCTA	CCTTCACATC	CATCTGAAAA	1800
CCGTAATGC	CGTCACACGT	ACCTGCTACC	TTGAAATCCA	TATCACCGAG	ATGGTCCTCC	1860
TCACCCAAAA	kaTCCGAAAG	AATCGCATAT	CGCACGCCAT	CGGTGATGAG	CCCCATCGCG	1920
ATTCCCGCAA	CAGGCTTTT	GATTGGGACC	CCTGCATGGA	GAAGAGAAAG	CGTCCCTGAG	1980
CACACAGTCG	CCATGGAGGA	AGATCCATTC	GACTCCAAAA	TTTCTGAAAC	CACACGCACG	2040
GTGTAAGGAA	ACTGTTCTGG	ATCCGGAATG	ACTGCCGAGA	GGGAACGATG	CGCTAGACAC	2100
CCGTGCCCAA	TCTCCCTCCG	ACCAACCCCC	ATTCTCCCTA	TTTCCCCCAC	TGAAAAAGGA	2160
GGAAAATTAT	AGTGAAGGAT	AAAATTCTCC	CGTCTATCCC	CTTCGATGTC	GTCGTACACT	2220
TGCCCCTCCG	ACATAGCACC	GAGCGTGACC	ACCGCGAGCG	ATTGAGTCTC	CCCCCGGGTA	2280
AACACCGCAG	ACCCATGCGG	ACGCGGCAAC	ACCCCGACCT	CACAGGCGAT	GGGCCGAATG	2340
GCATCAATGG	CACGGCCATC	GATGCGCAAA	CCCCTGTCAA	GAATGTTTCA	CCGTAGTATC	2400
TCATACTCCA	TCTCGTGGAA	CAACGCGTCG	AACAACCTGC	GCTGCACATC	GTTCTCAAGC	2460
TGAGCAGCAT	ACTGCTGTGC	AACATCACGC	TTCAcCGCGT	CGCAGGCACT	GcgCCGCTCA	2520
CCCTTCCCCT	GTGCATACAA	AGCCTGCGCA	AGACGCGGAT	AGGCGAGCTC	ATAAATACGA	2580
TCGCGACCTA	CAAGcTGCGC	AGAAGAAGGG	ATAACCGTCT	GTTTCTCCTT	GCCACACAGT	2640
CCACGCAGAC	GCTCCTGCAT	ATCGCAAAGG	GCTTTAATAT	GCTCTTGTGC	CTGTTGAGC	2700
GCGCCGAGCA	TGAGGTCTCT	GGACACCTCT	CGCGCACCAC	CTTCCACCAT	GGTAATGCCC	2760
TGCCTAGTGC	CTGCAACGAC	AACCTCCATA	CTGGCGGCAT	CAATCTGAGA	AAAGGTAGGA	2820
TTAATAACAT	AGGAACCGTT	CAGATATGCA	ACGCGGACTG	CAGCAACCGG	TCCATGGAAG	2880
GGGATATCCG	AAAGAGTAAC	GGCAGCTGAA	CTGGCAACAA	TAGCCAAGAC	GTCATGAGGA	2940
TGGACCATAT	CCGACGATAT	GCACGTAGGG	ACAACGTGTA	TATCACGTCC	AAACTCCTTT	3000
TCAAAGAGCG	GCCGCATCGG	ACGATCAATG	AGGCGCGAAA	TGAGAATCTC	TCTGTCTTTC	3060

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GGACGGCCTT CACGCTTGAT GAAGCCGCCA GGCATCTTCC CCACCGCATA ATACTTTTCG	3120
TTGAAGTCAA CAGTGAGCGG GACATAGTCG AGCCCTTCCT GTCGCTGAGC AGAGGAGCAT	3180
ACGGTCGCGA GAATCGCCGT ACCTTCACAC TGTAATACA CGGACCCGTT CGCTTGCCGC	3240
GCCAGATACC CACTTTCAAG GAGAAGGGGG TGGTCCCCAA TAGTGCCGGT TATGCTGTGT	3300
TTCATACGTT TCCTAAGAAC AGAATGTATC GCAGGCCGCA CCAAGCCCTG GCACAGCCAC	3360
CTGCGAAGCT AGACAAAGAA AGCAGAACGG ACAACCGTCC TATGCACAAC CCCTCGGCGG	3420
CACGCACTGC GAAACTTCCC CATGCAAAGC CCCTACTTCC TCAAACCGAG GCTTTTGACA	3480
AGCGAACGAT ACGCCCCCAT ACTCACGCGC CGGGAATATC TCAACAGGCG ACGACGACGC	3540
CCCACCAGAA CGAGCAACCC CCGGTTGCTA CTTTTGTCTT CGGATGAACC TTACAGTGGT	3600
CAGTCAAcTG CCTAATCCTC TCAGTGAGAA GAGCGATCTG CACACTCGAA GATCCTGTAT	3660
CCTTTTCTCC TGAGCCGTAC TGCTGCACTA CCGAAGCAGT ACGTTCCCTT GTCAGTGCCA	3720
TTCTCCTTCT CCTTTCTTAC TCGAACTCGA TAGAGTCAAG CGCCTCCCGC CCATGCGACA	3780
GCGCCTCGGT ACCGAGCCTC AGCTGCACGA GAGAGGAACC CACACTAAGT GCGCACGCAG	3840
ACCCACCCCA CTCCCCTGTA CAAGGGTACC GCATACTCGC CCTCAGGTGG AAGCGTCTGA	3900
CTCACACGCC CACGCTCGGn GCACAACGTG CGGGCACACC CCyCGCTCTG CTGCCAGGGA	3960
ATTACCTCCC CGTCAAGCGA AAACGCACGC CCCAGCAGAC GCCGCGCGCT CTCAAAGTCT	4020
GCGCAGCGcA cckCACGGGT ACCGCGCTCG AACTCACCCG AACTCCCTCG AGAGTGTAGT	4080
GACCCACCGC GTCaGACAAA GCTATGCGCA TCACCAAGCC GACGCAGCTC ACGGACCCCG	4140
GTGTCCAGCC CATGTCCACA CCGAAAGTCG ACACCAACTG CGAGGTAGCA CACCCTCACT	4200
GCACGCAACA GGGTGTGAA GAAGACACCA CCCGGGATTC TAGCAAAATC CTTGGAAAAG	4260
TCAATGAGCA CGACGAAATC AAAGCCGCGC GCACGAAAAT AACGGAGTCG CAAACGCAGC	4320
GTTGACAGAT CCCCCTCGTA AGAAGAGGTT TTGTGCTTCC TGGGAGGATG AGTAAAGGTG	4380
ATCAGCCCGG TGCACCGCGC CCGATCGGCC ACAGGAGCGC ACGCAGCGGC AAACACCTTA	4440
TCGAAGAGAA AAGCATGTCC CCGTGAGGA CCGTCAAACC CCCCACCGA TATTGCTGCT	4500
CCCCGATCAC ACGCTATACA TGCACCCTCC TGCAACTGAG ACCAACGAAA AATGCGnCAC	4560
GCCTCACTCC GTACAAAATA CCGCCATCAT ACGAAAACCC ATTCGCCGCT TTCCTTATTA	4620
TCCAAGACAG CGACCCTCGG AAAACACCAA CGCACGTTCC CCGGGCTTCG CGTACCAAAC	4680
GACTGGAACC AACATGCGCG TATTCTTTCC CCATGCAAAA ACCGCGAACG CATACTGCGC	4740
ATGCACTGAA CACGCCGTAA GTCCAATACG ATTCGCAAAAG TCCACATCAC AGCTAACCAC	4800

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TGCCTGCTTA ATCTCACGCA CCGTCAAGTC TTCACACCCG AAAGAGACTG AATCGGTCGC 4860  
 CACGCCGCCT GAGGACGGAG GCGGTGGAGC ACCCACAATCA AAGCAAGCGG CACCGCAAGA 4920  
 CGCACGCTCT TTGCCCCATG TCCAGGACCC GAGACGAACA CACCCGCC 4968

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AGTTTCGCGC GGGCTAAAGT GGGTTGGTCG CGTGTGGGTG CCAGCGCGCT GTACTTGTCG 60  
 CGCGTTATTT CGTGCAATGA GCGTTCTAAG GTGGTTTAGC GCTTATGAAG GAGAATTCCTT 120  
 GCACGGCGTG CAGCAGACGG CTCGCCCTGT TCGTGGGCGC TGCGGTGCTT GTGGTAGGCT 180  
 GTTCATCCAA GACGGATGTC ACGCTCAACC GTGACAAGCC CCTAGTGTTT TTTAACCGAC 240  
 AGCCCTCTGA ATCCCTCAGG GGGAAGGTTG ACATGGCTGC CATGAACCTGG AACGACAAAA 300  
 CCTATTACGT GGGTTTGTGAC GCTAAGTTTG GTGGTTCTAT ACAGGGAAAG ATGATTCTAG 360  
 ACTTCCTCGC CTCTTCTGAG TCCTCGGTTG ACCGCAACGG TGACGGCATC ATCGGTTATG 420  
 TGCTTTGCAT CCGTGACGTC GGGCACAATG ATTCGAAAGT CCGCACCGAG GGTATTTCGCC 480  
 GCGCGTTGGG CACGTGGACC GGCTCCTCGG ATCCGGGACA GGCGAAAGAA GGCCAGGCAG 540  
 TGGTAGGAGG GAAATCCTAC AAGGTGGTGG AGCTCGAGGG AAAGGCGATG ACGGGAACCTG 600  
 ACGGTTCCAC TTGGAATACG AATTCTGCAA CCGAGTCAAT GGGAAGCTGG GTGGCAAAGT 660  
 TCGCGGATAA GATAGACCTG GTCATCTCAA ACAACGACGG GATGGCAATG GGCTGTCTGC 720  
 AGGCGTCCAA TTATCCGCGG GGGCTGCCTA TTTTCGGATA CGACGCAAAT GCGGACGCGG 780  
 TCGAGTCGGT TGGTAAGGGT GAGCTCACGG GGAAGTGTCTC TCAGAACGTC GACGCGCAGG 840  
 CTGTTGCAGT GTTGCAGATT ATCAGGAATT TGCTCGATGG CTCCAGCGGG GAAGATGTGG 900  
 TCGCCAACGG TATTTCAGA CCGTACGCCC ATGGCAACAA GATAAGCGCG CCCGTGCAGT 960  
 ACTGGGAGA TGTAAAGCG ATTATGCGG ATAACCTCGGA GGTCACGAGC GCMAACTGGA 1020  
 AAGAGTACAC CAGGGGAGCA CGGGATGCAG GGGTGCGACA GGTAAGTGCG CCGACGAAAA 1080  
 AAGTGCTGCT CACTGTCCAC AACGCGAGCA ATGATTTCTT TGCTTCTGCC TATCTTCCCC 1140  
 CACTGAAGCA TTACGCTCCG CTCCTGAATG TCGATCTCAC TGTCGTGCAG GGCGATGGCC 1200



AAAACGAGCT AAGTTGCCTT GATAAGTTCA CTAATCTCGA CATGTTGAC GCGTTCGCGG	1260
TaAACATGGT AAAAACGAAC TCGGGCGCTG ACTATACAGA CAAGCTCAAA TACTGAGCAG	1320
CCGGGTTTGG ACGTGCCTTG GGTAGCTGCT GTTCCTGGTG CACGTCCTGT TCGTTGAATA	1380
GGTAGGTCTT ACCGACCTCG CACCGCTTTC GCGCGCGAGA GGAGTGATAG TTGCGATGTG	1440
CGATGTACTC ACCATAAGGG ATCTTTCTAA GTCTTTTGCG AGGAACAGGG TTCTCAACGG	1500
GGTGAAC TTC CGTATGGGAA AGGGTGCCGT GGTGGGGCTT ATGGGAGAAA ATGGTGCGGG	1560
AAAATCCACG CttATGAAGT GCCTCTTTGG AATGTACGCT AAGGACACTG GTCAGATTCT	1620
CGTGGATGGA AGCCCGGTGG ACTTTCAGTC TCCCAAAGAA GCGCTAGAAA ACGGTGTCGC	1680
CATGGTCCAT CAGGAGCTCA ATCAATGCCT TGATCGCACT GTCATGGACA ATTTGTTTCT	1740
CGGCAGGTAC CCTGCCCCTT TCGGGATAGT TGACGAGAAA CGCATGTTTCG ACGACTCCCT	1800
CACTCTGTTC GCTTCCTTGA AAATGGACGT AAACCCGCGG GCCGTCATGC GCAGcATkTC	1860
TGTcTCTCAG CGGCAGATGG TAGAGATTGC CAAGGCGATG TCCTATAACG CGAAGATTAT	1920
AGTCCTCGAC GAGCCTACTT CCTCTCTCAC GGAGAGGGAG ATTGTCAGGC TCTTTGCCAT	1980
TATACGAGAC CTGAGCAAAA AAGGAGTGGC ATTCATCTAT ATCTCCCACA AAATGGATGA	2040
GATCTTTTCAG ATCTGCAGCG AGGTGATTGT GCTGCGGGAT GGTGTCCTCA CGCTCTCACA	2100
ATCCATAGGG GAAGTGGAAG TGAGCGACCT CATCACCGCT ATGGTCGGGC GCACTTTGGA	2160
CAAGCGCTTT CCCGACGCTG ACAATACCGT CCGTGACGAT TATCTTGAAA TACGAGGTCT	2220
TTCTACAAGG TATGctCCGC AGCTGCGGGA TATTTCCCTT TCTGTGAAAA GGGGCGAGAT	2280
TTTTGGCTTG TACGGGCTGG TCGGTGCGGG GAGGAGTGAA CTGCTTGAAG CGATTTTCGG	2340
CCTGCGTACC ATCGCAGACG GTGAGATCTC TTTAGCAGGA AAAAAAATTC GCTTGAAGAG	2400
CAGCAGGGAC GCAATGAAAC TCAATTTTCG CTTTGTGCCC GAGGAACGTA AGCTCAACGG	2460
AATGTTTCGA AAGGGGAGCA TAGAGTATAA CACCACGATT GCAAATCTCC CTGCGTATAA	2520
GCGTTACGGT CTACTCTCAA AGAAAAAGCT GCAGGAGGCA GCGGAGsGGG AAATAAAGGC	2580
CATGCGCGTG AAGTGCGTTT CTCCAAGCGA GCTTATCAGT GCGCTCAGCG GGGGTAATCA	2640
GCAGAAAGTC ATTATTGGAA AGTGGCTCGA ACGCGATCCC GACGTCCTCT TGCTTGATGA	2700
GCCGACCAGG GGGATCGACG TGGGTGCGAA ATATGAAATT TATCAGCTCA TCATTCTGAT	2760
GGCGCGTGAG GGAAAGACAA TCATTGTGGT TTCTAGTGAA ATGCCTGAAA TTCTTGGAAT	2820
CACCAACAGG ATCGCAGTCA TGTCCAATTA TCGATTGGCT GGGATTGTGG ATACAAAGAG	2880
TACCGATCAG GAAGCCTTGC TCAGACTTTC TGCGCGATAC CTGTAGGGAG GAGCAGATAC	2940

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ATGCGCGATC	GTACACAGTG	TGTGGCGGTG	CCAACTCAAG	CGTTCAATGA	GATTTTAGAT	3000
CAGGACGGTC	AGCTCACCGC	GTACGCCCAA	AGGCTCGAGC	AGTTACGAGA	GCGCGGTTCC	3060
CATAGGGTTG	CCTTGCTCCG	CGGGGAGCTT	GCGCGCATAC	GGCAGGATCA	GGTCTTGGGC	3120
ATGCCGGAGA	AAAGGGTGCA	GGTTGCGGCG	CACAGGCTCA	AGATTTCCGA	AGCGCAGGCC	3180
GTTCACGAC	AGTrmAAAAAC	TGAGGAAACG	CAgTTGGtTA	GGAArGsTGT	CGCGCGTGTA	3240
AgGGGGCTCt	TTCGAGACTT	TGACTGCTCT	GTGCGCGACG	CGATGCGCGA	ACAGCGGCTC	3300
TTGCTAAAGC	AAGTTGCGAC	GGTGCaGCAC	ACCTCTGCCT	CATCTGACCA	AAGAGAGCAC	3360
TGTCTGGCTC	AGCTCCGGCA	ATGcmAGGAG	GCGCGACACC	ACGCCTACCG	TTCTTGGTC	3420
GAAAGaGct	GCGCTGCGGA	ACGGGAAAAT	GaCGTTTATC	GAGCGCGTGG	TGCGTGCTCT	3480
TAGAGAATAT	TCGTTCAATT	TTGACGCAAC	CCAGTTCTTC	CTCGCAAATG	GTTTGTACAT	3540
TGCTATTGCG	GTATTCTTTA	TTGCGTGCAT	CGTAgtTGCA	CCTTTCTCTG	GTAATGGCAA	3600
TCTTCTTACC	ATTCCCAACA	TTCTCACCAT	ACTGGAGCAG	TCTTCAGTGC	GCATGTTCTA	3660
TGCGGTGGGA	GTAGCAGGTA	TTATCCTGCT	GGCAGGAACT	GACCTCAGCA	TTGGGCGTAT	3720
GGTGGCAATG	GGGTCTGTAG	TCACGGGTAT	TATTTCTTCAT	CCGGGACAGA	ATATCGTTAC	3780
ATTTTTTGGA	CTGGGGCCGT	GGGATTTTAC	CCCTGTCCCC	ATGGCTGTCC	GTGTAGTCAT	3840
GTCACTTGcA	GTTTCTGTG	CACTTTGCGT	TTCGTTCAGC	CTATTTGCAG	GATTCTTTTC	3900
TGCTCGCCTC	AAAATACACC	CTTTCATTTT	AACTCTTGCA	ACGCAGCTTA	TCATCTACGG	3960
GGTTTTGTTT	TTTGGGACAA	GTGGTACGCC	AGTTGGCTCT	ATTGACCCAT	ACATCAAAGA	4020
CCTATTCGGT	GGGCGGTGGA	TTCTAGGCAC	CATGCAGGGC	ACACTCGTGA	CCTTCCCAAA	4080
GCTGATAATT	CCTGCCACCA	TTGCGGTGGC	CATCGCGTGG	TTCATTTGGA	ACAAGACGAT	4140
TCTAGGAAAA	AATATGTACG	CCGTTGGAGG	GAATGCTGAG	GCAGCGAATG	TTAGCGGCAT	4200
CAGTGTTTTC	GGGGTGACTA	TGAGCGTTTT	TGCAATGGCA	GCTGTGTTTT	ATGGCTTTGG	4260
CGCGTTTTTT	GAGACGTTCA	AGGCAAATGC	AAGTGCGGGC	ACTGGTCAGG	GTTATGAGCT	4320
CGACGCAATT	GCCTCCTGTG	TGGTAGGGGG	TATCTCCTTC	AACGGGGGAA	TCGGAAAAC	4380
CGAGGGTGCC	GTGGTAGGCG	TAATCATTTT	CACCGGTCTT	ACCTATTGTC	TGACTTTTTT	4440
AGGCATCGAT	ACAAATCTTC	AGTTCGTGTT	CAAGGGTTTG	ATCATCATCG	CTGcAGTTGC	4500
ACTCGACAGT	GTGAAGTATC	TGAAACGCCG	CTAGTTCTTG	CCCcGCTGGG	CGGGAcGTCA	4560
ACGTTCACAA	TACGAATAAG	CCGGGCGCCT	TTCTGGGcCA	TTGTTCCCTC	TTTGGCTAAC	4620
TCAGGGTGTG	GGCTGACaG	AAGGCcTCCG	CTGTCCGAGC	TCTACCGTGC	TTCAGATGAG	4680

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CCcTTTtCTT TTCTCAGTAG TTCGAACGnc yTCGCGCGCA ACTTGGAGGA TAGGGTAATC 4740  
 TCTTACTGGA TCCGCAACCC GAAATCCACT GTACCCAGAT TGCTCAAAGT TCTTGGTATC 4800  
 TCCCACATCC CcTGGTCCTC GTAACCTCAG ATCCTCTTCG GCGATAACAA ATCCATCCGC 4860  
 aGTACTTCCC ATaATTTTCA GCCTGCGTTT CGCACACTCA GTCATTTTCGT CCCCATGCAT 4920  
 TAaGAAACAA TACGACTGCA CATCACCCCG ACCAACCCGA CCACGCAGTT GATGTAGTGC 4980  
 AGAGAGGCCA AAAACTCCGC gTGCTCTATA ACGATACAAT TCGCATTTGG TACATCCACT 5040  
 CCCACTTCAA CAACGCTTGT AGCAACCAAG ATATGGACGG TACCTTCGCT GAAATACTTC 5100  
 ATGATACGCT GCTGCTCTTC CTCAGTCATT TTTGAGTGAA TCATCGCAAC AGCATATCGT 5160  
 GCAAAATAAT TTTTtagata CATATACATA CATTGCACCG ATTTTAAATC GGTTAATCCT 5220  
 ATGTCATGAA TACGTGGATA AATAAAATAT GCCTGCCTAC CTTTTTCTAT TTCATTTCCC 5280  
 ACAAACTCAT ACACCTTTTC TGCTTTTCGTC TTTCTTGCAA TATACGTAAT CaCTGGTTTT 5340  
 CTTCCACCAG GCaTAGATTT AATTATTGAA ATATCTAAAT CACCAAATAC AGAAAGTGCa 5400  
 AGCGTACGTG GAATTGGAGT TGCGCTCATC ATAATAATGT GTGGAGTCTT TCCCTGAGGG 5460  
 TTCCCTTCCC TTCCTTTCTG AATCAAGGCC GAACGCTGTA ACACTCCAAA ACGATGCTGT 5520  
 TCGTCAATGA TAACCAACCT CAGATCATGG TATCTTACGC TCTTTGAAAA CAGCGCATGT 5580  
 GTTCTACAA CTAAATTGAT TTCTCCTGCA ACAAGAGCTT CGAGCAAGTA CGCCCTTCCT 5640  
 TCACTTTTCA CATTACCTGT CAGGAATGCA AGTCGAATCC CAATAGGAGC AAGTAATCGA 5700  
 GCTGCaGTGT CAGCATGCTG GCGTGCAAGT AATTCAGTTG GAGCAAGCAG TGCGACCTGT 5760  
 CCACCTTGTT CAATAATTTT TAAACAAGAA AAAAACGCCa CTAACGTTTT TCCTGATCCA 5820  
 ACGTCTCCCT GAATTAGCCG TGCCATCGGT TCTTCTCTTT CAAGATCCTG CGTAATTTCT 5880  
 GTAATTACTC TTTTCTGATC CACTGTCAAC TCAAATGGCA AACACCGGTG AAGTTTCTTC 5940  
 TGTAACAAAG ATAATTCAGA AACAACGAC GGAATAGCCG ACTGCTGATC AGATTCTCCC 6000  
 TGTGTAAGAG GCAATCTCCC CCGCTTCTGT AAAGAGCGCA TACCGATAGT CATTTGAAGA 6060  
 GAAAAAAATT CTTCAAATAT CAAAGA 6086

(2) INFORMATION FOR SEQ ID NO: 100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GCAGCGGCCG GTGTGGGCGC CCACCGGCGG GCGGTATGCG TCTTTGGACG GTGCGTTTAC	60
CGCGCTGGCA ATGATGCAAG TTTCTTTGAG GCAAATCCGG CAGGAAGTGC GAACATGACG	120
CACGGGrAGC TGGCTTTCTT CCATACCACT GGCTTTGGCT CGTTTCACGC CGAAACGCTC	180
TCTTACGTTG GCCAGTCGGG CAACTGGGGA TACGGCGCGT CGATGCGTAT GTTTTTCCTT	240
GAATCTGGGT TTGACTTTTC TACCACCACG GAGCCCGTGT GCACACCTGC TTCGAACCCC	300
ATTAAGCAGC GCGrGGCAAT TGGAATCATC AACTTTGCCC GCGGTATCGG AGGTCTCTCC	360
CTGGGAGCCA ACCTGAAGGC GGGGTTCGCG GACGCGCAGG GCCTGCAGCA CACCTCTGTC	420
TCCAGTGACA TCGGCTTGCA GTGGGTGGGG AACGTTGCCA AGTCCTTTAC CTCTGAAGAG	480
CCCAACCTGT ACATCGGGCT TCGGGCCACC AACTTGGGAT TGACCGTAAA GGTCTCGGAC	540
AAGATAGAGA ACTGCACGAG TACCTGTGAA AAGTGTGGTT GCTGCAAGGA GAGGTGCTGC	600
TGCAACGGCA AGAAGGCGTG CTGCAAGGAC TCGGACTGTA ACTGCCCCTG TCAGGACTGC	660
AACGACAAAG GTACGGTGCA CGCAACAGAC ACCATGCTGC GTGCAGGGTT TGCATACCGG	720
CCCTTCAGCT GGTTCTCTT TAGCCTTGGT GCCACCACCA GCATGAATGT GCAGACCTTG	780
GCTAGTAGTG ACGCCAAGTC GCTGTACCAG AACCTGGCTT ACAGCATAGG CGCCATGTTT	840
GATCCCTTCA GCTTCCTGAG CTTGAGTTG AGCTTCGCA TCAACCACAA GGCTAACATG	900
CGAGTGGGAG TGGGTGCAGA GCGCGCATT GCCCGCATT AGCTGAACGC GGGATACCGC	960
TGTGACGTCA GCGACATCAG CAGTGGGAGT GGGTGACAG GCGCGAAGGC TTCGCACTAC	1020
CTTTCCTTGG GTGGCGGAT ACTGCTCGGC CGAAATTAAT TCATAATATG CCGGGGCGCC	1080
CGCCGGTGCC CTGCTGAAGA ATGCGGaCGG cAAGACGTGG AGGGGGTTTT GCCGCTTTTT	1140
TGGTGCGGCG GCCGTGTGTG TCGGCTGCGC CAGTACCGT AGGAGGACGA TTGGTGTTCG	1200
GTTTTCACG CGTCGGTTCG CGCGGGCTCT GCTTGGGGC CCTCCTGCTC TCCCyTCGA	1260
TCgTGTGGC ACAGCACGTT GCTGACGCTC CTTTGGGCGC ACGCGGGGT GTTCCGCGCA	1320
GnTCCTTGCC TCGGCGCACG CGGGCGGCC GGGCTACGAC GCTGCGATCT CGGGGCGGCG	1380
TGGTCAGTTC CgCGGAGCG GGGGAACGCT CGTGGTCACC GCGCAGAAAC CGAAGGTCAT	1440
GGCACGAAAT GACGTGGACT ACCGTCCGCT CTCCCTGCAG GCCGGCGGCA GACAAGGCTC	1500
GTGGACCTT GTTGCCACgC AACGGCGGAT GACGCCAGCT TCTTTGAAGC GAACGCCGcA	1560
GGAAGCGCCA CCATAcCGCG CATGACGCTC GCCTTTTTC ACACCATGCG CATTTCGAC	1620
TCCCACATAG ACGTACTTTC CTTTGTGCGG CGGGCGGGC GCACCGGCTA CGGCGTTTCG	1680

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GCACGCGCCT	TTTACCCAGA	CATGTCCAGC	AAAACCACCG	GCTTCGTGGG	AATTTTAAAC	1740
GTATCGCACG	CTTTCTCTTC	CGCCTATCGC	TTTAAGGGCG	TGAGCGTGGG	CGCAAACCTT	1800
AAGGTGGGGT	ATCGCCACAC	CCGGGGGGGG	GGGTAGCAGC	CAGTCAAAGA	GCTCCAACGG	1860
GAAGGAGAAC	CACCACATAG	TCCTGACCGC	GGACGTAGGG	GTGCGCGGTG	CGTGGACGGT	1920
GTCTAAAAAC	TTTGGTGCGC	ATGAGCCAAA	CCTGTGGGCA	GGAGTAGCAT	TCCGCAACAT	1980
TGGCGCGTCA	ATCAACGCCA	CAAACCTTCA	CGGAAATAAC	GGCGCCGGAG	GCAGCGGCGG	2040
CGGTGGAGGG	GGCAATGGCG	ACGGGAAACC	TGCCCACGTC	ACGGACTCCC	GCGTTATCCT	2100
TGCGCTTGCG	TACCAGCCGG	TGCGGTATTT	TCTTTTGGC	GCCGGGCTTG	AGTGGCTCTA	2160
CAATGTGGGG	TCTATCAAAG	CCGTCAATTC	GCTCCGGTAT	GGGGCGGCGT	TCATGCTTTT	2220
TCCGCTCAGG	CAATTGGCAT	TCAGCTCGAG	CGTGGTTATG	AAGGGGATGG	GTCCACAGCA	2280
GGTCCGCGCG	AGCGCAGGGG	CAGAAGTGCA	GTTTTCTCAC	GTGCGGTGCA	CCGCCTCGTA	2340
TTCGTATCTT	TGGAGTGCGA	CACCCACACG	GCCsCACTAC	GTTTCAATTG	GGGTAGCCGG	2400
TTTTCTCAAA	CCGGTTCCCG	AACAACCCCT	GTGGCAAGAG	GTGTACCGCT	CCTATTTGCG	2460
CGGTGCGCCA	CTACCACGCG	CAgCTaCGCA	GAGGCCATCG	CCGAGTGGAA	GCGCACGCTG	2520
CAGCAGGGCG	TCAGTTTTGA	GCCTGCGCGG	GAAGGCATCG	AGCGCGCCAC	CAAGCTTTTG	2580
CAGCTGAACC	AAAAGGTTCA	CGATTTTAAAC	ATTTTCTAGC	CGCGCCGCCG	cGCAtCATCT	2640
GCTCCGTCCT	GTGCCACGCT	GCCGGCACCG	GCGGAAAGTG	GGGGCGGACC	CCTTACTCGA	2700
CCGTCACCGA	TTTTGCCAGG	TTCCGCGGCT	GGTCAATGTC	AGTCCCyTTG	AGCAGGGCAA	2760
TGTGGTATGC	CAACAGCTGC	AGCGGTACGG	CGTAAAAAAT	CGGCGCGGTA	AGGGGAGATA	2820
CCGAAGtACG	GTGACTATCT	GACTGCACGC	CCCTTCCGGC	GCGTCCGCCT	CGGGCGTGCA	2880
TACCGGGCCA	AAACGCTCCG	GCACGTCCGT	AAAGATGTAG	AGCATCCCGC	CGCGCGCGCG	2940
AACTTCCTCG	ATGTTTGAGG	CCATTTTTTC	AAACAGGACG	CCAGGTGACG	CCGGCGCGAT	3000
TGCAACCACC	GGCATCTGCG	CGTCCACTAA	TGCAAGGGGC	CCATGCTTTA	GCTCCCCCGC	3060
TGCGTATGCT	TCGGCATGGA	TGTACGAAAT	TTCTTTTACG	TTGAGCGCCG	ATTCAATTGC	3120
AATCGGATAC	AATTCCCCAC	GCCCCAAAAA	GAGCgCATGC	TGCGCATGCA	CAAAATGCCG	3180
CGCGCACCGc	GCAACGTCTG	CCTCACACTC	AAGCACGTGC	TCCACATCCT	GAGGCAGTCG	3240
CTGGAGCGCC	GCAGAGAGCG	CGTCCTCGGG	CTCtTGCGTG	AGTATCTTTT	TTGCCTGCGC	3300
AATCATGCGG	GTGAGCACGA	GCAAGCACAC	CAGCTGGGTG	GtAAAAGAtT	CGTTGAAGCA	3360
ACCCCTATTT	CTGACCCCGC	GTGGGTGAGC	AGCAtGCGTC	CGACTCACGC	ACCAACGTGG	3420

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AACGTGCCCC GTTGCAAATG GCAATCGCAC AGAGATACCC TTGCGTTTTT GCCAGGCGCA	3480
GTGCGGCAAT GGTGTCAGCC GTTCTCTCCG ACTGAGAAAT CGTCAGTACT ATTTCACGCG	3540
CGTGACGAC GCTCGTGCGA TAsGGTACTC TGAGGCAATC TCCACCTGAC ATCCCACCCC	3600
TGCAAATGCC TCAAACCAGT AACGCGCCAC TAACCTTGCA TGGTACGAGG TACCACACGC	3660
GATAATGCGC ACCCGTGTTA TCCGTCTAAA CAGCCGCTCA AACGTCTTAC ACGAGGTACC	3720
GTCCAAGACC CGGTCTCTCC CGAACGTCCG CACCTGTGCG CGAGAAGACG AAGAAAACGA	3780
CATATAGGCA TTCAGCGTAT GCCGTATAGC GTGTGGCTGC TGCCATATTT CTTGATGCaT	3840
ATGGTGACGG TCGGTACCCT TATCCTGCGT ACAAAGCTGC ATCTGATACG TAACAACAGG	3900
ACGCGCCACA ACGTTTCCCT GCGCGTCGTG GACGCACACG CTATCTCGGT GGACGTCTGC	3960
GATGTCTCCT TCCTCAAGAT ACAAAAAACG CTGCGTAACA TGCGCAAgcG CAAGsgGGTC	4020
TGACGTAACA AAATTTTCCC CACAGCCGAG TCCTACCGCC AACGGACTGC CAGAACGCGC	4080
AgCAATCAAC CGCCCAGGAG ATGCAGCGTC CATGCAAAGT AACCCGTAGt ACCCCGAACC	4140
TGCGTCAACA CTTTTTTTAC CGCAAGCAGG AGGTGCGCCG TGTACCGCAA CTCCCAGTGC	4200
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AGCATTTTAC GCAAAGACCG ATGGTTTTCA ACAATACCGT TGTGAACTAT CGCAACGGAT	4320
TCAGAACAAT GCGGATGCGC ATTGCTTGCA CACGCTTGC CGTGCGTTGC CCACCGGGTG	4380
TGCGCAATGC CCATGGTCCC GCAAAGAGGA CTCTGACCTA ATAGCGCGCA GAGCGACTGA	4440
ACACGACCCT CACAGCGTAA AAGGCGGAGc GCACAGTCCG AGCCAACGAC AGCGATCCCT	4500
GCAGAATCAT ACCCGCGGTA TTCAAGACGA CGCAGCCCCT CAAGCAAGAG ACCTGAGACA	4560
TCACGCCCCG CCACCATCCC AACGATTCCA CACATAGACG CCTTTTCAGT GCAAAAGCAC	4620
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CAACCAAGCC ACGAGCCGCC TCGCAGGCTA CGGTCCAGCG CACCAACAGG GAGACTCACC	4740
ACCTCCCCCA AGGGGAGACC CGACGAACGA GCAAGGTAAC CCACAGGTCA CAGGCGATCC	4800
CATGCCCATC CGTTGCCTTG CTGCACATCG CTCACTTTTT CGAAGCTGAA TCTGGGAGTA	4860
TTTCCTGTAA CTCTATCTCA AAAACTAGGA GCGCACCTGG AGGGATAACC CCCTCGATAC	4920
CACGCTCCCC ATACCCCAAG GAAGAAGGCA CATAAAACCG ATAGGTAGAA CCCACCGGCA	4980
TCAGCTTTAA GCCCTCAGAT ACCCCAGGCA CCATACCATC CACCGGAAAC TCCGCAGGCT	5040
TATCTCGAGA GGCATCAAAC ACCGTTCCAT CAAGCAGCGT CCCCTTGATC TGAGTGCGCA	5100
CCCTCTGAcC GCctGCGGCT TTGGACCATC TGCAGCCTTT ACCACCTCGT ACTGCAACCC	5160

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CTGCGCATCC	GCAAGTGCCT	GCTTATCCTT	GTCTGCACTG	ACTGTCTTCT	TTAGACCCTT	5340
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CCCAAAGGCA	TACCCACAC	TCTTCTTTGA	AAGCGGCGTC	TTCTGcCGCT	CCTGCTCCTG	5460
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CAGAACGCCT	TATATTCACT	TCAGGCGGGA	GCGAAGCAAA	TCAACTTGCC	CTCCTTTCTG	6000
TCCTTACTCG	TCTTCCTCAC	GCAGAAATCA	GCGTCAGTAT	GCTAGAGCAC	GCGTCGGTCA	6060
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TGTGCGTGAG	CGCCGTACAT	AGTGAAACCG	GCGCCATCCA	GCCGCTCCCT	GCTATTGCGC	6240
ACGTGCTTGC	ACATACAGGC	ACACGCGGAC	GCTCTATCCA	GCTCCACGTA	GACGCCGCAC	6300
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GCGCCTTCTT	CCGTACTCTA	CATACCACTC	CGGAAGGCCC	TACACCGCAT	ACGAAGCCCA	6660
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GCGATTTACC	GCGGGTGCAA	CTAGTCCCTG	CAACGCGCAA	AGAAGACGAA	GCGCACTTCT	6780
CTCCCTACAT	CGTCTGCTGT	GCGGTACAAG	ACGCCAGCGG	cGAGGCATTA	GTACGTGCAT	6840
TCTCAGACGC	AGGTGTGTGC	ATCTCCACCG	GTTCTGCCTG	CTCGACAAAG	AAAGGTGGCG	6900

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GACTCGGCTG	CCTGACTCAG	GAATATCGAG	GGTATCAGGA	CTTTCATGAA	ACGAAATTAT	8400
CTCTTCCTCA	AGGGGAAAAC	GGGGAACAAG	ACGGTTACGC	GTACGAGCGC	GCGCACCCCC	8460
GCTATCGGAA	AACGCACTAC	TTGAAAGAAC	TGCGCGGCGC	ACTTCTGCAG	GGCTCGGACA	8520
CACGCTGAAC	GGCTCACATC	CCCGCGCATG	ATCCGGAAct	AAGTCCGCAC	CCGTGTACGT	8580
AATCACGTCC	ATAACGGGCG	GTATCGGAAC	ATTTATTCCA	GCGGTGAGC	ATTTGCCTG	8640



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gTATGAAGTG	TATACTTCCT	TTTCCAAGTG	CTTGCCTCGG	TCTCGATTAA	AAAATCCTGC	9000
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GCCGTATCTG	AATCTATTGT	TGTCTGCAAA	TTCTTGACAG	TTGTACTTCC	ACTCAATCCC	9240
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TCACCCCTT	GCGAAGACCA	CGCGCCCAAA	GAAGCTGTCC	GCGCAAAAAG	CGGGGCAAGA	10080
CACAAGGCAG	ACATCCCAAT	ACGCATCCCC	AGAACCCGAA	CTGATAGAAA	gCTGCGGCAC	10140
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CGCGTAGAAA	CGTACGACAA	GCAACTGGAA	AAGAAGGAAC	GGGAGCTGCG	ACACAAGTAT	16920
CACACCATGG	ATGGCGCGCT	TCGTTCTCTA	CAAAAGCAGT	CTGACGCAAT	TCAGAACTTC	16980
AACCAGTCTG	TTCGCAACAG	GAATTAGTGG	GAGTCTTAAT	GGACATTACG	ATTAACGGAC	17040
ATACACTGCA	GTATGTCATT	GAACATGAAA	AACTATTGG	GGAGGTTCTA	GGCGCGATAG	17100
AAGCTGCGTG	TAAAAAAGAA	AAACAAACGG	TATCGGCGGT	GACGGTCAAT	GGTAGGGAAC	17160
TGTCTGCTAA	TGAATTGGAT	ACACTTTTTT	GCCAATCCTT	GGATACCGAC	GTCACCCTTA	17220
ATCTTACCAC	TCTTTTCAGG	GGAGACGTGC	GTGCACTCTT	GCGTGAGATT	AGTACCACTC	17280
TCCTTGCACG	CACAGCTGCG	TTACAAGAAA	TCGCAGTAAA	CATGCATAGC	GGTAATCTTG	17340

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CAGAgAgcTA	CGCTATGGTC	AGTGACTTTT	CTGCTCTCTT	GAAAAGTCCT	TATCACTGCT	17400
TTACTCTCTC	GGACATCGCT	GATTTGGATC	ATGGCCTGAG	AATTAAGGGA	AAAGCCCTGC	17460
ACGATTACCA	GCGCGAGATT	TCTCCCCTGC	TTAAGGGCTT	ACTAGAAGCA	ATGGAAGAAG	17520
GGGACAGCGT	TGCTGTCGGT	GATATTGCGG	AGTACGAGTT	GGCACCGGTT	GTTCCGGGATT	17580
TAAGTGACGG	TATCTTGTCAT	ATGGACATGG	GTGTACAATG	AAGTTTGACG	GA CTGATTCTG	17640
CAATCTCGAC	CACATTACGC	GAAAGGATAC	GTATCTCTAC	TACCGGGAGG	AGTTTTCTGC	17700
TGTTGCATGT	TACTCTCTCT	TCGGTCTGAAT	TCATTTCAGGA	AGGGTTGAGT	TTTCGGTAGA	17760
GACCaCTCCC	GTTGGGGAAA	AGAGCGTGCA	GGTAAAATTA	GTTGATGCAA	TTGATTATCC	17820
GCTCTTACCG	CTTGTACAAG	CACTCAAGCG	TGTAGTGAGA	CTGTTGATCG	AGAAGAATCA	17880
GTTGCCGCGT	TAGATCTTGT	CCAGTTTTTT	TAAAAACGGT	AGACTCGCCG	CGGTGAGGTG	17940
CGTCAGTCGC	TCAGCGCAGG	ATACTGCgCG	GtGGGGCACG	G TAGTCGGAA	GGCTGCTTGA	18000
GGAAGGTTCC	G TAGTAGTCT	TGCAGGGGGC	GTTAGCGGCA	GGGAAAACCT	GTTTTGTAAA	18060
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GGCAGTCTAC	CACGGcAGGc	tGACGCTCTA	TCATATGGAC	GTGTACCGGC	TCGCTTCCCT	18180
GGAAGACTTC	TTTGATATCG	GTGCGCAGGA	GTGCGTATAC	GGCACGGGAG	TCTGTGTCAT	18240
TGAATGGGGA	GAACGGGTCTG	CGTCAGAACT	GCCGGAGTAC	ACTGTTACCA	TCTCGTTGCG	18300
TGTGCTCGCA	GATGGTAACC	GAGAGATTAC	CGTAGCGTAs	CgCAGAGTGC	TTCTGTCTT	18360
GCAAAAAGGC	AAAGAGGGCG	GGGTGTATGA	ATATACTTGC	CATCAACACC	GTTGCGCATG	18420
CCCTCAACGT	TGCAGCTGAA	GGAGCACAAG	GCACCGCTGT	TGTGAGCATC	GAAGGTGCGC	18480
ATTGTTGCAT	ACAGCAACAG	CTCGTGCGTG	CGCTTGACGT	TGTCGTAAAA	CGCGCAGGAT	18540
TTCTGTACA	GGAAACACAA	ATCGTTGCCT	GTCCTCGGGG	GCCTGGTTCA	TTTACCGGCT	18600
TGCGTACCGG	TTTTGCAGTT	GCAAAAGCCC	TACAGCTGGG	TGTCGGAGCC	CGTTTTATTG	18660
CCGTGCCTAC	GCTGCGCcTT	GCGGCACATC	CGTTCCGCGC	GTTACAGGA	CGGGTGTGT	18720
CCATAcTAGa	TGCAAAACGT	GGTCGTTTTT	TTTGGAAC TG	CTTTAAGTCA	GGAGAGCCGC	18780
TCTTTGAAGA	CTCTCACAAC	CACGCACAAG	AAATCGTAAA	AAAAGTGGAC	ACACGGGTTC	18840
CATGCCTGGT	GTGCGGCACG	GGAACAGCAC	TTTTTAAAAG	TGTAATGGAA	AGCCAGGACA	18900
ACACGGTTCC	TTTCATGTAC	G TAGAACTG	ACGCTCATGA	AGGAGCAAAG	ACACTCCTTG	18960
CTTTGGTAAA	AGTGCTCAAT	CACAGCGCCG	CCACTCCGGG	GGAGCGCGGA	GCGCCGCA GT	19020
ACACAACACG	AACTTACGCA	AAAGGAAGCT	AATACTATGG	GCAATTCAGA	TATCTGTTCT	19080

GACATTAATG ATATCGAAGA ACTTCAATCT GAAGAAGGTG ATGCACCTAT ACGAGAAAAT 19140  
GCCAATCCAA TCAGAGAGGA TTACAATTTT ATACGTGAAC AAAACCCCAT TCTCGGCTCA 19200  
GGACTTGATC TTATCGGAAG TGCAAAACTG CCCATGCTCT TTTTAGACAG CAATCTGCTG 19260  
ATTGAATATA TCAGCGCCGA AGCGAATTCT CTTTTTAGAG GTTATTACCA TCTGGAGAGA 19320  
AAGCCGTTCT TTAATGTGTT TGGGAATATC CTCAGCCGTA AGGAACTTGA AGACTTTTTC 19380  
TCTTGTGTCC GATCTCACTC TAAAGGATTT ACCTGGAGAG GCACGATGGC CCATAAAATT 19440  
CGTGCAAAAA GAGCGCTATA CACGCGCACA AGTTTTATCC CGCTTTCCAT CAGCGACGCC 19500  
CAACCTTCTG GATATATCGT TCTTTTCGAA GACATTTTCTG ATATGTACTC GCAGCAGATC 19560  
AGTAATATGC TGAGTAGTTT GCTACAAGCG TCAAAGCTTA AAGACAATGA AACAGGGTTG 19620  
CACTGCGAGC GCGTTAATCA CTATTGCAGA CTCATTGCAG AATACCTGTA TGACATCAAC 19680  
TTATACCCCC AAGTCGATAC GGACTTTGTA GAGAATATCG CCTTCTTGC AGCTATGCAC 19740  
GACGTGGGGA AAATTGGTAT TCCCGACTAC GTTTTGAAAA AACGTGGTGG ATTAAACGAA 19800  
TTAGAGTGGG AGCTCATGAA GGAGCATACT ATCAACGGTG CGCTCATTCT TTCTTCTTAC 19860  
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TACCCCTTCA AATTGGAAGG AGAGATGATA CCGCTTTCTG CACGTATTAC GAGCATCGCC 19980  
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ACTACACACA TGATTTTAGA ACAGTCTGGA CAAAGCTTTG aCCCCATTTT GGCACGTGTA 20100  
TTTCAGAAAA TACATACAAA GTTCAACGAC GTGTGGGACA gCTACAGGAC TGAGCATCCT 20160  
CAATCCTAGT CAGAGATAAG GTTTTCTTCG GTGTCAAATT GCTGCAAGGA GCTCATAACCA 20220  
GTTTCTGTCT GCATGCGGGA AATGAGAGCA AACAGGTACC GTGCGGTGTA AGCGCTCAGG 20280  
GTGTATGCGT GCACGCTCTG TGCATCCCAC AGAGTCCACT CTGGTGAGC AGCAGGCTGA 20340  
AGACGAAACC GTATAATCTT TCCGTCTCCC CGGTGAATGA CAATTGATTC TTTCCATTGA 20400  
GTCGGTGTAG GTCCAACATC AACATAAGAG AAACGTGCGA AAAACTGCTC GACCTCTTTA 20460  
AACACTACAG ACGTCCGACT CCTCACGATG TATTTCCCTG AAACCTCCAT CATTTGTATC 20520  
TGCGATTGTG TGAAGAGTTC ATGGAAGTGC CGCGTATCAC ACCAAAACCG CTTTTCATCT 20580  
CTGAAAAAAG GGGTAAAATC ATCCTCTGTC AAAAAACAG CTGCGTTATC TCCAATTCTGA 20640  
ATATAACGCC CAAGTCCTGT ACCGTTCAAC GCACCAAAGT ATATGTCGCC TATAGCAGCG 20700  
CCATTTTTTT TTGTAACTT CATCTGCACT GCAGGTTGTT TTCCGAGAGC ATAGTCT 20757

(2) INFORMATION FOR SEQ ID NO: 101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AGGAAGGAGA GGATTTTATC GTACGCGGTT TTCTCGATAG CGGATAGATT ACGATAATCT	60
TGCACGTCAC TGCTCATGTT GATTTCTTCG GGGATCCAGA AGTTGTTcAT TGCctGCCGA	120
TACCACTTGC TGACCCAGGG ATACTTCATA TTGTTaAAGT CGTTGAGATT GGTAGTGTTC	180
CCCCGACCA TCGTCGCTT ATGAAGTTCA ATGTCTCCTG CctCATTAAG CAGCGCGCGT	240
CTTTGCAGTA TCGTTGAACT TTCCATCATG ATGAAACCTC CTCCTGAGTG CGGGCACAGG	300
GTAGTATACT TGATGGACTT TGAATTCTCA ATTGCGGCGG GCGTAAAAAT GTCTGTCTGC	360
AGGGCTCTGT GTCTTGTGTG GTGGTCCCTG TTTTGTGGGT AGGTTTGGGG AAACCTAACA	420
GAGACGTAGG AAATCCGTTA TGCTCGAGCA CATGAAGCGT GAACAAGCAC GAAGTCAGCT	480
ATCACACGAG CCTCCTAAGC GGCGCCGAGC CTCTCTAACC GTCTGCGGCC TCGGTGCTGT	540
GGAAACGCTT GGCAGCATAC ATCCAGAGAA AATTCATCGG TTC'TTTTTTA CCCCTGTGCG	600
TGCGAAACGC TTCGGACCCC TGTGTGCATA CCTTGCTGCA CGAAAGAGGC TCTACCGTAG	660
CGCTAATACG CAGGAACCTG AGCGATTGAC GCAATCCGTT CACCATCAGG GGGTTGCTGC	720
TACCATAGAC GAGCCGCGCT TTCCAGCCGT GACTCATCTT CAGGTTGAAT TTTGGGTACA	780
ACGGCGTGAG TTTGTTGTGT TACTCGATCG CGTAGGAGAT GCCACAATC TGGGGGCGAT	840
TATACGTAGT GCTGCTTTTT TTGGAGTGCA CTCACTGGTG GTGAGTGAAT GTCGACAGCA	900
GGCGCAGTTA CAAGCGCAAC ATATCGGGTT GCGCAGGGAG GAATGGAGTT TGTGCAATTG	960
TTGCGCTGTA CAAATGCGCA GGAAGTATTG GAAATGTGTG CAGGTAAAAT GACCCGTGTG	1020
GGAGCCTCCC CTCATGCGTT CAGATCGCTT ACACGGCTTT CAAACATACT CTCGCCTGAA	1080
GAAGCGGTAA TATTAGTACT GGGAAACGAG GAGACAGGGC TTTCTGAGCA TTTGACTGCG	1140
CATTGCGATC ATCTCTGTG GATTGCAGGC AGTGGTCAGG TGGAAGTCT AAATGTTGCG	1200
CAAGCGGGTG CGCTTTTTTT GTCCACTATC GTACAGTTGC GTCAATCTCC TCAGGACTAC	1260
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GAGGAAAAGG GGCAGAAAAA TGGAGCACGT GTTCTTATTC CCCGCTCGGG GgCGGTGCC	1380
AATTCCTGTA AAAGTTGAGA GTAGGGAAAG TAGACGGGTG TGAGGTATGG AACCTACAGC	1440



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GCAATTGGTT TTGCAGTCCG TGTGACGTG CGTCCGCGTG TGCCTCTGAG AACGCAGCCT	1500
GCTCTGTTGT CGCGTAGGAA AACTTGTAAG GAGCTTGCAC AAAGCGTCTT TTTTMTTTTAC	1560
CCTCGACCCC GTTCGCCTGA ATTCATCACG TAGGAGTTGC CCGCATGAAT CAGATCCGCC	1620
TGTTTGCCCA GAGTGCCTT GTGAGCGTCA TGGGTATGGG GATGGTTTTT GCCTTCCTCC	1680
TTTGTCTCAT ATGCGTTGTG CGCTGTGTGG GCGCGCTTGT CTCTTCTTTC GGCTGGGATC	1740
GCGGTCTGA CGAAGGTGTC GCGCTGCAG TCCCTGCAGG AGGAGCACTC GCCGCGGCTA	1800
TCGCAGTCGC CGTTCATGAG AAGGCAAGGA GTACTTCATG AGTACCCCGG TTCGCATTAG	1860
CGAAATGGTC CTACGTGATG CGCATCAGTC TTTGcAcgt ACGCGCATGA CTACCGAAGA	1920
CATGCTCCCT ATTTGTGACA AGCTAGATCG CGTTGGGTAT TGGAGTTTGG AGGCGTGGGG	1980
AGGCGCCACG TACGACGCCT GCATTCGCTT TCTAAATGAG GATCCCTGGG AGCGTTTGCG	2040
TGCTCTCAAA TCTCGGTTAC CTAAGACCCC TATTATGATG CTTTTCGCTG GGCAAAACTT	2100
GCTAGGCTAC CGGCATTACG CGGATGACGT TGTAGATGCG TTCGTAGAGG CCGCTGCACG	2160
CAACGCGCTT GATGTGTTCC sCATCTTCGA TGCACCTAAT GACCCACGTA ACCTCAGTCC	2220
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CACACCCTAT CATACCGCAG AGAAGTACGT AGAGTTAGCA AAGGAGTATG CGCGCTTCGG	2340
TGCGGATTCT ATTTGCATTA AGGATATGTC GGGGTGTGCTG AcCCCGTACG GGGCGTACGA	2400
TCTGTTTCTT GCCATTAAAA AGAGTGTCGA TTTGCCCGTT GAGTTGCACA CCCACGCCAC	2460
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CAGAAGGACT GCGGTTATAT CCCGCTTGTG ACTCCTACGA GTCAGATTGT AGGTACGCAG	2880
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CTCACGGGTC AGTATGGCCG GACTCCCGCC TCCTGTGATG CAGGTTTGGT GGAGCGGGCC	3000
TTGAAGGAAG AAAAGTTATC GCAGTCGCTT GTCTGCCGCC CAGCGGATGC CTTGCCTCAT	3060
GAGCTTGATC GCATGAGGTC TGAGGCcgCs CCGCAGGCCG ACAGGATACC ATTGAGGATG	3120
TGCTCACGTA TGCTATGTTT CCCAAGATCG CTCCACATT CTTTGCTTCC CGTGCGCAAG	3180

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GGCCTATTTC GTTCAGAGGA AAGGGGCAGG GGCAAAAACA GAAGGGTGAG AGTGCAGGGT	3240
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CTGTTCTCCG GGTAATGGT ACTCCCTACA CCGTTAGGgT TGAGGCAGGC CCGTCCGTTG	3360
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GGGGGAGACG GTGCTCATGG TGGAGTCCAT GAAGATGGAA CTTGAAGTGA AGGCCACCGC	3540
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GCTTTGGTTT TTGATGGTGA CAGGAACAAC AGCACATATT TCCTCGTATA GTCTTATAGT	6720
GACGTGATAG TTCCCCACAC ATTTTCAGAGT AAGACCAGGG ACCTCCACAC GcTTGCGCTC	6780
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TTCTCGTGCG TCATTGTGTA GAGAAGGAAG CGTGGTGATG GTGCACCGAC CAAGAGAGAA	9660
AAACTTGCG GATAAAATCG ATTCACTTGT GCGGACCGAT CAGCGTGTGT ACGGGCGCTC	9720
GGTAGTTGAT TTTTACCGCA GGATAAAGCC GGTCTTGCGT AGAACTGAAA CCCGTTGTAG	9780
GATCTTGcTg TTTTGTGCG AGGGGATGCA GAGGGTGCTg AGAGCGACAC GCCGTACTTC	9840
GTTaAAGGTA TACAGCGCCC TGTTcCACT CTCTCCGATC GCGACCGGg CGCTGCTAAA	9900
CAGGCGGGGc AATGCATACC TGAATGAgGG GAAGCTGCAG GAAGCGGCAC GCGTTTTCAT	9960
TACCACTGGT TACCACGATG GATTGACCAG GATTGGCGAT GTGTATATGC GCAAGGCGGA	10020
CGTGTGaCC GCACTGCGgT TTTATTATTT TGCTCGCAAT GAGCAGAAAA TGAGGCCCAT	10080
CGTTTCAGCG CTCTCAGTGT TGATTGATG TCTTATATAA TTTTGACGCC GGGGGGGGGT	10140

ATGGGGCTTA	TGGGGTGCGA	GTGTAGTGTT	CCGCCTTTTG	AAACGGTTGA	AACGGGCAAA	10200
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GTCAATGACC	TTGAGAGGGC	AGAGAGCGAG	TTCGGTAAAA	TTCTCCAAAT	TGAAGCGGAT	10320
AACAACATATG	CCCTCGTGGG	GCTCGGGGAT	GCGGCGCGCA	AGAGACGCGC	GTACCAAGAG	10380
GCATCTGACT	ATTACACGAG	GTGCTTACAG	CATTACCCTC	GCAACAGCTA	TGCGCTCTTT	10440
GGTCTTGCGG	ACTGTTATAA	AAACATGCGT	CGGTACGTGA	AGGCAGTGA	AGTGTGGCAG	10500
CAGTACCTGG	AGCAGGATAG	CCACAACATT	GCGGTGCTTA	CGCGCATGGC	CGATGCTTAC	10560
CGTAAAATAC	ATGATTTTCA	AAACTCGAGA	AACCTTTACT	CCCAGGTTAT	CGCCCTGGAT	10620
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CGTGAAGCAC	TCATCTACTG	GA AAAAGCTC	CTGGAGTGTG	CAGAACACAG	TGTGGATATC	10740
CGTGACTCA	CCTCTATCGG	GAATTGTTAT	CGTAAAATGA	AACTCTTTAG	TCAGGGATTG	10800
CCCTATTTTC	AGGAAGCGCT	GAAGCGTGAC	CCAGGTAATT	TTTATGGATT	TTTTGGGATG	10860
GCTGACTGCT	ACCGCGGCAT	GAACATGCAG	GAGCGTTCCA	TCCAGTACTG	GGAGAAGATT	10920
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ATTGGGGAAT	ACGAAAAGGC	CCATCAAACG	TATAAAAGGG	CGTTGGATAT	CGATTACGAT	11040
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TGTCAAACAG	GCCAGTTGGG	TTTCGCGCGA	AACCTTTCTG	CCTCAGAGAT	CGTCGAGCAG	11880

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GCAGCACGGG	GATACCGCGT	ACCTTCATAG	AAAAAGCGTC	GGCGCAAACA	GAAGGTGTAG	12960
AATGCTCGCT	GCGAGAGAAA	ACAATCCCCa	AGGGTTTGGC	ATACTGCACC	AGCGTGCGCG	13020
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TACCGCCGGC	AAGGGTGGGT	ATGAGATCCC	CAAGCACGGG	AAGTTGGGCA	CCGATAGGAT	13140
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ACCCCGTGG	GACCGACACA	TAAGAACTG	CCAAGAGGAC	GGCGCGTATC	AGAAAGTCCT	14220
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(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5420 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

ATCTTTTCTG CACAAAAGTT ATAAAAAGAT TTGATAAAGC TTTTCGATTTC CTCCATCGGT	60
TTTGAGCnCG CACGCCAAAT GCGAGAAAAG TCCTTCATCC TTAAAAGnTT GCGCnTTCAC	120
ATTGGGGAAA AAACGCGGCC ATACGCGGCC GCACATCGGT AAAACGCCAG GGAAACTCTC	180
CACCAAACAC TTTGGCCAAC TGCCTGCGCA CCACCTGCTC ATCCCATACG AAAACTTCCT	240
GACCTCCAG GAAGGCACCA AGACGCGTAT GAGATGGCAG GAGCATACGT GGGACCACCG	300
TTTCCGAAAG ACGGTCCACC ACCTCCATAT TACACATTTT TACAGCCTcA ATCGTATACG	360
CCCCaGTCAC CGGACGAACG TGTAAGCA CCACAGGCCG CTGATACCAG CCGCTGGTAC	420
TGAAACGGAG CGCCGTtACC ACCTTCCACG CAGTTGCACA GCCTGAGAGA AACTCGTGCG	480
GATACCTGC ACCTGGCACT TTTGCATTAA TGATAATTGC ATCAGGGAGT GTCTCAGGGG	540
CCGCATGGTG ATCAATAACC AGTACGTCAA TACCTCTGTG ACGCGCATAC GCAATTTCTG	600
CGCGATTAGA AATACCGCAG TCAACGGTCA CAATGAGAGT ACCCCCTGCG GCCGCATGCT	660
CATCTACTGC ATTGCACGAG AGCCCATAGG GCTCATCGGC AACCAGGCAG CGCCAGCACA	720
CCGTCAAGCC AAATGCACAG AGAGCCTCAA AAAGAAGGGT GGTGGCGCTA ATACCGTCTG	780
CATCACGATC ACCAAAGATG AGCACCTTTT CTTTCCGCTC ATGCGCAAGA CGCAAACGGT	840
CAACTGCAGC GCTCATCGCA TGGAAACGGA AcGGTcCTGG CAGATAGCGT AGATCACGCT	900
CAAAATGAAA AAGGAGTGCG TCAGcATnCC ACTACCTTGC GACGCACAAG GATGGCCGCC	960
TCAAGCGCCG AGCAGCTATA CCGCGCGGTA AGCTCGCGGA CACGCCCTTC GTCAAGTGCC	1020
TTTGCACGCC ACCGTTTCAT GCGTA <sub>s</sub> CCTT CCTCCGAGAG AGTACCACCC GACGCAAGAG	1080
GACCCGCCAG AACGGCCACA CGCACCACAC ACGCGCCCCG GTGCcGCGAC GCTTTCCGTC	1140
GGCGAAgcaT CtTCCTCTAA AGAGACTGCC CAATCTTTCT TACGGACCGG TATCCAGACT	1200
CTGCACACCA CGAGCAGGAT CGTCCTGCAC GTCTTCTGAC TCCTCCTCTG GAGCGTCACG	1260
CGACGGGTCG GATGCAGACG GCACAGGCAC ATGCGGCGCA TCAAAAAGCG GCGCTTCCTG	1320
CGGATGCACC GGCGCAAAAG GATTGCTCGG GACAAGCACC TCCCCTGCA CGCCCGGTGA	1380
ACCCAGTGGC GGATCTTCAA AGACGCGCGG GTCTATATGC AGCCCTTCTT CGsTcACTGC	1440
CGGCCAGAAC CCAgTGCTGT ATCCA <sub>c</sub> TTTC CTTCAACCGT TCTTTAGCCA GTTCCTCAAG	1500

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CATCTTCCCA CTTTCATGGT ACGAACAAAA GCGCTCAGGC AmCGTGcCAr GCAAAAATGA	1560
CAGAGAAACA AGCTCATCCC CACAGTACGG GGTAGGCAGC AATCCTGATT TTGCACACAC	1620
CGCCTGGTAC ATCAACCCTG TTTCAGGACG AACAAATGCC CGGTGCGGCT TATCCTGATG	1680
AATAGCCCGC ATAAAAACGC CCCACGGAGG ACCTGCAAGC GTCGCGCCCG TGCTATGCAA	1740
TCCGAGCGAT CGGTCTCCTT TGTCAAAGCC AAACCACAAC ACTGCAGTGT AATAAGGAGA	1800
GTATCCAACC GCCCACGCAT CAGACCAGTT TTGCGTAGTC CCCGTCTTCC CCGCAACCGG	1860
CATAACAAAC GATCGCcCCG TTGCAGGGTC TTGGTATGTA AATGCGCGCC CCCGCTCAGA	1920
GGCCACCGCC AACGTCCCCA TCGTTACCGT TTTCTCTAGC ATATTCTGTC TGAGCGCCGC	1980
GTTCTCCGCA GAGATCAGTT GCGTTGCCGC ACCcTGCGCG CGCAGgCGGG CCCGCACTTC	2040
CCGTCTTGGA TCCAAAATCA CCCGCCCTAA ACGATCCTCC ACTGAACGCA CTGCAATCGG	2100
TTCTACCGCT TTGCCCCCAT TTCCAAACGC TGCAAATGCA CGCGCAAGCT GAATCGGCCG	2160
GAGGGCAACT ACGCCCAACG CAAGCGGATA GACGCGTGGG AAGGTGCGCT CAATCTCCTG	2220
CCGATCGGTT ATATGCAGGA GCGTCGCCGC ACGCTGGATT ACCGCGTCGA AACCGACCAT	2280
ATCCAGTACA CGAATAGCAG GAATATTGAG CGACTGCGCA AGcGCCTTCC ATGCAAGCAC	2340
TACCCCTGC CATTTTCCCC CATAGTTGTT GGGAAATATAC GAAACACCAT TGCGGCTGaA	2400
mACCTGCGGT GCATcGTGcA AtGCGTTGCC ATCGTGAGCT TTTTGCTATC CAACGCCGCA	2460
GAATACACCA GAGGCTTAAA TACACTGCCT GGCTGCAACA ATCCTTGCGT TGCACGAATC	2520
ACTTGGTAG AAGCACCAGAA TCTGCTGCCC CCTACGAGAG CTGTAATGTA TCCGGTATCG	2580
TTCTCAAGCG CGATGAGCGC ACCTTCCACC CGCTTACGTG CAATTTCTGTC GCGCACCAGA	2640
GAGGCGCCTT TGTCAGACAA CGTTTTAAGA TTGTCGAGGC CGAACATCAG CGCCATAACA	2700
TTCAACAGGG GACTGAGCGT ACTGCGGTAA TaCGCGCCGC TTTTGCCTT CATGCGCCGG	2760
TCACCGACGT GCAACTGCGG AACGTTGAAC ACCAACCCCA ATAGCTCGCT GATATTGCTG	2820
TACAGTTCTC TGCGCGCAAC GTGTGTGAGA GAAGATTTTT GCACGTGTGC ATTGGCCTGC	2880
TCCAGCGTTT GCTCAACTTG CTGCTCTGCA ACCAACTGAT GACGCAAATC GCACGTGGTA	2940
TGCACGGTAT ACCCGTCTTG GTACAAATTC ATCGTGCCGT ACATCATGCG GTCCAGCTGC	3000
CTCCGCACAT ACTCGGAAAA CCAACGCGCC TTATCCGCAC GGGCATAGAA CGCAGAACTT	3060
GTGGTGCGAG TGTAATCGAA ATGCGCCCAG TAGTGCTCGT AGGACTCATC CCGTTCTTGT	3120
TCACTGAGAT AGCCAAGgCG CGTCATTTCA TGGAGTACGT AACGCTGACG GTCTTGAGCG	3180
CGGTTAGGAT ATTCAAAGGG ATTGTAGTGT GCCGGGTTAG AAAGCAAAAT AACCAAGAGC	3240

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GCCGCCTCTG CTGCGCTCAT CTGACGTACC GAATGGCCAA AGTAGAAGCG GGCAGCCGCT	3300
CCTACGCCGT AGTGCCGCCA CCGAAGTAGA CGCGGTTCAT ATACAACTCC ATAATTTCGT	3360
TCTTGGAATA ACGCCGCTCC ATATGGAGTG CCCACCACAA CTCTTTGATC TTACGCCTGA	3420
GACTGCGGTC GCTGCGGTCT GAATAGAGAA GACCTGCTAT CTGCTGGGTC AGCGTACTCC	3480
CGCCCCCTAA GCGCGGACCG GTGAGGGTGC CGACAAGGC ACGGAAAATA GCCTTGATGC	3540
TGTAGCCGTG GTGGGTATAG AAGGAGCGGT CTTGCGGGT GAGTAGAGCG TGCACAAGGT	3600
GTGAAGACAA GTCAGCAAAG GAAACGATTT CGCGCTTTTC GTCTGAGGAA AACTCAGTGA	3660
TCAAATCACC CCGAATGTCC AGGATTCTGG TGGGAAGCGC CGGATTAAAG CGGGTGAACC	3720
GTTGCTCTG CTTAATGTTT TCAATGGAGG CAAGCAAGAA CCCAAAGAGC GCAGCTCCCC	3780
CCACCAACAG ACCGCACAGC AACACCAGAT ACAGGTAACA AACGCGACGC ATGGGCCAAG	3840
AGCGGAACAC AAAAAGGCGA AAACCTCAAG GCAAGAGGCA GAAGACCGTC AACGGCGCAC	3900
ACCGCACGAT GCACTCAGGC AGACACACAA AAAGGCCGGC TTTCTCAAAC CGGCCCCACT	3960
ACGTACCGAC CGCGCGATAG GTGGGAGGGG AACCACGCAG CCGGCGCCCC CAGTATCGGT	4020
TCTACCTGCA AAACCTTGAG CCTGGTGCGA ACCCCACGCC CAACGGTAGT GCCACAGAGA	4080
GGAGGAGCGC GTCGACACCT CACCTGTCGG CGCCCCGACC GTCACGTATC AGCGGAACCT	4140
TTCCATGAAT CGCTCAGGAT TTTGGGGTAC CCCCCTTCC CGTACCTCAA AATGCAAGTG	4200
TGGCCCGGTC GATGCGCCTG TCGATCCCAC ATTGCCGATC ACCGCTCCCA CACTCAGTTT	4260
TTGCTGTACA CGGACGCGCA CTGCACTCAA ATGTCCGTAT AAGCTGTGCC TTCCGTCTGT	4320
GTGCTGCAAA ATCAGTACT TGCCATACAG ACGATTGTAC GCAATCGTCG CCACCTGTCC	4380
GCTCGCACAC GCATACACCA GCGCGCCCAT GGGAGCGGCA AGATCTATAC CTGGATGATA	4440
ACTCAGCCgC CCGGTGAACG GGCTTTTGCG TGCGCCAAAC CCTGAGGTGA GTCTTCCGGA	4500
TGCCAACGGA AAACGATAAA ACGGCTTAAG AAAGAAGGCA CGCACCGTTC CGTCAAACAA	4560
GGCCTGAGGC GCGCACACTA CCTCCCGCTT TTCTCGCGTA TGcgTTGTCT GCGCAGTCCC	4620
CGGAAGGGAA AGAAAAAAG ACGGCCCTTG ACCCTTTTTT ATCAGTGCGT AAATGAGCCG	4680
CTCAAAGGGA AGGTGCGGAT CCGCAGAAAC GTACAGTCCC GGAACGnTTG GCAAAAGCAA	4740
CGTACGCCCC TCAAGGGGGG TATGCAGCGT CTCAATACGG TTCAAACCTAG CCACCGCGTC	4800
ATAGGGAATA CCGCAGCGCG CGGCGATACG GATGATGGTG TCTGCCTTTT TTACGCGATA	4860
TGCATAAAAA CGCAAGGGTA AATCGTTTCC CCGCTTGCC TCGGCCAATG CCaCGCgCGC	4920
aGCAcGtCAT CGCTATACTG ACGAAAGAGC GCATCCTGCC CTTGCAGcTG CGCTATCAAC	4980

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GGATAGGGAC CGCACACCGC AGGATGTGCC ACACACACAC ATAGGCAGGA GCACACgcTG	5040
CGCGCACCAT CCGCACGCGC AGGAGAAAGG AGAACGGAGA AAATGGGCAC AGACGCATCA	5100
CACGCAGCCG CTTAGCACTC CTGCGCGGGG CGAACTTCCG CGGAGGAAGA GAGCCCCATA	5160
GCACCGACTT CCCCTGCTTG CACTAAAACG CATGGCTCCT GCGCGCGGGC CCTACGcCCT	5220
GCACGTGCA CCCGTGCATA AGAAAGArCG TTGCACACGC GTcTCAGTCC CCACAGGACC	5280
GCACCGCCGC CATAGAGCAA ACCGCTCAAC ACCGAGAAAA CACGCGGACG ATGCACCGCC	5340
AACGCCCAGA GAGGGTAGAC GAGCGCGCAG CCGAGCGCAA ACGAAAGTAT CAGCAAGCAT	5400
CGCAGCGAGT GCTCCAATGC	5420

## (2) INFORMATION FOR SEQ ID NO: 103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GGGATCAGAT TGAAAATGCA GAATATTTTA GCGCACACGG TGCTGCGTGC ATCCTTCGTG	60
CTCAAGATGA AAAGGGACAT CAACTGGTGT CTTTGCTCAC AGAACTGTTC CATCCTTCCT	120
GCGCTAGGAT AGAGGAGATG GCACGTGCGT CTTACACACT TGGAATTGGC AATGCCGCGT	180
ATGATATTGC GCAGCAGTTG CAGACTTTCA TAAAGGAGGG GATGTGACAA TCAGTACCCT	240
GGATCTCATT CTTGGAATCA TCATGGGGAT AGTGACCGTC CGTGCCACCA TGCGCGGGTT	300
TGTCGATGAG TTCTTTTCTA AGGCAAGTAT CCTGTGCGCA gCAGTTGTTG CAATACTGTG	360
TCATAAAAAGG CTCGTGCCCT TGACACGTGT GTTGTTAGGC CACAGTATTC TGCTTCCGTG	420
TATAACGTTT TTGATTACCT TTATGGGCGT CTATTGCGTT ATGCTCTTCC TCCGTTACG	480
TATGCGCACG TaTGctACGC GCGATCTTAT CAGTGGTTTT AATCAGGTGT TTGGCTTTTT	540
TTTCGGGATA ATTGAAGGGA GTGTACTACT CACTGTTATC CTTTTGCTTT TACACGTGCA	600
GCCTTTTGTA TCTGTTTCGC ATATGTTGCA TGAAAGCGTA ATTAACACTG TTCTCTCTCC	660
CCTTGCTCTTA GATGGCGTTC GCTATATGCG CCTGAAGATG TAGGCGCGTT TTCGTGTTG	720
AGAACATTGT CGGACAGCCA GCTACTGACC TTCTGCGCGA TGATGTTATG CACGCGCGTC	780
TTCTGCTGCG GCTCTTATTT GTTGGAACAC CCGCTAGTGG CAAGCTAACT GCTGCACTTG	840
AGcTTGCGCG CGTGCTTTCC TGTACGCAGG GGGGCGTGTG GCAGTGTCTT TGTGCACCCT	900



GTGTGCAGCA TACGGAGTTA CTTTCTCCAG AACTACTCGT GATGGGGATA AAAGATCTGA 960  
TCCTCGAAAT ACGCGCGTCG GCACGTGCCT ATATGTCAGT GCACACGCAG GGTACGCGCT 1020  
ATCTTTTGT GCGGGCAGTG CGTAAACTCA TTACACGCTT TGACGAACGA CTGTGGGATA 1080  
GTGATGATAC TCGTTTCTCT GCCGCGGTTT CGAGCATTCG TGAGCTCGAC CAGGAGCTCG 1140  
CATCACTCCC CGcACAGGGA GACCGACGTA CCACTCCAGA GCAAAAAGAA AGAGTGCAAA 1200  
GGATATGCGT GATCGCCGAA AGGCTACAGC AGGAGTCACT CTATACCCAA TTACCCGTAC 1260  
AGCAAATACG AAACGCAATT CAGTGGGTGC GTCTTACACC CTCAGGAAGA AAGAAAGTGC 1320  
TGATCATAGA ACACGCGCAC GCGATGCATG AATCTGCACG AACTGCTTTT CTAAAGATAT 1380  
TAGAAGAACC TCCGCGCGAT ACGCTTTTTA TCCTCACTAC CGCTACAAAG TATGCAATCA 1440  
TGCCTACTGT CCTTTCGCGT GTGCGCAGTT ATTCTTTCAG AGAAAGAAGT GTTGAAGTCC 1500  
AATGTGCAGT AATTACACGC GTATTTTCATG ACAGACCGAC CGATGCAAAA AACACACAGG 1560  
GTGTACTCTT GCACTATTTA TATCAGTTTT TGTCGTTTTT TTTAGAAGAG GTGCAAACGT 1620  
CCGTGATGTA CTTTTCGCTG TATGTGTGCC AGCACGCTAG GTGTATCGGA CGCATCATTC 1680  
CTGATACTTG GGTTCGCGTA GGTACTCAAC CTCAAGTATC AGGAATsGAT CTTACCTCAC 1740  
TTGATTCTAC GCTGCATTTT TTCCAAGCTC ACAAACAGCA ACACGCCGTG TCCC'TTTT'TT 1800  
TCTCCTTACT CGTCAGGCAC ATGCGCACCC TGCAGCGCAC CACCGAGTAC TCCGCACGGA 1860  
ATACAGAATG tTCGCACACA TTGCTCACTG TATCGAACAG GCACATCGCA ATGTGCAGTT 1920  
GTGGAATCTA ACAATACAAG GGACTCTCGA ACACTTAGCA CACACCATCG CGAATCATCT 1980  
ATGAGAGATT TTATTGCACG CGCGCTAAAA AAGTCAGCGA AAATGAATGA CTCTCAACTG 2040  
AGAAATATGA TTGAAGTTAT TGCCAACGAG TACACCTTGT TGGATGCACT TATGGATTCT 2100  
CTGAATTAcG GACTTATCGT GTTGGACTGT TTACACATTC CATTAAGAC AAACCGAGCA 2160  
ATTGCACGGC TCTTGGGTAA ACCACTGCCT TCAAATCCTC GCAGGCCACT GTGGCATTAT 2220  
CTTGATGACG AACACATTGC GCAGTTCATT GTGGCAATTA TTAAAAATGA GGTAGGAAAA 2280  
GCACGCGCAG AATTCATTGT ACAAAGACAA GGTGAAACAT TGTATCTGGA AGTATCCTTA 2340  
TTCCGCTAA TTTGTGACCA AAAGATCCGC GGAAGTATTA TCGCAATACA TGATATCACA 2400  
GAGAAAAAAC AAGAAGAAAT CTATAACCGA AGCTAGAAAG TCTTGCAAAT TTAACGAATC 2460  
TTGCAGCAAC CGTTGCGCAC GAAATCAAGA ATCCCCTAGG AGCAATGAGC ATTCATCTGC 2520  
AATTACTACG TAAGAATTTT AGTACCTGTA GTTTCGAAAC AAATAAAAGA ATCCAAAAAC 2580  
ACCTCCATGT GGTAGAGGAG GAAATCGAAC GGCTCAATAG AATTGTCACC GGCTTCCTTT 2640

CTGCAGTTCG TCCCTTAAAA CTAAATATCA CACGGCTGAG CGTTTTTGAT CTTGTTACAT	2700
CCATACGAGA CACATTTATG AAGCCTTCAC CAAAGCAGAA CTGTCTTTCT CTGTACATAT	2760
GCCACACAAT CTTCCCCACA TACGAGGCGA TGAACACCTG CTAAGACAGG CATTTGGTAAA	2820
CATTATCACT AATGCTAAAG AAGCCATGCA AAGAGGAGGG GCCCTTGAAG TCTTTGTCCA	2880
TAAACAAACT GACCACATCA GTATCAGTAT TTCGGATACA GGAGAGGGAA TTGATGCCCCG	2940
AAATATTCAC AATATTTTTG AGCCGTACTT CACTACTAAA ACTGAAGGTA CGGGGTTAGG	3000
GTTAACCTTA ACGTTTAAAG TGATTAAAGA ACATGGCGGT GACATCAGTG TGTCTCTAC	3060
TGTTGGACGG GGTACGTGTT TTA CTCTCCT TTTACCCATA GATAAATTGG GACGATCGCT	3120
TTTACAAGAA AAAATATCCA CCCACCTAAG ACATACGAGT AAAGAATAAG GAAATGCGAT	3180
GAAATTCAGT ATTCTCGTAC TAGATGATGA AAAAAATATC CGTGAAGGTT TGCAAATGGC	3240
CCTCGAAGAT GAAGGATATG AGGTGTTTAC CGCAGAGGAT GGAAATACAG GGGTAGAGAT	3300
TGCCCTCAAA GGGGATATCG ATCTATTAT CACTGATTTA AAAATGCCtC GTATGAGCGG	3360
GGaATTGGTG CTGCaACATG TGCACGCGGT GTTGCCCGAT ATTCCTAtCA TTATTCTCAC	3420
CGGGCATGGC ACAGTAGAAA ATGCAGTTGA AGCAATGCAC AAGGGAGCTT ACGATTTTTT	3480
AACTAAACCA TTGGATCTTA ACCGATTGTC TTTGCTTGTG CGCCGGGCGC TACAAAACCG	3540
AGAGTTGATC GTTCAACATC GAGAGTTAAT CAAACAAATA GGAAATCGCA CCTCATTCTGA	3600
GAACATTGTA GGAGAAAGTC CTGCAATGAA CAAAGTGTTT GACATGGTAA AAAAGGCAGC	3660
CGCCTCAAAA GCGTCCGTGC TCATTACTGG AGAAAGCGGG GTCGGTAAAG AACTTATCGC	3720
GAATGCAATC CATAATCTTT CGCCGAGGAA GGCAAAACCT TTAATTAAAG TACACTGCGC	3780
TTCTTTTGCA GAAGGAGTGT TGGAAAGTGA GTTATTCGGT CATGAAAGGG GTGCCTTTAC	3840
CGGTGCGGTC AATCGCATGA AAGGTCGTTT TGAAC TTGCG CACGAAGGAT CAATGTTTCT	3900
TGATGAAATC GGAGAAGTAA GTATGGCTGT GCAAATAAAA CTACTCCGTG TGTTACAAGA	3960
ACGTTCAATT GAACGTGTAG GTGGAAGAGA AACAATAAAA GTTGATGTAC GCGTAATTTT	4020
TGCAACAAAT CGTAATCTTT TAGAAGAAAT TAAACGCAAT TTGTTTCGAG AGGATCTTTA	4080
TTACCGATTA AATGTTGTGC ACATTACAGT tCCTGnCTGC GCGAGCGcAA GGAGGATTTG	4140
CCATTACTGA TTGCAACATT TCTTAAAGAG ATTGCAGAAG AAAACGGTAA AAAAATTACC	4200
TCTATAGATC CTCAGGCCCA GTCTGCACTG CACGCGTATG ATTGGCCTGG TAATATTCGT	4260
CAGCTGAGAA ACTGCATTGA AAGCGCTGTC ATTATGAGCT CAGGTCCTGT TATCCACATA	4320
GAGGATCTCT CAGAGCCAAT TCGATCTCTC GGTGAAACCT CTTCCATACG CaTTCTCTATA	4380

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GGAGTGAGCa	TGGAGGATGC	aGAAAAaGGAA	aTCATCCTCC	AGACACTGGA	AGCACAAAAA	4440
GGTAATAAGA	GCAAAACCGC	AGACGTGCTT	GGCATTGGGA	GAAAGACGCT	CTATCTAAAA	4500
TTAGATCAAT	ACACGAATAC	AAGCTTTGAA	CCTGATGCCG	CAGCAAAATC	ATGaAACGTG	4560
cTTTGATAAT	CACCGGAGGT	GAATATGCAC	CCTATGAGTT	TGTGCAATAT	TACCTGCCTG	4620
CGTACGATCT	GCTCATTGCC	GCTGATTGAG	GGCTTGATAC	CGCATTGCAA	TTTGGTCTTG	4680
TGCCCCGATTT	TGTTATTGGA	GATATGGATA	GCGTTAAGGA	CAACCTGTTC	ATACAGGCGT	4740
GTGATAAAAC	GCGCACACAC	CTTTTCCCCC	GAGATAAAGA	TTTTACTGAT	ACTGAGCTTG	4800
CAGTCACCCT	TGcGCACCAA	TTGGGAAGCG	ACGATTTGAG	CATCGTCGGA	GGGGGTGGGG	4860
GAAGGGCAGA	TCACTTTTTA	TATTTTCATGC	GTCTTTTTGC	CGCACCTCTG	TCACCGCGTC	4920
TGTGGCTGTA	CAGACATGGA	CTGGGATATT	GCTTTGGGGA	AGGATGTGTT	ACACAACAGT	4980
TATGTATTGG	AGGAGTGGAT	AATACTTCTT	TTTCTTTCTT	TCCCGTTGGA	GATGCTACAG	5040
ACTATTCGCT	CTCCTCTGAA	GGATTGCATT	GGCCCCCTCGA	TGGGgTGCCg	TGGCACACTC	5100
ATGTAAGTAT	GAGTAATCGC	AGCAGCGCAC	CTGTCGTGCG	CGTCGAAGCA	CACCGGGGGA	5160
GATTTTTGCT	TTTCCTTTCT	CCCCTCGGAC	GTTACACCAT	TGATCATCAC	GAGCGGGGTA	5220
TTGCGTGCAC	GCACAGAACG	TAGATATTGC	GCCGGGCAGT	ACCTCGACCG	TTCCATCAT	5280
AGTGGGTATT	GACCCAGGAC	TTGAATCTAC	CGGATACGGC	GTTATAGAAG	CAGGGGGAGG	5340
CAGTCTGCGC	TGTCTTACTA	CGGGGTGATT	GTTACCCAAA	GCAATCAGCC	ATCTGCTGCA	5400
CGACTCAGAC	ACATCTTCGA	TACCCTGCAA	CAGGTAATCT	CAATATATCA	ACCTCAGTAT	5460
TGCGCAGTGG	AGACAATCTA	TTTCGCAAAG	AATGTAACCA	GTGCGTTGTG	TGTTGCGCAA	5520
GCGCGTGGGG	TTGTATTACT	TGCTATGGCA	CAACAGCACA	TTTCAGTAGC	TGAATACGCA	5580
CCGAATGCGA	TTAAAAAAGC	AATAACTGGT	ATTGCCCAAG	CAGAAAAAAG	ACAGGTACAG	5640
CATTTGGTAA	AAATTTTACT	CAATCTTAAG	GATATACCTC	ATCCTGATCA	CGCTGCTGAT	5700
GCCCTAGCGG	TTGCTGTTAC	CCATGTACAC	TGTTGTATGT	CTTCAAACCTA	TGCGGTAGGT	5760
TCAACGCGCT	CTAGGGGAGC	GTACGTTACG	CTGTACAAAA	AAGGTAAGAG	ATGAAAAGCA	5820
AGAGTTCTTT	GTGAAAAGT	GGGTTGCTGC	TTTCTCTTTT	AACACTTGTC	TCTCGTGTAT	5880
TGGGTTTAGC	GCGAGAAGTA	GTGAAGTCTA	CGCTTATGGG	GACCAGTGCG	ACAGCAGATG	5940
CATTTACCGT	TGCATTTATG	ATCCCAAACC	TTTTCCGCCG	ACTGTTTGCA	GAAAACGCCA	6000
TAAGTGTTGC	CTTCATTCCC	GTCTTCACAC	AGCACTACTC	AATGCCGAGT	TCAGCGCAAG	6060
TGCCATGTTC	TTCTAAAACG	AAGGAGTTTC	TTTCAGCTAT	CTTCACACTG	ATGAGTAGTG	6120

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TCACTGCAAG CATTTCTCTT ATCGGTATAC TCGGTGCTCC GTACATCGTG CGATTATTTG 6180  
 ACACTGATCA GTCATTAACC GTTTCATTAA CCCGCTTGAT GTTTCCTAT TTATGGATGA 6240  
 TCTCTCTCGC AGCTTTCTTT CAAGGTATGC TGCACAGTAT TAAGGTATTT GTCCCCTCAG 6300  
 GATGTACCCC AATATTTTTT AATGTCAGTG TCATTTTTTTC GATGTACTTT CTGAATGTGT 6360  
 CACATATGAA CGTGGCTATT GCTGCAGCAA TAGGTGTTCT TATAGGAGGA TGTGCGCAAG 6420  
 CACTCTTCCA GCTAATATTT GTATATATGC ATGGGTTTCG TTTACGCTC CAGTCTCCTT 6480  
 TAAAAGCAAT GCACGATGAA GGTGTGCGAC GAATCATTGC GTTACTTCTA CCGACAAC TG 6540  
 TTGGCATTGC AACCTATCTT CTAAATGACC TGGTGTGTAC TGCCTTGCA ACCTCTGT TG 6600  
 AGATAGGAGT TGCTGCGAGT GTGCAATATT CATTCGTATA CAAGAACTTT TATTAGGrAT 6660  
 ATtLATCGkT TCTCyAAGCT CyGtGGkACT TCCTGAtCyT TCyTTCCaTG tTATGAGAAA 6720  
 AGATTGGCAA TCGTTTGAGG ACCTCCTGAT AACA 6754

## (2) INFORMATION FOR SEQ ID NO: 104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCCAACGCGT TGGCGGCCCT ATGTGCATTT CCGTTCTGCT TGGTGGTAG TGGATTGTGG 60  
 AACACGCTC ACCTTTACGG CGGTGGATGG CACGGGGTTG ATTtCAAGGG GTGGCAATTG 120  
 CGCCTGGTct GCgcACTGCG GTGCAGTCTC TCCATACAGG AACGGCACAA TTACCACTTG 180  
 TTCCTCTTGC CCTGCctGAT TCCGTTCTGG GCAAGGATAC TACGCATGCG GTGcAGGCGG 240  
 GTGTGGTGCG GGGCACGCTC TTTGTTATTC GCGCTATGAT TGCACAGTGT CAGAAAGAGT 300  
 TAGGGTGmCG CTGTGCAGCG GTGATAACGG GGGGGCTTTC GCGTCTTTTC TCGTCAGAGG 360  
 TGGACTTTCC TCCTmTCGAT GCACAGtGAC GCTCTCAGGT CTTGCACATA TTGCGCGGCT 420  
 GGTGCCGACA TCTCTCCTGC CACCTGCTAC AGTGyCaGGT TCATCGGGGA ATTGAGGAAA 480  
 CTGTTATCCG CGCTCCCCAT CTTCCGATAC TGGATCGGTG TCGGGGGAG TAGGAGTGGG 540  
 GAAGCGTCTG TGCTGTATCG CGCTGGTGAT GCGCGCGTTC TGGTACCTCa kTsCGAAGGG 600  
 AgTCAGTaTc GCTTACGTGC CCgTTCaTcG CAGTGGGGGC TCTCAAGATT cGAGCATGAG 660  
 CACAGCAGTG GCGGATACGC TCyTTAACGC CTTyTTGAC GAGGrAATGG TGGTTACGgC 720

AGTACCGCCG	GGTGACACG	ACGGCCAGAC	TATAGCAGAA	ATTGCTGCAT	GTTTTGAAGT	780
AATGCCCGAT	TACGCGTTGT	TGGTGCAGTT	TCATTCCGCT	CGTCTCCCTG	GTGGGGAAAG	840
CCCTACCTCC	CGTGCCCGCG	GCGCTTGGTC	TTCAGAGAGG	CCGTGCTG	TGTGGACATT	900
AGTGGATTTG	CATACGCAGC	GCGCGTGTGT	CTATGCGTGT	GTCGCCCCAT	ACAGGGAGAG	960
TATTCCCGTT	TCTGAGTGTG	TTGACGTCGT	TACCCGTTGT	ATTGCGGA <sub>g</sub> C	AGG <sub>c</sub> AATTTC	1020
GTACATACGG	GTGGGCACGA	GCACCGATAC	AGCCGGAGTT	CAGTTATAGA	AAATAGGGAA	1080
TACGTAAGGT	GTCTGCAGCG	TCGCTTCAGC	TGGGAGGAGT	CTTATGATTA	AACGCCACAT	1140
GTTCGCAAAA	AGGGGTGTCA	AAGGAAGATC	TTACCTGGTT	AGGGTGAAn <sub>a</sub>	mTGC GTTCTT	1200
AGTGCTTTGT	GTGCTTCTG	TCACGCCGCT	TTGGGCTGTG	TGGGAAGGGA	ATGCAGAAAT	1260
TGGCCCCCAG	GGAAGTTTTT	TGCAGGACGG	CATGTTTGTG	CGCAGTGACA	TGTTCCCCAA	1320
AAACACTGCT	GTTGAAATTA	GCAACTTAGA	AAAGAAATGCC	AAGGCTCAGG	CAGTGGTTAT	1380
TGGGCACGCA	GGGATCCCCG	GTCTTCTAGT	TAGCCTTGCA	CCCGCTGCTG	CAGCACAGCT	1440
TGGGATTGGC	GTATACCAAG	CTGTGCGTGT	ACGCGTACGT	ACCTTGGGTA	CCGTGCGCGG	1500
TGGGTCTCAA	ACAAGTCAGG	ACGGA CTGTC	CCTTG CATCT	TTGCCGTCCC	GTGTGCCTGC	1560
GCGCCCCGCC	AG <sub>c</sub> gTGATCC	TCTGT CATCC	CCGCCG CAG	GTCACACTGT	ACCGGAATAT	1620
CGCGATACGG	TTATTTTCGA	TGACCCGCGT	TTGGTTTCCC	CTTTGTCTCG	TGAGGTGGAG	1680
GACGCGCCGA	AGtAGTGAG	CCGGCCTCTG	AGCGTGAGGG	AGGGGAGCGT	GAGGTGGAGG	1740
ACGCGCCGAA	GtAGTGAGC	CGGCCTCTGA	GCGTGAGGGA	GGGGAGCGTG	AGGTGGAGGA	1800
CtGCCGAAG <sub>g</sub>	TtAGTGAGC	CGGCCTCTGA	GCGTGAGGGA	GGGGAGCGTG	AAG <sub>g</sub> TGGAGG	1860
ACTGCCGAAG	GTAGTGAGC	CGGCCTCTG <sub>c</sub>	AGCcGTGAGG	GcAGGGGAGC	cGTGAGGTGG	1920
AGGACGT <sub>g</sub> CC	GGGGTAGTG	GAGCCGGCCT	CTGGGCATGA	AGGAGGGGAG	C <sub>g</sub> TGAGGTGG	1980
AGGACGTGCC	GGGGTAGTG	GAGCCGGCCT	CTGGGCATGA	AGGAGGGGAG	CGTGAGGTGG	2040
CTTCTCAGCA	TACGAAGCAG	CCATCCC ACT	CGGTTTCCAA	CTCAGCTCCC	AATCAGTTTC	2100
GGAACCCTGA	GGGGGAACTC	CCCTTTACGC	TCCCTGACCT	ATCCGAGTCA	GAAATGTGTTG	2160
TTCCGAGGA	ACAGAAAGGA	CGTGCGCATC	CCCAGGTGAT	ACCCGAGGGT	GCGCCACGTG	2220
GACTGCAACC	TGGTGAAT <sub>a</sub> c	TACGTACAGA	TTGCAGTCTT	TCATGACGCT	ATCCAGGTGC	2280
AGAGCATTGT	CCACCGTTAC	GGGGTAGAAT	ACCCCATCGC	AGTGGAGCAG	GACATCCATG	2340
AAGGTAAGGT	GCGTTTCACC	GTATGCGTCG	GTCTGTCCA	AAAAGACGAA	CGCGGCGCGt	2400
ACTAGAGAAC	TTCCAAAGGT	TTGGATTCAA	GGACGCCTTT	CTGAAAAAGG	CGCGATGATC	2460

AGGTCGGCCC	TCCTCTTCCC	CTCGTGACCG	TGGTGACTCG	CCCCGAAGc	GnCaCAGAGC	2520
CCGAAGaACG	GAAGGGAAGG	GGCAGACTTA	ACTATTTCTT	TGTTTTTTTG	AGCACGTAAA	2580
ACGGCGCCAT	CTCCTTTGAA	GGCTTTCCTG	CGCCGGGAGC	GCCCATGTAG	CGAACGGAgT	2640
TACTGTCTAT	CAGCTCGTAC	AGCTCTTCT	CGTGCGGTGC	CTTCGATTGC	TCCGAGGACA	2700
CAAGCGAGAG	TTCGACAATT	CCGTCTTCAC	GTACCATCCA	CGTACCGCGA	TACGTAAGAG	2760
GAGAAGGTGC	CGACTTCTTC	TCAAGGGCAA	GCTCTACCTT	TTGCGCAtGC	CATCCGCGTT	2820
GAACGTCACA	GTCGTATCGA	TTCCCGGGCA	ATCGGCCGCA	GTAGCGTACC	CCGAAAGATA	2880
CCTCCCTTCA	ACGCGCACTC	TAsCTTTTCC	GCTTtGGCCT	TCCCGGCGTG	CGGACACAgG	2940
TTGTGCACGA	GACACACAAA	GCGCTAmCGA	GCGCTCCAAC	ACCAAGGAAC	GCGCACAGgs	3000
CGGsACAGAT	CtTTCATCAC	AGAAAACCCC	CTTGTCACGT	CTGTAAGnTC	AGGGGAGAAA	3060
AGCCCAACGA	TGCAAAAGTT	ACGCTCCCTC	TTGCCAAAAG	TGAGAGAAGA	GCGCAGGCCA	3120
CgCGCACGgr	GGCAAAACGTG	GGGTTTAGGA	GCGCACCTGC	GCCCCGGCCG	CGGGTGACG	3180
CATCTGAGCC	TCAAAGGCAG	CAACAAAGCG	GGGTAACAGT	TCATCAACGG	TGCCCTCGAT	3240
ACGAAGGCCA	GCAGCGCAGC	GATGACCTCC	ACCCCCGAAG	CGAGCGGCGA	TAACGCTTAC	3300
GTCAATCGAT	CCTCGCGATC	GAAACCCAC	CGAACAATGT	GTGGGAGATT	CCTGACGTAC	3360
CACCACAATT	GCCTCGACGC	CCTGGATGCT	CTGGATGAGC	TGATACAGAG	CATCGGAGTC	3420
TCGCACATCA	AGCCCCAACT	GGACCGCGTC	TTCGCAAGTT	TCGTACGAGG	TCATGAGCGC	3480
GCCACCATAA	TACGGCGTCA	GTCGAGAAAG	CACGCGCGCA	ATCAACATGC	GCGAAGCAAG	3540
GGATCTCCCA	CCGTTTCATGG	CAAGAAACGT	GTCTTCGGAT	TGGCGCCTGC	ACGTACAAGA	3600
CGCGCAGCAG	AAGCGAAcGT	GTCCGCACTG	TGCTCGTCGA	GGTGGCGAAA	AAAACcTGTG	3660
TCCGTAGCCA	ATCCCCAAAA	AAGTGCGCGC	GCCTCGGCTG	CTTCAAGAGA	TCCGGCCATC	3720
GTCTCGATTA	ACGTTTGCAC	CAATGTAGTG	GTGGACGGAG	CTGTTTTTAC	GACGAACGAG	3780
TGCGCGCAGT	GGTCGCCGCA	CGTTTCGTGA	TGGTCTATGA	ACGCGCGCGC	AAAGGGGGCA	3840
AGCTGCGAGG	CGAGCTCAGC	GCCAACGCGG	CTGAGCTCAG	AGCAGTCGAC	CACGATGAcG	3900
gCCGTCTGAT	CAGACGGCcG	TnAtCTGCGC	AGAGAGACTT	GGACGGAAGA	GTGTCGCGTA	3960
CGCAGCGATC	TCTCTACGCT	TGAAAGGACC	CGCAGACAAA	AGCTCAACCT	CTTTCCCTAT	4020
GCGTCTTAGG	AACGAGGCAA	GCGCAAGACT	GGAACCTACA	CAGTCCCCAT	CCGGCTTCTC	4080
ATGCCCCACG	ACCGCAAACG	CGCGATGCGT	GcaATGAACT	CGATGAGCCC	GGAAAGACCC	4140
CTCCCCCGAT	CCCCTGTACG	CGCCGCGCAC	GGAGAGGGGG	AGGAAACGGA	CTTAGGAAGA	4200

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GAACTCGGGG	GACTGGAAGT	GAACATCAAA	CTTATCGTCG	TACTCAGAAG	GACTTTTCAG	4260
CGTTCCCCAC	ACCGGGCTGC	TCAGGCTGCG	AGGGAGTGTG	AGCTTTACGT	AGGTAAGTGT	4320
GTTCCCTTCC	ATAAAAAACG	AAAGGTAGGG	ATCGACGCGC	ACTGGAGcGT	GCCGCAAGAG	4380
CGCCTTACCC	ACCCTGGGCG	AGAACCAGGC	GGACGGCAGA	TAGATCTCGG	CCATTTTCGAA	4440
GTTAGCACGC	CGGTAAATAA	CCCATAGGCC	CAAGCGGTGA	GAGAAGACTT	TCACCACAGG	4500
AAGATTGACG	TAgTACATAC	GAGAAGAGTT	GCTCTCTGTG	AGCCCTGGGG	GAGGGGGCTC	4560
TAACACACGC	CCAGCAGTAT	CAGATGCATC	CTGCGCACTC	AGAGCGACAG	CAGAAGCGCA	4620
CAGCACAAGG	CGTAGACAAC	GAGTTGAAAA	TTTCATAGCA	AAACCTCCGC	GGCGGCAGGA	4680
TTCTAGCCTA	GGTGTGTCCC	TTAATACAAG	CGTCTGTATC	ACGCTCCTTG	CAGGTAAGTG	4740
CGCCGTGAAA	AATGCGCGCG	GTTGATTTCT	TGCGTAGAGC	TACAGTATGC	TGGTACATGC	4800
GCATTTATCT	TGCGTCAAAC	AACGCGCACA	AGCACGCGGA	GTTCTCCTCA	CTTTTCCCCA	4860
TGCACACGAT	TCTCCTGCCG	AAAGACGAGG	GTATCGATTT	TTTCTCGCCT	GAGGACGGGT	4920
CTACTTTCTT	TGCTAATGCA	AGGCAGAAGG	CTGACGCCCT	CTATGACGTG	GTACATGCGC	4980
CTGTGCTCGC	CGATGACTCA	GGTCTCTGTG	TGGATGCTTT	AGACGGGGAC	CCAGGGgTGC	5040
ATTCGGCGCG	TTTTGGTGCA	CAGCATGGGG	TACACACAGA	CAtGCGCGCA	TGCAGCTCCT	5100
TCTGGAACGT	ATGCACGGAC	GGCArgACCG	TGCCTGTTCC	TTTGTGTGTG	TGGCGGTACT	5160
GAAGTTGGGA	TCGGTGCCGT	TGTGCGTTGG	GCGGGGGGTG	TGCCgGGGAG	TGTTGACTAC	5220
AGAAATGTCT	GGGGTAGAAG	GTTTTGGCTA	TGACCCGATT	TTCTGTGTGC	CACACCTGGG	5280
CAGGACGTTC	GCTCAGCTCA	GCATTGAGGA	GAAGAACCGC	GTCTCTCACC	GGGCACTTGC	5340
GGCGctGCGC	CTCGCACAGG	TGTTGGCCAT	GATGCAGCTA	CCCCGTkgsT	GCGCTACGAG	5400
TTAAAGCTTT	TGCGTGGTGC	TCGTGCTATG	AaCGCGCGGC	GGCGTGCTGC	GGCCTGGCGC	5460
CCCCTGTGCG	CAACGTAAGG	GACAGACCGC	GCAGACTGCC	CGAAGACACA	AATTTTATGC	5520
ACGCGCTCGG	AGGTGTGCCC	GTCGCATACA	TCGTGCCTAG	TGCTCTGCAA	GGTGCGTGAg	5580
CGAACGGAGT	GCaGGACACG	CGCTTGACTG	CAGCTGAGAG	GAGGGATTGT	ACGAAGACGA	5640
TGTTTTTTGT	ACCATGGCCC	CACGCTGCAC	CATCGGAGGG	TCCCCATGGC	GGTAAACGAC	5700
GAACAGTTTC	AACTCGTTAC	CTTCCAGCTC	GGGGAGGAGC	TTTATGGCAT	CGACATTATG	5760
GGTGTCAAGG	AGATTGTGAA	GGTTCAGGAC	GTTCGTCCTA	TTCCCTGTGC	GCCTGCCTTAC	5820
GTGGAGGGCA	TTTTTAAACCT	GCGCagcGAG	ATTATCCCTA	TTATTAACCT	GCACAAGCGC	5880
TTTCACCTAC	GCGAGGCTAC	GCTCGAGTCG	GGCGACGAGT	ATCTCGGCGG	CTTTGTCATT	5940

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CTCAATGTGG AGGACAGTAA GCTCGGCATT ATCATCGACC GCATCGCGCG TGTATCGCT	6000
GTCTCGCAGG AGGACGTGCA GTCCCTCCC CAGGTTATCA CCGGcATCGG GGCGGAGTAC	6060
ATTCATGGGG TCGTGCGCCA GGGGACGAGT TATCTTATTG TTCTGGATAT CCACAAGCTG	6120
TTTAGCTCCA AAGAGTTGCA AAAGCTCGCG AACCTCTAGT GCCCCACCGC TGTCTGTCTC	6180
CTGCCTGCAG CTCCAAGCGC CGTGCGGGGT CCATCCCCGT CCACAGCCCC GCCATCCGAA	6240
GgTCCGAAAT GGACGCGGTG CTCACCTGCT TGGTGGATGA AAAAAATTGGC CCTGGTTTCG	6300
TTGGCAGCAC CCTCATCCAG TTGGTGC GCG AGGTGTTTTT TCCAATCGAT GCATAcGTgc	6360
TGCGCAGCCC ssTATCGCAC TTTCTTTgC ACTCCGTGCA CTGAAATTGC CTCCTGCTTC	6420
CCCTGTACTT CTTTCTGCGC TTGCGCCCTT CTGGCACTAC CGTGAGGTGC TTCACCAGGG	6480
GCTGCAGCCG CTTGTCCTTG ACGTAGACAT TCACAGCGGT TTGTTGTCCC GTGATGTGGT	6540
GGAAACTGGC AtCGCGCGTG GCGCTCGTGC GCTTCTTGTG CCTGAAACAC TTGGAAATGT	6600
GCCTCCTGCA GCGGTGTTTT TGGAAGTGGG GATACCCGTC ATCGAAGACA GCTCTCAGAG	6660
TGTCGGTGCA GTATtGGGAG AAAAGAAGGT GGGAAAcTTT GGCTCGTGTG TCATCGTGGG	6720
ATTGGAGGCA CACGATATGC TTACCGCAGG CGGCGGCGCG GTACTCATGG CTTTGAGGC	6780
CGCCTGCGCG CGTCGGCTTC AGGCGCTTGT GCCAGAAGCG CTTGCCGTG ATATGCTGCC	6840
GGATATGAAC GCGGCGCTCG CGTGTGTCCA AGTAAAGCAG CAAGAAAAAA ATATTGCCCT	6900
CAGGCGCGCA ATCTACGACC GATACTCCTC TGCGCTTTTG CGTACGCGTC ACGGTACGCT	6960
TCACCGGTGT GAGCAATTGG AACACAGTGC CTACGCTTTT CCTGTTGTCC TTGCTTCTGA	7020
TCTGAAGGAA GTGACGCGTT ACGTGCGGCA GCGCTCCATT GAGATTTCTC CTGCCTTTGA	7080
ACATTCCATT GTGGCAGCGT TTCAATTACC TGCTATGCGC AGACGGTGGC CTTTTCGCA	7140
GTTTCTTCCT ACTTCTGCAT CGCACACGGC ACCTTTTCAG GGTGAGGACA GGGAGGTACT	7200
AGAGACCACG CAGGGCGCGG AAAAAACCTG TCAGGACTCT AGCTGGGAAA GGGAAAGTGC	7260
TGCGTCTGAG ATTACGCCCTG AGATGTGTTG GCCACATGCA TCTGCGCTTT TGTGCGCTG	7320
CGTGCGCTTT CCGTTGTACC CGCGTCTTGC GCCTGCACAC GCACAGGAAA TTGCGCGCAT	7380
CCTTGGGACA CTGCCGTGAG CAGCCGCGTG TGTCTCAGC GGCTGTGTC AAAATCATCG	7440
GGGGACGCGA AgGTGTTGCT TATTGTCAGC ACGTACAAAC CGCGCGCTGC GtGCTCGCTG	7500
CGGACGTTGT GAACTTTCTG AGCATACGTG GATTCCAGTG CCACACCATT GAGTATGATG	7560
GATTGAATAA AGAAAGCTGT GCTCGCGCAG GCTATATGTT TGCAGTCAGT ATTGGGGGGG	7620
ATGGTACTAC ACTGTTTGCC GCGCGCTGTG CTTCTCCTTC TGGTATTCCC ATACTTGCCA	7680



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TAAATTTAGG GCGTTTCGGC TTTATCGCTC CTATTGAGCC ACGGTATTGG CAACAGGCGT	7740
TGAGCGATTA TTTGGCAGGG GGGGTGCGCC CTGCTGAGCG TCGCTCATA TCGTGCACCG	7800
TCACGCGTGC GGGTAAAGAG ATTGCTTCGT GTCTGGCGTT AAACGATGTT GTCCTTTCAA	7860
GTGGACCGTC GCGCGTCTTA CCCGGGCAGA GGTGTGCTTC AACGACATT CTTTTGGCGT	7920
GTATGAAGCT GATGGCATT TTTCTGCGAC GCCTACAGGA TCTATGCGTA CTCGGCGGCC	7980
TGTGGCGGTC CCATCCTCGA TCCGGACCTT GATGCGTTTG TCCTCACTCC CATAAGCGCA	8040
CTGTGCCTTT CTAATCGTCC CGTGGTAGTT CCCTCCTCAG GGGTGGTGCG TATCAAGGTG	8100
TTGTCTATGC GACACAAAGA AACGGTGCTG TCTGTGGACG GACATGAATT GTGCACGTTG	8160
CAGGAAGAAG ATCAGCTGCT TGCAAGCAGG TCaTCGTGCA GCGCACGATt GGTTTTCTGT	8220
ACACCACACG TGTCTACCA TGCACTGTGC TCgAAACTGG CGTGGTCAGG GAGTATTTTT	8280
TCTCGCAGGG GAAGACGTCA CGATGATTGA GCAACTTTTCG GTGCGCAACG TTGCGCTCAT	8340
TCAATCTTTG GCGTTGGAGT TTGGTGACA GTTTACTGCC CTCTCAGGGG AGACGGGTGC	8400
GGGTAAGTCA ATGATACTCG GCGCGCTGTC CTTTCTCTGT GGGCAAAAGG TAGGGCCTGA	8460
TCTTATTCGC AAGGATGAGA ACGAGGCATG GGTTCCTGCG GTGTTTCGCT GTGAtCACgc	8520
ACCGCGTGCG GTGCACACAT GGTGGCAGA ACGGAGTATT GAGCCTGAGC ACCACCGCGT	8580
GTCCTTCGT CGGGTGATGC GCGGTACCGG TCGTGGCAG GCGTGGATTC AAAACGTCCC	8640
GGTCTCTCGC GCAGATTTGG AGTTTTTCAC GTCATTTTTT ATAGACCTCC ACGGACAGCA	8700
TGAACACCAA TCGCTGTTTC GTGTGCAGA GCATCGCCGC TTTCTGGATA CtACGGAGGA	8760
CTCCAGCAAG AAGTTGATGC GTTTACTGCG TGTTATGCGG CTCTGCAGA GCGACGCGCG	8820
CAgcTGCAGC GgcTCGCTTC CTGTGAACAC AACC GG CAGG AGCGGCTAGA ATTCTCTCC	8880
TTTGCCCTTG AGGAACTGGA GCACGCAGCG TTGGACGTGC ATGAGGAGCG TCGGTTGGAA	8940
GGAGAAGAGC AAAAGCTCTG CCAGCACGAA AACTCTGTG ATGTGATGCA AAGGGTTGAC	9000
GCTGCAATTA GGGGGGTGGA CCTGCAAGAG GCGCGCTGC TTTCTTCCTT AAAGAAAGCG	9060
CTTGGTGAC TTTGAAAGCGC CTGTGGGATT GATGGGAGTC TTGAGCCGGC GCGTGCCCGT	9120
TTAGAAAGTG CGTACTATGA AATCGAAGAC GTAGCGCATG TTCTGCGTAC GTATACAGAC	9180
GGTATTCAGT TTTGTCCCGA CCGTTTGAG CACGTT CAGG AGCGTCTTGC GCTCATATAC	9240
CGGCTGAAGA AAAAATATGG AGGAACAGTT GCGCAGTTTT AGAATACCGT GCGCGTGCGC	9300
ACAAGAGATG CAGGATCTTT CACAGGCGGT GGGTGATAAA GAGGCGCTTG AGCAAGATGT	9360
TCAGCGTCTG ATGGCTCAGT ATTACACGCG GGACGTGCCT TATCGCTTAA	9410

## (2) INFORMATION FOR SEQ ID NO: 105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTCTTAGAAA CCGGTnCACc GATcCACACT CCCTCTGAAC CGAGATATTC GGTACGCCGT	60
CCTTCAATCA AAAACTGCAC CGCATGCACC GTAGGAAACG CAGCTGCCGT GAACACCACC	120
TGCGAAAgTG CGCCAAGTAG CCCTCAATGC CATACTGATT GAACTGAAAC TCCTCGCTCA	180
GATCCAACAC CGCCACCCCT TCTTGCACGC GTGCAGAGCG CAGTCGCGTA CCTTCAGGGA	240
TGAGCGTACG CAgTCCGCGC ACCGCTTCTG CCTCAGACGG ACCAAGGAAC AATGCGCGCA	300
ACGCATCCGA AAGCGGCACC GTCGAATGAG GAAGCGTGCG AGCTACCTCC TCACGAGTGA	360
TCTTTCCATC TGCATCAATG CGCACCCAGC ACAGCGTAAT TGC GCGGGAC TGTGTGCAG	420
AACCGGGCGC CCCAGAAACc GTGCCGACAT CTTTCCTTCG GTACCAGCGT cAsTGGCGCA	480
GGGGATCCTG CAACAGGAGC GTCCGGCTGT GCCACATCCT GCGTAGGGAG CGTGGCTTTA	540
GCATCACTTT CAACAGCCGA GCCGGCCTGA GAACGACGTG CAGAGTCAAA AACGCGCATG	600
GAATCCTGGT TGCCGAACAT CCCTTGCACT GCAGCGCTCG AAAACACACG GTCAATATTT	660
CTTCTATTGA GAAAGAAAAG CACCGCCATT AACAAGGAAA ACGCAAGCCA GAACAGCAAC	720
CCCGCTGATG AGTGTtTCCC CTTCCCGGCC ATACAGCGCC ATCGTACAGG AATTATAAAG	780
CTTTTCCAAG ACATGCTGCA CACACGTCCC TTATCCCCGC CTTGCAAAAA ATATAGGCAA	840
AAAGAAAATA AAGCAGCCGA TATTGGGTcG TGC GCATGGC ATTCATGTTA CTGGCCCTGC	900
TTTTCTCTTT TCGTAATGCG TCCATTcAGG CAGAGGACGC GCGCCTGCTG CAGCCAAAAA	960
CCAACGCTTT GGATCTTGTC GTGCAGGGGG TAGATCTTGT GCTGTTTGCC CAGGATAAGA	1020
CGGCTATCAG TATCAGTACC CCTCCTGAAA AAGACGTGTT CTTACAGAA CACGAAGGGG	1080
TGCTTCGTGT CCGTACACGC ACAGAAAACG CGGAGGGTAC ACGCCGAGTG ATACGCATTG	1140
GCATACCGCG TGCACAAACG CTCGCATGGG TGAAGATCAT TGCGACGGGC GCACATACTA	1200
CGGTGCGCGG CGTACGcGCG GtGTGGTCAC TGCTTTTGTG CAACGAAGGC AACTCGCCC	1260
TCACGGAAAG CACGCTCAAG TCATGCACGC TGACACACAC GCGCGGCGAA CTCCGCTTTG	1320
AAGCGGCGGT ACTAAAACGG GCGTCATTCT GTTTGAATGA CGTGAACGCT CGTTTCACTC	1380

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TTCTCGGATC	GCGCGCCGAC	TACCGTCTTA	TCTGTAGCCC	AGGAGAACGT	GCGTGAAAA	1440
TTGAAGGCGC	CGAACACGA	GGCGCGCACT	ACACCGAGCC	CGCACGGGCG	AgacGCCACA	1500
TGGTTATCAG	CGCGAGTGCT	TCGTCGATAG	ATGTAATGTT	CAAAGCGCCA	CCTACACAAC	1560
AGGAAGCGGT	AGACACGACA	CAGAAGGGGT	AATCCAGGAT	AGACTGCCCC	TTTCAATATC	1620
ACCTCAGATA	GCAGATTAC	ACCGCGCACT	ACTCAAGCAC	GTCAGTGACG	ATGCGCACCA	1680
CGCGTTTTTT	CCCCGCGCGA	ACTATTACCG	TCCCGTCCAA	ATCCAACGCT	GA CTGGTCAA	1740
TTACCGCACC	GATATCTGCC	ACGCGCTGGA	GCCCGACAAA	AGCTCCTCCT	TGTGCAATCA	1800
AGCGCCGTGC	ATCACTCTTC	G TAGTACACA	ATCCAACCTG	TACAAACAAA	TCAGTCACTT	1860
TGATCCCAAC	TTGCAACGTG	CACTGTGTCA	GCTCGAACGT	CGGCAATGCA	CACTTATCGC	1920
CACACCCGCC	GAATGCCGCG	CGCGCTCCCT	GCAACGCCAC	CTGCGCGACA	gcCGTTCCGT	1980
GCATGAGGCG	CGTTACCTCG	TATGCCAACA	GCTCCTTTGC	ACAAATTAATT	CCCTGAGTCA	2040
ATATCGCCTC	GACATCGCGC	ACAGACAAAA	AGGTAAACAG	GAGCAAGAAA	CGCCGCACAT	2100
CTTCATCCGG	AGTATTTTCG	CAGTATTGGA	AAAAGTCATA	GGGAGACACC	AAAGCCGGGT	2160
CTAGAAGAG	CGCACCTTGC	TCGGTCTTGC	CCATTTTTTG	CCCATCCGCC	CGGGTAATGA	2220
GCGGAAAGGT	CAACCCATGC	ACGGTTTTTC	CGCGCACTCT	TCGAACCAAA	TCCGCCCCGG	2280
CAACAATGTT	GCCCCATTGA	TCATCGCCGC	CAATTTGTAA	CTCTACCGCG	TAGcaTnCAC	2340
TGAGCGTTAA	AAAATCATAG	CTCTGCAATA	GCTGATAATT	AAATTCAAGA	AAGGAAAGTC	2400
CTGTCTCCAG	GCGTTTCTTG	TACGCCTCAT	AGGTAAGCAT	TTTGTTTACA	GAAAAATGCG	2460
CCCCAACCTC	TCGCAAGAAA	TCAATGTAAT	TCAAATGTGC	CAACCAATCA	CGATTATTCA	2520
CATAGAACAC	ATGCCTGTGA	TCGAAGGAAA	GAAAATGATc	CAGcTGCGCA	ACTATCGCTC	2580
CCGCGTACGC	ATCGAGCGTT	GCATAATCGA	GCATCTTGCG	CATACTGGTT	TTGCCGGAGG	2640
GATCCCCAAT	ACGCGCGGTA	CCTCCACCGA	TGAGCACGCA	ACCGCGGTGC	CCCGCATCAC	2700
ACAAATGCTT	TAGCGCAAAC	ATAGGGAGCA	TGTGCCCAAC	GTGCAAACTA	CTGCCAGTTG	2760
GATCTACACC	GACATAAAAG	GTGAGTGGGC	CTGCATCCAT	ACGCGCCGAA	AGCGCCGAAA	2820
GATCAGTACA	TTGTCTAATA	AAACCACGCG	CCTGAAGACG	CGCAAGCgCA	GGaTTCATGG	2880
AGCCGATTAT	ACCGCGCATC	GCACACCCCG	ATCCAGGGCA	GGCGGTTTCAG	TCCCGAGAAA	2940
AAGACAAAAC	GCGCTGATGC	ACCCCCACCG	TCGCCCCGCG	TG TCACTATT	CCTTTAAAAG	3000
CGCTGCAATC	TTCGGACGAC	TCCAGCGCAC	CGCAACGTCA	TAGGGTGTCT	CTCCCGCCAC	3060
GTTTCGTAAA	AACTTTCCAA	AGCGATTTCAT	CGCCAGCAAA	CtTGCAGTGT	CTTTTCATCT	3120

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GCAACCTTTG CTGCGTAATG GAGAATACTT TCTCCAGCTG AATCTGTCTT ATTTACCGCA 3180  
AAACCCACCA GCGTTTTCAA GATTGACGTG TtCTTGCTCA GGACTAACAA GGCCGGAGnA 3240  
CTTCC 3245

## (2) INFORMATION FOR SEQ ID NO: 106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

ACAGGGAGGT TCAGGCATCA GAGAAGGACG TCTGTACACT CAGGGAACAG GTTGCCGTGG 60  
CGCAGGGTCT GATTGCTGAG GTTAATAAGG AGTCTTCTTT CGTCGACTCG CTGAGTAAAC 120  
gCGTTGCGGC TGCAAAGACG CAGCTGCAGC AAGTGTCGCG TGCGATTCCCT GATATGCAAA 180  
ATGCATTTAC GCGCGAGAAT ACCGCGCTTC TCCACCGGGT GCGAGATGGA GTACTTGACG 240  
ACGTACATAA GGAATTAGCG GTGTTGCAAA CAAGGCTGGA AAAAGCGCAG GGGGAAAGCC 300  
AGTCTCTTTT TGAAGTTTCT GCAGTTAAAT TGCGTGAGTT GTATGAAGGG GCATTTTCTG 360  
AAGCAACTGT GCGTGACAG GTGCTGGAAG AAAATGGATT CGGTCAGTTG AAAGTACAGG 420  
CGGAAAATCG CCTTCTCCAG TTGCAGGAGG AGTTTGAAGG GAGCCTCCTT TCTTTGCAGC 480  
AGCACGTTAT GCAGCGTGTC GAACAAACGG ACCAGCACAT CCAGGATTGT GCATCCCAGT 540  
GGTCTGTTTC GGCGCAGACA TGTGAGTCTG ATTTGAGTAT ACGTCTTGCG GACGTTACGG 600  
CGTGTGTGGA TGAAAGCGTG GCGCAACTGA AGGAACAGAT TACTACACAG GAGCGTGAAG 660  
TGCGTGCGCA CCTGGAAGGG ATCGAACAGT CGCTTTCAGG AGCAGAATCC GGTTTACcGA 720  
GCGCGTGAC AAGAGTGTA CAAGTTTTCA CGAAAACCTA AATAAGATTG CAGAGGCTTC 780  
TGATGCGCAG TTACAGCACT ACAGGAAGGA GATGGATGGA CGCTGTAGCA AGTTTGACAG 840  
AGAGCTTGAG GGTATTGATG TCCTTGAGTC TCAGTTGCaG CTTGCGCGTG AGCGTACAGA 900  
ACAGAAGGTG CGCGAAGAAT TTGAAGCGTA TGCGCAGGAT CGTGAGCGGA AGCAGTTAGC 960  
GTTTGAGGCA CAGTTGCAGC ACAGTATGGA TACGGTTGAG CACCGTATGA AGCAGCTGAA 1020  
TGACGAGCTG CGTGAGCTGA AGGCAAGTGC GTATGCAAAT GCATCCGAGA AACTGCAGTC 1080  
GGTGGAGGAT AACTTTTTTG AGGTACTTAC CAAGCGCAGm aCTCGTTGCA CGCGCGCTTT 1140  
TCCGAGTGA GTGAAGGGAT TGAGGGTCGT TTGACGCAAC TTGCTCTAGA GAGTGAGTCT 1200

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GCGCGAAAGG ATCTTGAGGA TACGTACCGC AAAGATGCA CACGCGGCTC AAgGATTTTG 1260  
 TGGAARAAATA CAAGGGGCAG TGTACAAAAC TGGGAGAGCA AATCCTCGCG ATTGAATCAA 1320  
 ACGTGAAGCA GCACATGCGC GCAAACG 1347

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AACTGTTTGC GAAACGGnAT TCCAAC TAAC CGACACATTC AACGTACGCG CAACTTTCAT 60  
 CGCAGACACA AACGCTTCAT CAGCAGAAAG ACACAGTGCA AAAAAGAAAA CACCACCTAT 120  
 CAAACACGAA CGCAAAAAC TCCATAATGCC CCTCGCTCGA GATACCCTGT CAAAGTACCA 180  
 ATGCACACCT GTCCCCCTCTC CCTACTCACA ATAAGCACAT ACGTCCACGC ACCACACTAC 240  
 CATACCCTTT GCGCATGCAA TCTCTCACCA GATGACAACC GGTGCAC'TTT ACTGAGAACG 300  
 ACACGCAAAG TACGCAAAAG CTCACGCGGT AGATATTCCA ACcGCTCCCC TAACAATAGT 360  
 CCTAACTCCT CAGTGCTATT CCATACATCa TGGAAAAGCG CGGTTTCTTC CGGACTCATC 420  
 AATCCAATTT GGAACCCAAA AATCATCACT CCACGCCGAC GCAGTTCC'TC TATCGTTCGT 480  
 CGACTCTCAT GAGGGTATGa GGAGCATCCG TCAGTAATTA CCAACACAAC CTTAACAAAA 540  
 GATGTATCAG ACGACACACG TGCACGCCGT CGTTCCACGT CTGCAAGAAT GTGTTT'TAAC 600  
 ACCTCTGCAT CATTTCGTCC TCCGAATCGT CCATCTAAGT TCACCGATGC TTTGATAAgT 660  
 GCGCGCTATT GAAGTCTTTC GATTTACTCT TTCCAAATGA CTTCACTTTT ATAAACTGC 720  
 TCCCAAAGTA ATACACCTCA GAATGAATAG TTGTTCTCTC ACGCCTACCT GCTGCGAGCA 780  
 TGTCTGAGTA CTCTCCAAAA TCTTTCAACG AAAGCATACT TACCGCAAGC GCTTCCCTTG 840  
 CACTCGCAAT CTTTTCTTTA TTCATAGAAC CCGAGTTATC AACAAACGAAT GAAACTTCTA 900  
 TCTGTGCCGG ACGTAGCGTA CACGCACGCA CTTCATACAC ACGATCATAC ACGCGCAnTT 960  
 GtACCTCTGA TCCCTACCCC GAAATTCTTG AAAATCAGGG AAAACTGAAA CAAAATCGCC 1020  
 TACGTTTAAC CTCCCC'TCG GGCAC'TCCC CTCGTAACAG TCTATCCACT GGACTGACTT 1080  
 TCCAATAAGT GATTTCCAAA ACGAGCGCAT ATCGATACGC AAACGATGCG TTGTACGCAG 1140  
 CAACCGCGCA AACTCTTTGC GTTCCTTCGG AGAAATAGAG AAGCGCTCGT CAAACTGAGT 1200

GGTACAAGAC TCAAAAACAT CTTCTCTTTT TTTCAGCTCT TGCTGCCCCGT CCCTTGAGTG	1260
CACAGCGTGC AAATTACTTT TAGTGATTTC GAAGGCACGC TCGTTTCTGA AAGGATCATA	1320
ACTTCTGTCC GTTATATTCT TTAACTCGAA TGTGATATTT GCCACACTCA GATGCCAAAG	1380
CCGCACAAAA TGCTCTAAGA GAAACACAGA GACAATACGG TCCCGGTGCT TGGTTGGGAC	1440
TACCTCGCCA GAAAGGGGGA AAAATTCTGA GTGAATAAAA TTACTCATCT CAGTACCAAG	1500
CACTAAAGTG CGTAgcCTnC CTGTACTACA GGATCCCGTG CGATGCATGC GCGATTGCAA	1560
CCCTTTGGCA TATCATGGAA CAGCACGCGC TCTGCAAGCG CATATGCAAA CTGCAAGTGC	1620
AATGCCGTTT CCGTATGTTT CCAATACACA CCCCCTTCTT TTTGATACAG AGAAGCCAGC	1680
AGCGCACTTC CTTCTGGAGT TGTGTAGTAC GGAGCTCTGT TCCGCACATA GTGGAAGGCA	1740
TACACCGCAT CGAAAAGGTA AAACAGTGAT GCCACTTCTG TGTGGCAGTA ATGCTGAACA	1800
AAGCGCGGAA CACGTATTTT ATCTCTCGCT TCGCGAGArA AAACGCCTC ATACATAAGA	1860
CGTCGCATCC CCTGTGCAGC GTCTTCAAAA AAAGACACAC GGTTCAGTA ATACGCGTAA	1920
TCCGCCTTTA ATTCTCGATA GTAAACAAGC TCCCGGAAAA GgTTCCACAA TATTTCTTTt	1980
CCGTCAAAGT CGTCCTTTAA AAACCACTGC AGTGGAAACC CTACCATCCC CTCCTGCGGA	2040
ACAAACACAA ACCGATCAGC TTGTAAAATA GGTACACAAC GAAAATGCGC ATCCCCCGCA	2100
AArGTGGCGA TATTCGGTGC TTCAGCGGAA AAAAAACGCG CAAAATTCTC TTGCGCACGc	2160
tTcGCATCAC ATTCATTAT TGTCATGCAA CGGCGGCGG ACGATCTTAC TCAGTCTCTC	2220
TTTAAACATA GAAGGTTTAC AAAATTCGTG CACCGTCAAA AGCCTGCACG TACCATTTTC	2280
TGCCGCAATA AACACGTTGA ATACCGACGG GTGTTCACTC TGCAATAAGA ATGCAGAAAC	2340
GACCGTCTCT GTTGTTGTTT CAAATGAGCG AGAATACTGC GCCGTGCCCG TAGCATCGAA	2400
TGACAGCAAA CGCGCTCCC CACCCCGGCC GAAAACAAGC ACCATGCGTG AAGAGAGCGC	2460
CAACGCGCAT AACACTACAC TTTTGAAACC TGTAATCCAT TCGCCATACG CATAGTCCCC	2520
CGCAGCCATG CCATGCTCGT GCCGAAGCac GCGACTTTCC CCGTCATCGC CAAAGACTAC	2580
CACTCGATCC TCAGAAAGCA CGACCGCTTC AGTGTATGGA TTTTCAAATC CATATATCGC	2640
GTCAGAATAC TCTTCATTGT GTAAAAGGCG TGTACCGCTA AAACCACTAA ACACCACAAG	2700
cTGCGCAGTA TTAAGAGCCC GTACTACCCG TATTCCCCCA CCTAAACCAA GAATCGGCCC	2760
ACGATACTCA TATCCGTGTG CACTCTTTTC TAAAATGAAG AGAGCACCTG TCTCATCACC	2820
TACCACCACT CGGTGAGCAT TTACTTTTTC CACACACAGC ACACGCTCAT ACACGCCTTC	2880
AACACGCGCA ACTACCTCAA ACGAAACCCT TCTTCTCTCT GCCTTCTTCG ATCGTTCCCTG	2940

AATAGAAAGC	ACGATCGTTT	CaCCACtTCG	GTAACGACAA	CTACTTCTCC	ATCACCCATA	3000
GAGATAAGCG	CACAAATACG	CCAATCCGTT	TTCACGCTCT	TATGCGTGGA	TTCCGCAACA	3060
AGCCATTGAT	CGTGCACCCG	GTATAAAAGC	CGTATATCAT	CTGTGCCACC	TGCGATAAGG	3120
ACAGAATCTT	CCGCCAAAGG	AATCGCTGCG	GTGATGCTTT	TTCCAAATTC	AAAAAACACG	3180
TCACTGTACG	TGCACTCATC	TCCACAGATA	TCGGGAAAGC	AGTGCCGAAA	CTCGGGAAGC	3240
AGCTCCTGAA	TCAATGCGTC	ACTTGTCTGT	TCTGCACGTG	CAAGATCATC	CCACAGTGCG	3300
CGCGGAGTTC	CTCCCTCACT	GCGCAATCGC	GCGTGCTCAG	ACACCAGTTG	GTCACACGAA	3360
CACTGCAGAT	GGGCAATCCG	ATCCGCACAC	TCACGTGCGT	ATGATTTCCTC	CTGCAAAAGT	3420
CTGAATGCTG	CACACACGCG	TACCAACTCG	TGTATCCGAT	CGTGCAGAAC	CAACATCGCA	3480
CCGGCATCTA	CCACATCCGG	CACTGTATTG	TGTGTATGCA	TGGCGTACGT	AGGTCCGTGT	3540
CCAAAGAGCA	ATACCACCAC	CTCAGCGAGA	GTTTTTACCC	CATCCGGCAG	ACGCGTGTAT	3600
TCGTAAGGAC	GGGTACGGAT	CTCTyCGTAA	GAgTAAAAct	GCCCCawTCC	CtTGGGCCGC	3660
ACAcTCCACC	cGTCyTTTTc	TTGAAAAAAA	CCAAaTCGGA	CTGCTTGCGA	TAAAATATAA	3720
TTTTGATCGT	CTGCATTCAA	AACACCACCG	ATAAAGCCGT	CCCACAGCGC	CTGATCCACA	3780
TCCTTCTCTT	CGCCCCGATT	CCACTCATCA	AGCACACGGA	TCACATTACG	AATGGAAAGC	3840
ACCGCTTCAC	GCAGCTCAGG	CTCCACATCC	CCAAGACCGT	CATGCGTCTC	ACTTCCCCCC	3900
GTGCTATCTT	TCCATTGCGC	GGAAAATACC	TGCTGCGTCA	CCTTTGCCAA	TTGCGCAAGT	3960
TTAAACAGCT	TGTCCAATGA	ACCATCAATA	TCCGGCAGGC	AAAGTGATCC	TCCAGAAGAG	4020
GCAAGACGCG	CGAGAATGAT	GCGAAAAAGT	TCATTTTTCT	CAGGATGCGC	CTGATTCGTA	4080
TAAAGACCTT	CTGTGGACTG	CGGAGGGTAA	TCATATTGCA	ACGTGTTAAA	GCGCGAAGCA	4140
AACGCGGGGT	TGAGCGCCCC	AGTGCCCTCG	TAATGAACAA	GTCCACTGCT	GATGTTCCCC	4200
GTGGAATTA	CGCCAAACCC	TGCAGCTATT	TTTACCGGGC	CTACCCCGGG	GATATAGGCG	4260
AAATCCCCTA	CCCGTTTTTG	CAAATATCA	TTGAGTGCGA	TGAGATGCTG	CATGGGAATT	4320
GCGTTGATTT	CATCGATAAC	AAGAGGTCGT	CCCTCTTTTA	CTGCGCGCAg	CACCTCACGC	4380
TCAATCTTTT	GTACCTCAGT	GCCAAAATTG	CCATACTTTG	CAAGATAGAT	ATCCAGCATT	4440
GGATCAAATG	CGTAACCACG	CTCAGTAAAG	GCATGCACAT	CCTGGTAACA	GTGTTCCGGT	4500
GTTTTTCCTT	CCAGACTGTT	TTTTAACACA	AGCGTCTTTT	CAAGAAACAG	ATCCTCTGTG	4560
TCGATGTGCT	TTGACCCCGA	AATAAATAGG	GGTTTGATGC	GCTGCAAAAG	CCGCTCGTCA	4620
CCGAGACGTA	GCGCCTGTTC	ATAATATGCC	GCGCGCTGAG	AAAAAAGGCG	TTGAAACTGC	4680

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GTACGCGCTT CCTGGGAGTT TTGTAAGGCA TCTGACACGC CACGCTCGCT GCCCCGAATC	4740
TCCGCACACG AGCCACCGGT TGCAGCAGTG CACCACTcAT TAAGCGCACA ACGGACATCT	4800
TCAGTGATTA ATTTATGAAG CGCAAAACgc tCCGCGGCGA GCACGGCGAG CTCAGTCTTT	4860
CCCGTGCCGA GATGCCCCGCG GAGTAGCACC GCATCCCCGC GGGCAAGGCT TGTGCTATC	4920
CTCTCAAGTG CAGCACTAAC AGAGGGGGTT TGCGCAAACA CCCCCGAGtG ACGCGTTCAA	4980
CTTCCCCAAG CCATTGAGCA GCATGGAGAA CGAAAAAGGA TTCAGGTGTT TCCAACGCGA	5040
GCGCTGCTCG TTGCTCCTCC AGATCCCGTA TGGCATCTGA GTGCACTCTG GTAAAAACCG	5100
TACTCCGCCT ATGGATACCG AAGTGGGCAC AGGCGACTGC AACTCCCAG TtCcGCAAAA	5160
AGCGCTCATA CACAATACGC GCGTCAATAT CTGCCAAACG TGCCCGATAn CCGTGCAAGT	5220
TCTATCCGCG	5230

(2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TTGGATTTCGC CAGTCTATCC TCAAGGCACT GAACGAAAAA GCACGCATCA TCCGTTGCC	60
CGTGAGTCGT ATTCTGTCTG CAAAGAGCAC GTATGAGTAC ATACCTCCTG TTACCTCGGT	120
GAATGTTGGT ATATCGAAAA CACaGGGAGG CaACAGATAT GGCaAAAGGC GTGCAACGAT	180
GTGCCGAGCT GTGCCaACAg TGAAGAAGT TCACATCTGG CACACGCCGC TATCTCTAGA	240
TGCTCCGCTT GGAGCCTCGG GAAGTCGTGG TGAGTCTGGG GATGTTGATG GACTGCGTAT	300
AGGTGACTGC GTGCCGGACG ATCTTTACGC GCAGcCTGAG GAGCATATGC TTGCATGTGC	360
ATTGCAAGCT GATATTGCAA AGATTTTACG ACTTTTGCCT GCGCGTGATG CGCAGGTCAT	420
CCGCTATCGA TTTGGACTTG GCGGGTATGA ACGGCGTTCT CTGCAAGAGA TTGGAGAAAT	480
TTTTCAGATA ACAAAGGAGC GCGTTCGCCA AATAGAAAAA AAGGCTTTGT TCGGTATCCG	540
TAGCTGTGCC CGTCAACACA GACTGGATTC CTACATAGCG TAGACATCAG AGGCGTATGA	600
AATAGGAGCA GGACGCGTTG GGCATACAAC TTATAGTGTT TTTAGGAAAT CCTGGTGCAG	660
AGTACGAAGA AACCGGGCAC AATGCTGCAT GGTGCTTTT AACGTACCTT TTCCCATCCA	720
TCGTGCTTCC TTGGCGATGC GGATGTCGGG GGTGATTGC GCGTATTGAA GGGTTTGAAG	780



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GGTCAAGCGA AGAAGTTTGG CTTTTGAAAC CGCTGACTTA TATGAACCGT TCTGGGAAAA 840  
 GCGTAGGGGC AGCATGTGCC TTTTTCAGAG CGGATGCGAA cAGCTcTTAG TAGTGCACGA 900  
 TGAATTAGAA TTACCGTTCG GTGTGGTGAG TTAAAAACAA GGCGGAGGGC TTGGAGGACA 960  
 CAATGGGTTG CGCTCTATCA AGGAAGTGCT TGGTACCGCA GATTTTTTGGC GGTTCGCGAT 1020  
 AGGCATCGGG CGTCCACCCA GTGAGAGTGT GAATATAGCG CAgTACGTCC TCTCTGCCTT 1080  
 TTACCCGGCA GAGATGGCTG CATTCCCAA GCTGGGGCGT GCCACGCGAG ATCTTCTGTG 1140  
 TCAGCTTGTA GTAACAGATC AGGCAGCGAC AGTCACCTTA CTCAGTGCCT GGAGAAAAAA 1200  
 ACGGTTGCTG TCTTTATGCG AATAAGGACA GGGTGACTCc CATACGGTGA AGGAAGGGTA 1260  
 AAAAGAGAAA GTGTGGGGAG GACTTGCATA AAGAAAGAAT GGTGGGTTAn TGGCGCGCCA 1320  
 CGTGATTAG CTAGGACGAG GAAATCATAT GGCATTTGAA ACAATTTTCGT CATGCTTAA 1379

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTGCCCnAGG CGCGTGTGGG TGGTGCGCAT AACCAGGGGA AGGATATCCC ACCGTGTTGG 60  
 TAGTAGAAAC CCGTGCTTCA GATTGTAGGG ACCGGTGCCC ATAAGTGCAC CAGGGGCTTG 120  
 GCCATGACTG CATACCCCCT TGCCATAGCT GATGCCCCAC TCAAGTGTGG CAGAGCCAGT 180  
 TAGCTTCGGG GAAAACTCCT GTCCGAGCAC TCCCCGCTC GTCCTACCC CCACCACCAC 240  
 ACACAGCACA CTCCCCCACC GCATGCACCC CATGCTACCT CACCCCCCCC CCGGCCCTGT 300  
 CTAGTAGCCC CCTCACCCTG CCACCTGCAC ACACGCAAAA ACTCACCCT CTTGCACCT 360  
 GCCTACCCGC CnGCATCGcG CGcACCCCAG GCGCAGACCT TTGCGAGCGC AAACGCACCG 420  
 ACACACCCAG CCACACATCC CATAAAAAGC GTAAACTGAT CCTGCATCCC GGCTGCAGTT 480  
 CCCCCTGGGA ACAACGTCAC GCTCGATCCC AGCAGGAGCC CACACACACA gCATGCGCGG 540  
 aCACCGGGTA CAACCGAAAC CATGCGCGGA GCACCCGCGC CGCCCCAGC AACCTATCC 600  
 CCATTCCCAC ACAGAGTGGG AACAGGAGCC CCCACACGTG CGCAGAACAC AACCTGCTTA 660  
 TTACCGACGC GCCAGTCACT CCTCCCCCCT GCTCCACCGC GCGCAAAGAC AACACGCTCA 720  
 AAAGCGGTTG GTACACCCCC GCCAGCAGCA ATACCAATGA ACCGAAAAAT CCTGGCGTGA 780

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gCATTGCCGC CGCCGCTAGC GCCCCTGCGC ACACGGTCGC CACAAATCCG CGCGTGTGTG	840
CAGTAGTAAG GACCGCCGTA GTCTGAACAG ACGCAGGGGC GGTCCGAGAG GATGCGTCAC	900
GCGCGTGTGTG CATGCGAGAA AACGCACACA CTGCCACAAA CCCAAGCAGC ACAAAGAAAA	960
TAATTCTAAC TGCACACCAC ACGCGGCGTG CCGGTTCCCC CACATGCCCC CGCGCTGTGC	1020
CTTCCGCTTG CACTGAGTGC TCCGCGGcAA CACTGGCGGC ACGCACCCGA TTGCGCAAAG	1080
ACGGCACACT TGCTAACAGC ACCCCGGCCA AAAAGGCATT CGTAAGATGA GGAAATGCTT	1140
CGTACAACGC ACGCATAAAG CGTGGgCACA CCCCTATCCC CAmCACTATT CCCCCGCAA	1200
gGGCAAGCAA GCGTCGCCAC TGACGGCACA GATGCGCTCT ATCCAATGCT ATTGCTGCAA	1260
TCAGTAaTTC CCaCgTGCCA CAGAGCAGCG CAACCGTACC CCCCgAAAGA CCCGGTACCA	1320
CGTTTGCCGC TCCTATTAAC ATTCTATCC ACACGTGCAT GACCGGTGAA CTCATGCTCC	1380
GCCTCCCTTG CTGGTCTTCT TTCTGCGAAA AAACGCACCC TCCCCTTCAT CCGGGCACTT	1440
CTCTCAGTTC AACCgCGTCC ATCGCATGCG CAACACACCC TCACCATACA AAAGGAGTCT	1500
GAAACTCTAC ATGCTCAGCG ACAATCTTTA C	1531

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TCTGCCCGGG TGTGGTGAAG CCGCnCAGTT GCCGGCGCGT TACnCGGATG GGATGCCAGT	60
CCAGTGAAAT GCCGCGTGCa GAAGCgTTGG TGCAAACTGC CcTTTGCCAG AAaGCTGCCg	120
TATCTAGAAaT CcAGTTACAC TTTGAWCcGG GTTGTCcTT TCTCTGAAaG GCTTCTACGG	180
TTGCaGAGAC GGTACGTGCC aACGAACTTT TTGCGCCAGC AGTCTGATAT TCCCTTGAC	240
CTTGGAGTAA CAGAAGCAGG CCCGCTTGTT TCCGGTATTG TCAAAAGTAC ACTTGCAATT	300
TCCCAATTAC TGTCACGCAA TATTGGTGCC ACGGTGCGGG TGAGTCTTTC AGATAGCATG	360
GAGCATGAGG TGcTGgyCG CGAGAAATTC TTGCTGAATG CCGTAAACGG GCTGGTGGGG	420
TTCGTTTAGT GTCATGTCCG CGCTGTGGCA GGATTGGTTT TGACGTACAC GCATTTGTGC	480
GGAGGTGGCA AAAGGAACTG TTCAGTTTGA AAAAGGATAT CACGGTTGCG GTTATGGGCT	540
GTGTAGTGAA TGGTCCTGGA GAAGGAAAGC ATGCGGATCT CGGTATCAGC GGTGCGGAGG	600

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ATTCGGTGAT TTTT TTTAAG CGGGGAAAGA TAGTGCGTCG CATTCAGGTA CGTGATCTTT 660  
 GCGCAGACGA GCGCAGCGCG ATAATAGACG CAGCGTTTAA AGAGGAATTG TCAAGTTTAT 720  
 GAATAACCTG aTCAAAGCAT ATGCGGcGGG TGTCATGAGT GCTGCGTTTC TTTTGGGTC 780  
 AGAGGGGCGG GTGCGCAgTG AATCCGATCG GGTGCGTGGG GAGGATCCGT GGCACCTGTT 840  
 ACAGTGGGCA CAGGTTGTCT ATGAGCGAGA GGAATTgGCG ATACGTTGCG CTATGCcAgC 900  
 GGGnCACGGG CGCTTCGGCG GGArcAA nTG GAGCACCAGT GCCgAaGTGC TACTGCGTGC 960  
 ACGCACACGG GCTGAGTCAG CGGGGATACC CGAAACACTG TCTGATTTAT ATGCACTTTT 1020  
 AAAAAGTCGA GGAGAGACAG ATGCCtGCGA AGTGCTTGAT GCTATTTTTTC TCACTCATGC 1080  
 GCCGCACGTT TTTCAAAACT CCGTTTCCAA ACTGCTCCAG TGGCTGAAGG ATTCAGCCGC 1140  
 TTTTCCAGAA GCGGAGTTGC TCTTGGGAAA GGTATTCGAG GGTGAAGGAG AGTACGCCCA 1200  
 GGCTTTGCAG CATTATCGAA ATGCGTGCGA TACGCGAGCG CAGCTTGTA TCCCGACGC 1260  
 TCGCTTTGAT ATTATCTACG CAATGGCGAA TGTGTCTCGT CTGCTCAGTC AGCAGGATGA 1320  
 ACGGGAGAAG TACTTGCTCC TTGTGCTGAG CGAAGATCCT CTGTACAGTG CACGTGAGGT 1380  
 GTGGGGCAAG ACGCTGCA 1398

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AACCGATAGA CGAAGGGACC ACACGCGCTC CTCCCCTTTT TAAATAGAGA AAAGAATAGT 60  
 CCCTACGGGA ATTGAACCCG TCTTCTGAGA TTGAAAATCT CATGTCCTAA CCGATAGACG 120  
 AAGGGACCAC ACGCGCTTTC CCTAGGGAGG ACTCGAACCC CCACACACAG AACCAGAATC 180  
 TCGGGTGCTA CCATTACACA ACCAGGGAGG GAGGCCCAGG CTAGTACGAC ACGTATTTTC 240  
 TGTCAGCAG ATAACGAACA CTCACTCAGA TCAAAAACCTT ACCCGGTACC TCCACTTGAC 300  
 CGACGCAGAC TGGGCAGCTG CCATCAGCAG CCCCACAGGC ACACGCGnCA TTCCGGGCAA 360  
 AGACACACAA CTGGCACATT GCCGGATACA ATTGTGGCAG TCGCTCCTTC CAGTTCAGTA 420  
 GCGCTATTGc AAAGCGCGCC TGGCTGcGAT ACAAGGAGGA GAACACTTAC TCCGTATGGT 480  
 TATTTcAGGa TTACGCGCCA TCGAAGAGTT TCTGCGCGgC AGtCCTnTGC GCTAGAAGGG 540

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TTACACGCGG GAGGAAAAA CAGCAAGACG CAACAAAGCT GCGTGCGTGT GTCACGCTCT	600
ATTATGCAGC GGAAATGCG CGCATCAAAC GACTCCTTGG TATGGCCGCG GCACGGGGGA	660
TACGGATCAA CACACAACGT GTGCTGTGCT TGATAAGTAG CGCGTAGTTT ACCCnCTGC	720
TGCGCGATCA CCGCGGTATC CTTGCTGTTC TAAGTTCACC GAGCGCAACG TCCGCAGGGT	780
TCTCATACAA GAAAAAACG ACTCCGCTGT GGACAGCTCG CAGGAACGAA CGTTGTTACA	840
TGCACTGGCA ACGCACaGC ACGCGCTTGT GCTCGTCTTA GACGCAATTA CTGATCCCCA	900
CAACGTTGGG GCAATTGTAC GCATGCAGAC CAATTTTCTG TCGATGCAGT GCTCCTGCCG	960
CACCATCATG GGGCAGGAGG TACAGAACT ATCACGCGAG TGAGCGCAGG CGCCGTTGCA	1020
TGGGTACCGC TTGTGCGTGT ACGCAACCTA GTGCGCACTG CAGGTATCCT CAAGCGTTCA	1080
GGATTCTGGC TATACGGTGC TGATGTAGCA GGAGAAGCAA TAGGCGCCCG TACTTTTCCT	1140
CCTAAGACAG CGCTGTGTT AGGCAACGAG GGGCACGGCG TTTCGCTTTG CTGCGCACGC	1200
ACTGCGACGC ACTCATCTCT ATCCCAACGC AGGGaATGTA GACAGTCTGA ACGTGTCCGT	1260
TGCCGCAGTA TTCTGTTATA CGAAATACGC CGGAGTCAGC AGTCTCCCTA CTCCGTACAA	1320
AGGCAAAACG AAATGAACGC TCAATGAAAA CACCAGGGc ATCTTCGCAT CTTTAATTCA	1380
TATTGCATCT TTCACCCCAT TGCCTTACct GAGGGAGTCT CTACGCaCGC GGTAcGGAgG	1440
GACCCCATGG CACATCTTCC TAAAGAGTAC GATTTTTCCTA TAGAGTCATT GGGGGAAAGC	1500
AAAATTCCCT CTCCCATCTA CCTGTCTCAC ACCCTTGGCG ACTTCATTCC TAAcTACGTC	1560
AgTGACAATG AGTACATCAG CCATGAACTG AGTGCGCGTC TGGGGGAGAC GGTAGGGCCC	1620
TTTACTCATA AAAACTTGAT GGAGCGTGCG GGCCCGCGCC AGAAGATTTT CTTCAACCCG	1680
CATCACGTTT ATGCAGGTAT TGTCACCTGT GGAGGGCTCT GTCCCGGCCT CAACGATGTC	1740
ATTGCGCCA TCGTCCGCTG CCTTTGGGGC CGCTATGGCG TTAAGCGCAT TAGTGGTATC	1800
CGCTTGCTA TAAGGGCCTC TTGCCCATT ACAACTTCGA TATCCTGCCG CTCAACCCTG	1860
AGGTCATCGA TAACTGCCAC AAAACAGTGG TTCGCTGCTA	1900

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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TTCGATAGAC GGACAATATC GTGTCCCTAC CGCCTTTATT CTGCCAGAAA AGAATGGAGA	60
ACGATGAAAA TTCTCACGGA TGAGCTGATG CGTTCTCTCC ATTGGTGTA TTAATATAAC	120
AGTCCCGCAT GTGGACGATT GATTTCCcAC GTGAGCmAG GAAAAAGGAC GCATGATAGC	180
GTCGGCTTCT TGCTTTTCCA TTACCGAAAG ATCTACAGAT TTTCGTAGTA CGCGCGCGGG	240
CGTACCCGTC TTCAGCCGTC CCATCTGAAA CCCCTTTTTT CTCAGCGCAG CTCCCAGCCC	300
TTCAGCGGCA TGTTCCTTA ATCGGCCTTC AGGTGCCTCA TATTCCCCAA TATACACACG	360
CCCTTCCATA AAGGTCCCCG TAGTCAGTAC CACCGCACGT GCAGAGATGC GTCTGCCGCG	420
TGCGGTAAct AyCGCATGCG CTGCCCCATA CGCTACATAT CCTGCATCAG TGGTATTGGA	480
ACACACAACG TCTACCACTG TGTCTGATA CAGGTGAAGA TGCTGCGTAC ATTCCAACGT	540
ATACTTCACC TTCTGGGCAT AAAAAACTT ATCTGCTTGG ATACGCGGCG CCTGCACTGC	600
AGGnCCCCGG CTTTGTGTTGA GCAGTCGATA CTGAATCATG CATGCATCCG CAACTTTCC	660
CATCTCTCCG CCGAGTGCAT CGATTTCTCT TACAATATTC CCCTTGAAA TTCTCCAAT	720
GGAAGGATTA CATGAGAGCC TGCCGATACT ATCGATTGTC TGAGTGATGA GTAACGTGTG	780
CTCCCCCATA CGGGCAGCGG CCAGCGCCGC TThCGGCACC TGCGTGCCA CCACCGACGA	840
CGATAACGTC ATAGTCAGAA AATCTGAAAC CCATGGGCAG CGGATTATAG AAGAAAGGTG	900
CAAAAGGCTT CAATCAGGAA GCACGACAGA ATTCAGGAAG CAACGCACAC ACAACATCTG	960
AAGCCTGTTT CTGATAATAA AGGTACCCGT ACATCACCGC TGCGGATAGG ATCTTCCTCC	1020
CGTACTCCCG AGGTCTGCA AGAGGCAGGG TTTCGAGGAA CAGATCATCG GGCAGACTTC	1080
CCCTCTGTTT TTTCATTG CGGACGCGCG ACGGTCCCGC ATTGTAGGAG AACAGGGCAC	1140
AGAACACGGA GCCATCAAAG CGACGAATGA GATCGGAAAA GAACAGACTG CCGAATCTAA	1200
CATTGATATC CGGGTCAGTT AAGTCATAGG TGTCGATATT GAGCTTACGA GCGATATCTG	1260
AAGCGGTTGG CCTCATCAAT TGAGCAAGAC CTACAGCGCC CGCCGAGAG ATAACcTGCG	1320
GCTGAAACAG ACTTTCACCTC CGGATGAGCG CAAACAGCAG ATACTCCTCA ATATGATACT	1380
TCCCTGcATA GCCTTGATG ACGTCAAGCC ACGGACGCGG GTACGCAATC TTCAAGTGTT	1440
CTACAGAATA GCGCGCACCG TGAGAGCGTA TTGCGTACGA CTGAATGCGC ACGGCATCGG	1500
ACCATCGTGA TCTTTGTATG TGTGCGTTCG CAAAATGCTC TGCAAGGTGG AGAGGAATGT	1560
CAGGATAGAA CTGTACCATA GCTTGGTAGA ACATATCGTC CAAGTGATAG TCTACATAAC	1620
CTTGAGAAT AGCACGCGAC TCATCGGGG TAAGAAAAGG ATGCGGTGTT CTCTTACTCC	1680
GCACCTTATA CAAAGCCTCT TCCAGAGGAA TGCCCAATGC ACATGCAGCA AGAACACGAT	1740

AGTAAAGGGA AGAATGCGCA gTTTCGAAGA TGGTACGGTA AGCGCGGCGC gcAcTCTCTT	1800
CTGAAAGCGT ACCTGAACGC GCAAGGACAT ACGTAACGCG CGCGGAnTTC GGGTAATGCT	1860
CTATGCGTCA CACCTCTTGC AGTGTAGCCA GACGCCCCCA ATCTTGCTGC GTAGTCAGCT	1920
GGACAATTGC ATAATCGACA AGGTCAGAAA ACCAAGAATC CGAACGCCAA CGTGGTGCAC	1980
TTTCAACAAG CACCTTAAAG AAAGAATCAA AGTCCAATGC ACGCagTACG TCCAAGTAAT	2040
ACCACAGGGC ATTATCAGCA TCTTGCCGCC TTGTGGCCAC TTTCTCTGCC TTTTTGAAAA	2100
GGGGAAGCGC TTGCTTCTTG TGAGAAGCGG ACCGCGAGTA AAGACGCGCC GCATAAAAAT	2160
AGCAATAAAA ACGCAtCGTG CCTCTAATTC CGCATTGGAC AACGTTGAGC GCGATAGATG	2220
TGCAAGATGG TCAAGAAAAA CCTGCGCGGC TTTAACAATG TTTTCACTAC CGTAAAGCGC	2280
TGCTTTCCCA AAATCGGAGA GAACCGAATT TGTAGCGTAC CgCGTGTGCC ACGCAGAAGA	2340
GCGCAACAAC AATCGCACTC TCTCCACCC CCGTTTGTAA TTCCTGTGAA AGACGTCCAC	2400
ACGAGCACCA TGACTTCCCT TAAAGATACG CGGCAGATCC GGCAGTGCCG CAATAAGCGC	2460
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CGTTCTCAGA CTGTAGTAGC GTTCGAGTTC AAAGAGCACC CTTGAACGCA AAAGGCGAAG	2580
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GACACACACC ACGCACCACA CGCGCAGGCA CAACCTGCCC TCCCGTAAGA GAGAGAAAAA	3000
GCCACCTCCC CACACGAGAT GCTTACCGTG ACGGAAT'TC AATTGAGGTT CCTGCAACGA	3060
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TGTAATAACT CCGCGCCAAA TCCCAGAGCG TATCCCCCG TTTGACCGTA TAACGCACAA	3180
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CAGCCCCGGG AGACGCAGGG GGgACGTCTT TTTCTTGTG GGTTTCTGGA AGAGCAGTCT	3300
CAGATGGGAG ATCGACGACA CGTGCC'TCAA CCGCAGTACG CTCAAGCTCA CGCGCTGCAA	3360
CATGCGCAGA AGACCTGGGC AGTTCAACTT TTTGTGACGG CACGACCGCA GGACGAGAGG	3420
CGCCGTGCAT GTACAGAACC CAACCTACCA AGACACCACC GAGCAGAATG AGAAATGCGC	3480

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ACACTGCCAA CAAAATCCGT CGTCTCCTCG TGAGGGTAGA ACCATCCCCT CCCTCGTCTT	3540
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CTGCGCACAC CTTTTCGCGA TCTCGTGCA ACCGCTCAGC ATGAGCTGCA CCTCGCGTGC	4320
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CAATGTTATG CTCATATCTG CACTTGCAAT CATACTCGTC CGTGCTCTGC GGGGGAAACT	7140
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AAGTGGAGCA GCAAACATCG GCGTCTCCTC CTGCGCCATG ACCCTCATTG TGGAACCAT	7440
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GCCAAATTGG ATCCGGTACC CGATTCTCAA TATTCCGCTC CTGCTCAATG GCCTCGTTTG	7560
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CGGTACCTG GTGAACACGG CACGCGGAGC AGTGATCGAC AGTCAGGCGC TCTTAGACAG	8640
CTTGACAAA GGCAAGATTG CAGGTGCTGC ACTGGATGCG TACGAGTTG AGGGTCCGTA	8700

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TGAAATCAAG	CTGTAACCTGA	CGcCAGGTGT	CCCTGGTCCC	GTGTGAGTCT	GA CTGGCTAA	8940
TCGGTCAGTC	TGGAGTCGCC	AGCTCAGGGT	GGGTGTGGG	ctCCGCGGGA	CCCCGTCCAG	9000
CCGGTTACGT	GCGGGCGCGG	CCCACCTGTG	TGAGCGCGAT	AACCAACATC	AGTACCACCA	9060
CCGAGACCAG	TGCGGTGAAT	CCCCCTGGGG	CCACGTTCAA	GTAATACGAG	AAGACCAAAC	9120
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CCCGCAGCTG	TAGCnTGTCG	CAACCGGTAC	GGTCATGAGC	GAGCTCAGCA	CCAAAATACC	9240
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CTGATGGTAG	CGCAACGCTA	GCGTACCCTAC	GCAGAACACG	CTGAGTGCGA	GCATGATCCA	9420
CAAATCGCGT	G TAGAAACAA	CCAGTATGCT	GCCAAACAGA	TAGCTGTCTA	TATCCGCCTG	9480
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ACCGATATAA	CCGTTACGTT	ACGTGATGTG	TTCAATCCCT	TCAGCAGAGC	GTAAATATCT	10020
TTCTGTCCTC	GAGAATCAAT	ACCTGTTGAC	AGCTCATCGA	GCACCAGCAA	ATCAGGATCT	10080
CCGATCAGGC	TCCGCGCAAT	GTACACCTTC	TGTAATTCTC	CTCCAGAGAG	GGTATACACA	10140
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GAGAAAAAAG	AGACCACAGC	TGCACAATGC	AAATTGTCTC	TCTACCATGG	TTTTCGAAGA	10620
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GCCCGTTTGG	GGTGAAGCC	CCTTCAAAGG	AGCCATCATG	CAACGCTGCT	CAGTAGTTGC	10740
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AACCCACACG	GATAAGCTGC	CTGTTGTGGT	GACATTTAAT	GCTCTCAAAG	AGTTAACACA	10860
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CGACTTTGAA	CCAAAAGCAA	AACACATGGC	CTTCATTAGT	GATGCCAAGG	TCATCGTGTA	10980
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ATTGCAATAG	GGAGTGAGCG	TGGATGGACC	GAATCTGAAC	GTTTACTTTT	CTCCGCCaTG	13020
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CsCGTGCGCC	GTGTACTCG	CCAACGCGCA	CGCGTGAAA	AGAAAAATCC	CTCGGCCAGG	13140
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GCCGAGATCC	ACGGGAGACG	CTCATCTCAA	GAGATCATGC	CCTTACGTAT	GACCAATCGA	13500
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CTTAATCATA	TCAACCCATT	CCATCTTGGA	TGCATCAAAA	CCGATGCCAC	GTTTCTCCTT	13740
TGCCTTCTCT	GCCACAAcTG	CGCCATCAAT	ACCCGCGTTC	TCTGAAATCT	GGCGTATCGG	13800
CTCCTCGAGA	GCACGACGCA	CAATCTTAAA	ACCAACCGCC	TCATCTGGAG	TCAGTCCACT	13860
CAAATCAGCT	TTCTCGAGCG	CCGCCGCAGC	CTGAATAAGC	GCTAAACCAC	CACCAGCAAC	13920

AATACCTTCC TCTATTGCCG CACGTGTCGC ATTTAAGGCA TCTTnCATa

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## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CACAGCACCC TACTGCGCCT TCAGGTACGC GACGCACACA TCGCAAGAGA AATTGCCGCC	60
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CCCACACCGG aCACTGCGCG CATTGCCCAG CCGGATACGA CACCTCAGGT GCAGGGTGCA	180
CAGACTGGAT GCAGTTACGA CTTTCTATTG CCACGCCTCC ACCGAGGCAC CGTTAAACAA	240
TTACTCTTGC GCCACGGATG GCCGGTGCA TATGAAGTGC CTCTCCGCGA GGGAACTCCC	300
CTATCCTTGC GCTTACGCAT CTCTCCGGCT TCGTGTCTCT CTCTTCTAC TCGGTATCCG	360
TGTTGTCACA CGCCAGGGAC ACCCTCGTTT GTGCCACGTG ACTACCAGTG GGAAGCAGCC	420
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ATTCTGACTC CTAATAGCGC AGCTGCACAG CAATGGAAAC kTGAATTgTG TGAAAAAACC	600
GACyTGGACG GGACATCCAT CGGTATCTAT TCAGGAGAtG CAgGAAATCA GACCAGTGAC	660
TATCGCAACt ACCAGATAcT CACCTGGCGT GCGCATGCAG ACGCTCCcTT TTCCCATTTT	720
CGTCTCTTTA TGGAACGCAG TTGGGGTTTG ATTATTTACG ATGAGGTGCA CTGCTCCCT	780
GCACCGCTTT TCCGTATCAC CGCAGAACTT CAGGTGGTAC GACGCTTGGG ATTAAC TGCA	840
ACGCTCGTGC GAGAAGATGG CTGTGCGCAG GATGTGTTCA GCCTCGTAGG ACCGAAGCGG	900
TATGACGTGC CGTGGAAGGA TTTAGAAGCA CGCGGCTGGA TCGCACGGGT GCGGTGCGTA	960
GAAGTTCGGG TAACGATGGA CCGGTCAC TCAGTACAGT ACATGACAGC TCCTGTGCGC	1020
CTGCGACATC GCCTTGCCAG CGAGAACGAA GCAAAAGTAG CCGTGGTACA GCGTCTATTG	1080
CGCGCACATG CAGGTGCGCC TACACTGATT ATTGGGCAAT ACGTGCAGCA GTTATTACAT	1140
CTCGCACACG TACTGCAGGT GCCACTGGTG AGCGGAAGAC AAAC TTATGC GGCGCGTGAA	1200
GCCATCTATC AGCGTTTTCG CGAGGGCACG CTCCAGGTGC TCGTTGTATC AAAGGTGGcA	1260
AATTGTGCGC TTGATCTTCC TGACGCGTCG gTTGCAaTTC AAGTTTCCGG GaCATTTGGC	1320

AGCCGTCAGg AGGAGGCGCA ACGCcTCGGA CGCCTCTTAC GGCCAAAGAT ATGCGACGCC 1380  
CATTTTTACT CGTTAGTTAC AGAACAAACG GTGGAAGAAG ACTGTGCacT GCGTCGCCAG 1440  
CGGTTTTTGG TAGAGnCAGG GTTACACGTA CGAAACCcTT CGCGTAAGCG AAGTaCACGA 1500  
ATAAAGGATA CTCCGTGCAG AGTCCTCCCT GTGTGTGTGA GGgGGGGGGG AGGAGGGGGT 1560  
GACCGTGCgG TCTCCCTTGT TTTTTTGGT CAAGACCGCT ACAGTACTCC ATGCTCGTAC 1620  
GCACTGCACT CAGGCTCATC TTTGGCTCCC AGCACGAGCG CGATCTGAAA AATCTCCTGC 1680  
CTCTTTTGAA TGCCGTCAAC GCCCAGGAGT CCTGGGTACT TCCTCTCCAG GAGTCTGAGT 1740  
TCAAACAAAA AACAGCTGAG TTTAAGGCGC GTGCCGCTGC AGGAGAAGCG CTTGACGCTT 1800  
TTTTACCTCA GGCATTTGCG CTTGCGCGCG nAGGCAGCTC GTCGTGTTTT AGGCGAGCGT 1860  
CCCTATGACG TGCAGATCCT CGGTTCCCTC GTCCTCCACC ACGGCAAAAT CGTGGAATG 1920  
AAAACGGGCG AAGGCAAAAC GCTCATGAGC GTGGCAGCGG CGTATCTGAA CAGTCTTTcG 1980  
GGGAGGGGTG TGCATATTGT CACGGTCAAC GACTATCTTG CTGAGCGCGA CGcggAnTGG 2040  
gATGCGTCCA GTATATGATT ATTTAGGCGT TTCCGTCGGC GTCATCCTCT CTTCATGGG 2100  
CAGTCAGGAG CGGCGGTGTG CGTACGCGTG CGATATTACc TACGGTACCA ACAATGAACT 2160  
GGGCTTTGAT TATCTGCGCG ACAACATGCA ATTTTTAAcG GAAGAAAAA CGCAGCGTGA 2220  
TTTTTACTTT GCCATTATTG ACGAGATTGA CTCCATTCTC ATCGACGAGG CGCGCACACC 2280  
GCTTATTATC TCAGGGCCTg CAGAAAATGA TACCCAGCAT TACGCCGAGG TTGACAGACT 2340  
CGTCGGGCAG TTACAGGAAG TGGAGCGAAA TCCTGCCACA GGTGACTACC CCAACGAAgT 2400  
GGACGGAGAG GAGGTTCGCG GCGATTATAT CGTTGATGAA AAGAATCGCA AGGTTTCCTT 2460  
CAGTGGTCCG GGGATGCTGC ACATTcAGGA wtGCTCACGC ACGCTGGGCT TATCCAAGGG 2520  
AGTCTATTTG ATGAAGAGAA CTTCAAGTAT ATCCACTACT TTACGCAGGC aCTCCGTGCG 2580  
CACTTACTTT ACCGCGCAGA CGTTGATTAC GTaLAAAAGA CGGACAAGTA CAGATCGTAG 2640  
ACGAGTTTAC CGGTCGCATC TTGGAAGGTC GGCGGTATTc TGACGGATTA CATCAGGCAA 2700  
TTGAGGCAAA AGAACACATC CGCATTGCGC AACGTAATCG CACTATGGCA ACTATCACGT 2760  
TTCAGmACTT TTTTAGAATG TATAAAAAGC TTTCTGGAAT GACGGGAACt GCGGATACCG 2820  
AGGCGTTGGA GCTCAATAAA ATTTATAAAC TTGAGGTGGT AGTTTTGCCc GACGAATCTT 2880  
CCCGTAGCGC GGGTGGATGA GCATGACGTG GTATACCTGA GTGAAGAAGA AAAGTGGAGT 2940  
GCCATTTGTG ATGAAATAAA GGAGGCACAC ACACGGGGAC AGCCGGTACT CGTGGGCACT 3000  
ATTTCTATAG AAAAGTCCGA AAAACTCTCT GCTCTGCTGA GAACACGCGG TGTA AACAC 3060

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GAAGTTCTCA	ACGCTAAAAA	TCACGCGCGC	GAGGCACTGA	TTATCGCCGA	AGCGGGGGCG	3120
AAGGGTTCGG	TGACCATCGC	AACCAACATG	GCCGGACGCG	GCACGGATAT	CAAGCTAGGG	3180
GGTAATCCTG	AATTTCTGTC	ACGACAGAGC	GCAACTGCCA	TAGCATCGAA	GCACGGTTCC	3240
TCCTCTGTCA	CTGTGCAGGA	ACATATGCAA	GCGTGCTATG	AGGCGGAATA	CACACGGTGG	3300
CGCGCAGATT	ACGAAGAGGT	TAAGCAGCTC	GGTGGTTTGT	ACGTCATTGG	CACAGAG	3357

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTGCCCCCAC	GnTGAAAGCG	CTCCTGGTnA	TCGGCGGCGC	ACATTTCGGCA	AATACCCAGC	60
GTCTACTCCA	CACCGCGCGC	GAAACGTTCG	TACCTACGTG	GCTGGTAGAG	CGTGTAGAAG	120
ATATTCCCCC	CGATATCTAT	GCCTTCAGTG	CGGTGGGCAT	CAGTGCAGGG	GCTTCCACCC	180
CAGACTGTGT	TATCGCTGCT	GTGGAgCAGg	ccTGCGCACG	GGCGGCGCGC	CTGTGCTTTC	240
TCGGGTGTCT	TCCTCTGCTC	TGCCCAAGGT	GAGTACCTGC	AGGGCTGTTT	GTGCGGCGGC	300
TACTTCTTCC	GTCGGTTTCAG	CGGGTGCATC	CGGCGCGGTG	TCGCCCAGTG	CTGTCCGACC	360
TTTTGCTGTA	GGCTCCGTGC	GGTGAAACC	GyTTCCCTTT	GTCTGCGAAg	TGCATGGCTG	420
AACGTTGCGC	TCGGCGGGGT	GCTGGGTGTC	CTTTCCGGTT	GTCGTtCTTC	GACGAAAGGG	480
CGGATGTGCG	CGTCGACCGT	ACGGGAAAAG	AATACCTCGA	TGCACAGGTT	GCGTGTGCAA	540
AAGAGGAGCT	GCGCGCGCGT	CCTCTGCGGG	CGCTTATGTG	TGCAATTGCG	CTCAAAGAA	600
ATGCCCCAGC	ACATCAGAAG	GTGGCTCAGC	TGTATGCCCC	AGGgcTTGCG	CGCGTCAAAG	660
AGGCGTTTCG	CTATTTCAGTG	GAGAAACAGA	AGTGGTCGGA	GGCACTTGTG	TTTTTTCGTT	720
CCCTCTCGGC	ACTTCGCATT	CCGCTGAAGG	ACTGGACGGA	GCGATCGCTG	CATCGTGC	780
AAATTGAACA	GTGGA AAAAG	GAGGGTGC	ACGTATTGGT	TGCGGCGCAA	GAGAAGCGCG	840
CCGGA ACTTC	TgCTGCGCGG	AGTCCGGCAG	CCATGATAAA	GGGGACGGTC	ACCATTTTGG	900
TAGATCGAGG	AATTCGCGTA	GAGCACGGAC	GCGGGTTTGC	AGATCGAGTT	ATCGGGTCAG	960
GTTTTTTCAT	CGACAAGAGG	GGCTATATCG	TCACTAACTA	CCACGTTATC	AGAAGCGAGG	1020
TAGATCCTGC	GTACGAAGGt	ATTGCGGTGC	GTACATCAAG	CTCCCCTCAG	ACAACACCGT	1080

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GAAAGTTCCG GTGCGCGTTG TCGGGTGGGA TCGCCTTGCA GATCTTGCAT TGCTAAAAAC	1140
AGAAATTACT CCTGAGGTGG TGTTTGGCTT AGGTCCTCA AAGAATTTGG ACGTGGGGAG	1200
TAAAATCTAC GCGATAGGAT CGCCTGCTGG GCTTGAACGA ACGCTTACTT CTGGCATCGT	1260
GTCTGCGAAA AAGCGCaAAC TGCTTTCAGT CGGTGGGGGA GTGCTGCAGA TAGACGCATC	1320
CATTAATCGA GGGAACTCAG GCGGTCCAGT TATCGACGAG GAAGGGTGCG TTCAGGCAGT	1380
AGCGTTTGCA GGTGTGGAGC AGCATGCAGG GCTTAATTTT GCCATTCTCTG TAGAATTGCT	1440
CAAGCAGGTG CTGCCAACTT GT	1462

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CTTTTTGATG ACGCACGAGC GCTTGTGCCC CCGCGGGAAT TTTACGGGGG ACAGGCTCAT	60
GCGCGGCAGC AACAAGCGTA ACCTGATGTC CCCTCGCGCT CAAACGACGC GTAAGTTCAC	120
GCCCATTTCGT ACCGCATCCA ACAACAATAA CCCTCATGTC CGAAGnCCAT AGTAGCACGA	180
AATTTTTTTG CATGGCCAGC GCGCAGAACA CGGCGCACAA CGCCTGCCAC TCATATCTTT	240
TTCAAAAGTA CCACTACCTG TGCGGTAACC GCCGCACCAG ATCCAACAGG TCCGAGGCGT	300
TCGGCAGTCT TTGCCTTAAC AAAAACACGT GTTACGTGcG TGTCCAGGGc CTGCGCAAgS	360
GATGcGCGCA TCGcTTcCCG AAATGGGTGT AATGCAGGCT GCTCAAGACA GACAACAGCA	420
TCGAGATTCA CCAGCCGcCA GCACGCTGCG CGCACCAGTT GcCAGGTATG GCGGAGCAAC	480
GCGCAAGAAT GTGCGTCTTT CCATCGTCCG TCACAAGAGG GGAAAAACGT GCCAATATCC	540
CCCAGGCCTG CTGCACCCAA AAGGGCGTCA ATGCTCGCAT GCGCAAGAAC GTCTGCATCC	600
GAATGACCCT GCGCTCCCTT CTTACTGGGa ATATGTATCC CTGcAAGTAT CAGcGGTCTT	660
CCTGcACACA GcGCGTGCAT ATCAGTCCCC AGTCCAACGC GCAGGCACCT TCTTCCGTAC	720
ACGGcAGGAC TGATATCCCC CTCGTGAGAG CAGGCTCCGA TGCCCGCTGC TcCAGATCCT	780
CCGGATAGGT AATCTTTACA TTACTGCGTT CACCGGCGCA GACATGTACG GTCCCTCCGT	840
AGCGAGCGTA CAGCTCcTgt TCATCAGTAT ACTGTTCCCC ATCAGTAGCA GCGCGGTGAT	900
GGGCAGCGCA CAGCGAsGCG TAgcAAAAAC CCTGAGGGGT TTGTGCTAAG CGCACTCGAC	960



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TCCGTATAAG ATGCGTTTCG ATACTCCCAT CGGCAGCAAC ACCCTTGGGA GTATCCGTCG	1020
CCTCTATAAC CGGCACTGCC GCTCCATAGC GACAGGTAGC CTCAAGTACA GAATGAATAA	1080
GCGCAACACT CACAAAGGGA CGTGCGCCGT CGTGACCAG GACCACATCG GGCGCATGCG	1140
TAsCATCGCG TCAAGCCCCG CGCGCACAGA CGCACTGCGT GTATGTGCAC CCGGCACGTA	1200
AAGAATGACT GGACGCGTAC GAGACGGGAA CGCCGAAAGA CGCGAATCAC ACGCCACTTG	1260
ACTTTCCTGCG TACGCAACTT CACCTGCAGG AACGGTAACA ACGACAAGGA AGAACGACCG	1320
CGCCTCAAGG GCACGCACGA GTATCTCAGA AAGGAGGCAG ACACCAGGCT GCCTGGAAGT	1380
TAACGGCAAG TACTCCTTTT TCTGCACACA CGCACCACCT CTGCGCATGC GTGCAGAGCT	1440
GCCTGCAGCG GTGACAAGCA ACGCGGCGCG GgTCACCCGG GcACATCCAC CGTACCCGAC	1500
ACAACTGGGT TTTCTTTTGC CTTTTCAAA TAGCCATGGA TGAGCGTTTC AACCTcAGGG	1560
GGTCGCAGCC CCAGCGCAA ACACATCTCA TCCTGAAAAA TACGGTATGC AGAATCATAG	1620
AGCCTTCGCT CCTGGATAGG CAGTTCCTTG ACTTTACTCC GGTGGTAGAG CGAGCGCACA	1680
ACGCCCGCAT TGTCCAAGAT ACCACCACTT TTAAAAAGGT TTAAATTGAC CTGATAACGC	1740
ATTTTCCAAT CAAGAGGACT AGGATCAAAA TCCTCAGACA GAAACCTCAA CGCGCGCTCT	1800
GCTTCCTTCC TTTTGACAAT GGTTCCTAATA CCCAGTTCCT GTGCTTTATC CACCGGAATA	1860
AGCACCGTCA TATCTGACTC TTCCAAGTAA ATGACGTATA TAGCAGCGTC TCGTTCTTAA	1920
ATGTTTMTTC GCTTATTTCC TGcACCTGAC CGACGCCCTG TCCTGGATAC ACCACGTGAT	1980
CGTGGGGACG AAACGCACAC GCCTTACCCA TGGGGCCAGC GTACACAAAC ACGGAAAAAA	2040
GTCAGTGGGA AGAGGAAGGG GAAAAACGAG GGAActCCAC CACGCCCAG TAGCCATAAC	2100
ACAAAGAACG TGTAGACTGG CGCACCCCTT TGTACTACTA TGCGCGCCAT GGCTTGCGTG	2160
CGCCGAGTGC GAAATTTCTG TATTGTCGCG CACATTGACC ACGGTAAATC CACCCTTGCT	2220
GaCCGACTCA TCGAAAGGAC GCGCGCGGTA GAAGAGCGTC TGCAGCACGC GCAGATGACC	2280
GACAACATGG AACTCGAGCG AGAACGAGGT ATAActATTA AAAGCCACGC CGTGTGTATT	2340
CCCTACACGG ATGCACACGG CACCGAGTAT GTGTTGAACT TTGTAGACAC GCCGGGACAC	2400
GCGGATTTTG CATACGAGGT GTCGCGCGCA ATTGCTGCCT GTGAGGGAGC GCTCCTGGTG	2460
GTAGATGCAA CGCaGGGAGT TGAGTCGCAG ACGATCTCAA ATCTCTACTT AGTTTTAGAG	2520
CACAATTTGG AAATTATCCC TGTATCAAT AAGATcGnAC yCTAcGGcAG ACGTGnCCGC	2580
GTGTGCTCCA ACAGGTAGAG CACGACCTGG GCTTGATCC CGCCTCTAGT GTGTTGATTT	2640
CTGCAAAAAC GGGAGAGAAT GTCGACGCGC TCTTTGATGC AATTATCACG CGTATTCCTC	2700

CCCCGCAGGG GAGTGGTACG GCCGCGCTCC AAGCGTTAGT ATTTGACTGT CACTATGACC 2760  
AGTACCGCGG GGTAGTTGTC CaCATTCTGTG TTTTCGAGGG ACAAGTCACA AGTGGCATGG 2820  
TTATTCTGTTT CATGAGCAAC GGGGCAGAGT ACCGTGTAGA AGAGACGGGT GTCTTTGTAT 2880  
TCAACCTTAT TGCACGTGAA GCGCTGTGTG CAGGAGATGT CGGTTACCTG AGTGCAAATG 2940  
TAAAAACGGT TTCAGATGTA CAGGTGGGGG ATACCATCAC AGACGCGTCC TGCCCATGTG 3000  
ACACGCCGCG TGCTGGATTT AGACGGGTAA AGCCGGTGGT CTTTTCCTCG GTGTATCCGG 3060  
TGGACACTGA TGAGTGTGAG CAACTGCGCG AAgcATTGGA GCGACTTGCC CTCAACGACG 3120  
CarTATTTCC TGGGAACGAG ACTCATCCTT AGCGCTGGGG cACGGATTTC GCTGTGGTTT 3180  
TCTAGGACTG CTTCATCTTG AAGTAGTGCA GCAGCGTTTA GAGCGAGAGT TCAACCAGAC 3240  
AGTCATTTTT ACTGCGCCTC AGGTGCAATA CTATGTGTTT CTAAAAACGG GACAGCGCAT 3300  
AGTGTGTGAC AACCCAGCCC ATTATCCTTT GGAGCAGGAG ATTGCACAGG TGCATGAACC 3360  
CTACATCCGT GCAACTATCA TTACGCCGAC AGAGGTGCTC GGTGCTGTCA TGACGCTCTG 3420  
TATTGAAAAG CGCGCGTACC AAACAGCGGT GAACTATTTA GATCAGAAGC GGGTGGAACT 3480  
GGTATACGAG ATGCCCTTGG CGGAAATTCT CTTTGGGTTT TACGATAGGC TCAAGAGTAT 3540  
TAGCCACGGC TATGCGTCTT TTGACTATGA GCTTATAGAG TCGAAGCTCA CAGATCTGGT 3600  
GAAAGTTGAC ATCCTTATTA ATGGGAAGCC GGTAGACGCG CTGCGCAGT TGTGCTATCG 3660  
ACCGCATGCC CGCAGAAGGG CGCAGGCGGT GTGTGCTCGC CTGAAAGAGG AGATTTCCTG 3720  
TCAGCAGTTC AAGATTGCAA TCCAAGGCTC AATCGGCGGG CAGATTATCT CGCGCGAGAC 3780  
GGTTAGTCCG TTCCGCAAAG ATGTACTTGC TAAATGCTAC GGAGGTGACA TCACACGTAA 3840  
GCGAAAGTTG CTGGAGAAAC AGAAGGAAGG GAAAAAGCGA ATGAAGATGG TGGGGGATGT 3900  
GGAGATCCCG CAGACTGCCT TCCTGTCGGT GCTAAAAGAG GCTTCCGACG CCTAAGGGTT 3960  
TCAGCGCTGT TTTT TAGAGT CCTCTCCGTC TTGCAGGGGa TGTGCAAAA GCGATGGTCC 4020  
GTCATGCTGC GGTGTAGACT TAGGTATCTG GATAAGTAGA CAGAACACAC ATTATACGCA 4080  
GCAAAAACAG AAAAAGAACA GGCGGGGAGG GCGACGCGGg CCCTCCGGGC CGCAcTAAaT 4140  
CTTACCGATT AAaTCAATAC CAGGCTTCAA CGTCTTTGCT CCAGGCTTCC AACGAGCaGG 4200  
ACAAAcTgAT CCCCATGCTT AGCCACAAAC TGTGCTGACT GAACCTTGCG CAAAAGCTCA 4260  
TCCGCATCGC GCCCAATACC CATGTCGTGT ACCTCGAAAG CTTTCACAAG GsCTTCAGGA 4320  
TCGACCACGA ACGTACCCCG CAGCGCATGC CAAGTGTCTG GCAACAACAC TCCAAAGrAA 4380  
CCCgCAAGCT TTyCCGCCTT GTCAGAAATC ATCTCGTAGG GcAGATTCTT TATCGTGTCT 4440

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GTCGCATCCG CCCATGCCTT GTGCACGTAC TCACTGTCCG TAGAAACCGA ATATACCTTA 4500

CAACCAATAA CTATAGGAAA CAAACGGGGA AA 4532

## (2) INFORMATION FOR SEQ ID NO: 116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTGGTTAGAT TCCCTTTTGG GGATGAGTTG GATGGTGCTG ACTCTGTGTG TCTGTGCGCT 60  
GTTGTTTTGC CTGAGGAGGA AGTACGTACA TCTCTTTTTT CCTCGTGGGG TTTCGGTGCA 120  
CACGCCCCCT GCGTCTTCGG ACGTGCGGAG TGTGTTGCCG GATATGCCAG TGAGAAGGAG 180  
GCGAGGAATC TTTGTCTGAC TCGAATGGGT TGACGCGCTC ACCCAGGCTG CGTGTTCAT 240  
GCTTTTGGTG AATTTGTTTCG CGTTCCAGTT GTACGTTATC CCGAGCGAAT CGATGGTCCC 300  
CAGCTTTATG GTCGGCGATA GACTCCTCGT GTTCAAGACC GCCTCAGGGC CTGTATTCCC 360  
GCTTTCTTCG TTTCGTTTGC CACGCTGGCG TACCTACAAG CGCGGAGACA TCGTCGTTTT 420  
TTCCAATCCT CATTACCCTG AACTCCGCA GaTAAGCTCC GCGCCTTTTT AGCCCAATTA 480  
GTGTACATGC TCACCTTTAC GCGCAAGAAC ATTAATGTGG ATCCTGTAC CGGTGCGCCG 540  
AAAGCTGATC CTCTCGTCAA ACGCATTGTT GCTCTGCCAG GGGAAAAAGT TATGCTCGTT 600  
GACGGTGTGC TCTATACGAA GACCAGGCAT GATGCGCACT TCAAGCCTGT CGCACAAGAC 660  
CGTACGTACG CCACGTGGGA TTTGAATGCG TTGCCCCGAC GCGATTTGGC GCGTGTTCAA 720  
CGGGTCATAT TTAATGCTGA GGAGCTCGCC GCCATCCATC TGGTAGAGCG CCTGCGCGCC 780  
CAGGTGGATT TTCGCGATTT AGCAGAGAAA ACGCGCGCGT TGGTTGCCCA AGCGCACGCG 840  
TaCGCGGGGg CGGCGTCACG CACCCGACAG GGCATTGGCG TGGCGCAACC GATAACGCAC 900  
ACATCTGACA TTCCTGCTTT ACCTCTGTTT GAAAAAGAAA TCGCGGGGGC GCGGGAGATC 960  
ACACAGCTCT TCGCCACCGT TGCAGACGTT GCCACGCATA TCCGCGACAC CTCCCAGGGG 1020  
TTCGCnCatT CGCTCACTTT GTGCAAAGCT GGATCCCATT TTGGGGGCAA GGAACGTATG 1080  
GCTTGACAC GGGACAGGAA GGTCCGTCCC tGCACGCGC AGGCCTCTCG CTCTACCAGA 1140  
TAAGATTTGC GCAGCTGAAC GCGTTGGTGA AGTACACGTT CGCCAGCTA GTGGTAAAAG 1200  
GCCTCCAGGT GACAGCACAC CGAACGTCGG AGGCTGGGCA GGACGAAACG CTCACTACAC 1260

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TTTTGCAGGA CGCGGCCCGG TACATCTTTT TCCTGGGTGC GGCGCGTGGA TTCAACATGG	1320
ACGAATTCCC CGCTGGCGCC GAGCAGTACC TTCCAGAACA CAACTACTTC ATGATGGGAG	1380
ACAACCGATT GAACTCTACT GATATGCGCC ACGCGTACAC CGAACACCTC GAGGCAATCG	1440
ACGCGCACGA CCCGTTCCTT ATTTTCTTTA GCTCCAATGT TGCGCCCAAG TACATTCCCG	1500
ATAGCCACAT CCTCGGTGTG GCGTCGTTC GATTCTGGCC GCCCTCCCGC ATAGGCACCC	1560
CACAATAGGC TTAGGGGGAG CGGAGAGAAA GCTAAGAAAG GCGGAACCCG CCCAGGCGCG	1620
CAGCAGGcAG AAAGCCCGTA CCCTCAGACA sGTCCCGTTA CACAACAAGC GGGATAGGGA	1680
AGAGCCCTCG CTTACAAGGG CtCAGGAAAG ACATCCCTT ATCGTGCAGAA gcGCTcGCCG	1740
AATGCTTTAC AGCTTGCTG GGCTTCTTCA CTGGGATCGT CGTACGCGAT CTCCCCCTTC	1800
CCCTCGAAGA CATCAGCGCC AgCCGCCTTA CAACGCTCGA CCCAGTTGAC CATCCATTCTG	1860
CCGCCTTCCC CTTCTCCAGC CCACTCATAG GATCCGAAAA GCGCAACTTT TTTCCCCGAT	1920
AACCTTCCCT CAATAGAGGT AAAGAAGGGT TCAAACCTCGC TTGACTCTAG CTCCTCAGAA	1980
CCAGctGCAG AGCAGCCAAA GGCGAAGsGG TCATAGGAAT CAAAAGTACC AACGTCGAAG	2040
TCCATGACGC TAAAAAGGTC AGCTTTTGCA CCACCGACAT TCAAACCTC TACGATGCAG	2100
CGAGCCATCG TTTCAGTGTG CCCAGTGCCA CTCCAAAAAA TGACAGCAAC TTTTGCCACA	2160
AACTCCTCCT CGGGAACGTC ACGCagTGGG TGcACTCGCA AAATAGTGCA GCCACGACAC	2220
GCGCACCCCTG CCCGCGCAAG GGTAGGGGAA AGCTCTGTTG CTGTCAACCG CAGCCACAGC	2280
AGGATCCGgT GCCACCCTGG ACACCGGTAG ACTTGACGGG CCGACATTTT CCGGTACACT	2340
GGGGCTGCG CGCCAACTTA GCTCACCTGG CAGAGCAGCA CCCTCGTAAC GTGCAGGTAC	2400
CCGGTTCGAG CCCGGGAGTT GGCTTTCTGT TTGGCGTAtT CCGCGCTGTG GGCCGGTAGG	2460
TGAGTCTTGG AAGAGGTGGG GGGGsGCGGg AACGGCGTGC TGTCTGTTC CTACGCGTTT	2520
TTCTCACTT CGGGTGGGGT GTTTTCCCTT TGAAGAACTG GGCAAACGGC TGkTATCGCG	2580
CGAAATCCTG TCCCGGCGCG GGGGATGTGC CCCGTGTCTT TGCGCGCTCA GGGGAGGTTT	2640
TCCCTTCAGG AGCCCGGGGA CGGGGTGCTC TCCGTGAAGG TGTCGCCGTG TGATCCGCAG	2700
gTGCACGCTG CTCTGCCTG AGACTGAGGG AAATACGTCT CTTGCCTCG TCAAGCCCGA	2760
TGATGGTGCA GGTGTACAG TCACCTACCT TCACTTTTTT GAGGGGGTTG GAAACAAAGT	2820
GGTCGCTCAT CTGCGACAG TGCAGAAGCG CCGTTTCCTT TATTCCAATG TCCACAAAGG	2880
CCCCAAAGTC CACCACGTTT TTTACCTTTC CCTGTACGGT TGCCCCCACT TTTAAATCTG	2940
CAAAGGATAT CAGACCTTGG CGCAGCACCG GTTTTGGATA ATCCTCGCGC GGGTCACGAT	3000

TAGGTTTTTG	CAGCTCTGTA	ATGATATCTT	CGACGGTTCG	ATCACTGACT	GCGCATTGCG	3060
ACTGCACCTG	TGCCTTTTTGc	GCTGCGCTCA	CTGTACCGCC	TGCGCGCAGT	ATATCAAAAA	3120
TTATCTTTCC	CGTTGCATAG	TTTTCTGGGT	GCACCCACGA	GTTGTCCAGC	GGGTTTGTGC	3180
TTTCGGGGAT	TTTTAAAAAT	CCTGCACATT	GCTCAAAGGT	TTTTTGTCCT	ATACCACTGA	3240
CTGTTTTTCAG	TTGTTTCGCG	CTAGTGAATA	TGCCGTAGtG	GCACGATGGT	GCACGATCCT	3300
TTTTGCCAAC	GCGCTATTAA	CGCCAGATAC	GTGCTTTAAG	AGAGATACGC	TAGCCGTATT	3360
GAGATTAACT	CCTACGCTAT	TGACTACAGC	ATCTACTACC	GCGTGGAGCT	CCTCAGATAG	3420
CTTTTTTTGA	TTAACATCGT	GCTGATAGAG	TCCCACCCCA	ATGGATTTCG	GATCAATTTT	3480
TACCAGCTCT	GCTAGAGGGT	CTTGCAGCCT	GCGTCCAATG	GAGATTGCAC	CACGGATGGT	3540
CAGATCTAAG	TCAGGGAACT	CCTCTCGCGC	AATATCTCCT	GCTGAGTATA	CGGAAGCTCC	3600
GTCCTCTCT	ACCACGGTGA	ATGCAACGGC	AGAGTGTGTT	TCGCTAATTA	TGGAGGCGAT	3660
AAGCTCCTGC	ACTGCATGGG	AGCCGGTGCC	GTTCCCAACG	GCTACGAGCT	GAATGCGGTA	3720
gCGATCAAGC	GCCTGCGTCA	AAGCGGCGCG	TGCATGGTCC	GTGTTGTGCG	GATATATGAC	3780
AAAGGAGCCG	AGATATTGGC	CCGTTTCATC	CAGTGCCGCA	CACTTAGTCC	CTGTGCGGAT	3840
GCCAGGGTCT	ATGCCGAGCA	CGCGCGTGCC	CTTGACCGGC	TGGGTCATGA	GCAGATTCGT	3900
AAGATTTTCA	CTAAAAACGT	TGATACCGTG	TTGCTCTGCC	GAAGCGGTAA	GGTCTGCGCG	3960
TATCTCCCGC	AGGACGGCAG	GAATGAGCAG	GCGCACCACG	CCATCTGTAA	TGGCATCGCG	4020
ATGATACCTG	TTGTTGGGGT	GCACCGCCTC	TTGAACCTGC	TCGACAGCGG	CGTCTAAATC	4080
GACGGTGATT	TTTACGTCAA	GGATTCCCTC	ACGCTCCCCC	CGATTGATGG	CTAACACGCG	4140
GTGCGCCTTG	ATGTCGCGCA	CTGCCTCTGC	GTAATCCCAA	TACATTTGkT	AGACGGACGT	4200
GtGgCAGCGT	GCGCGTcCCC	GATTCCGGTA	GCCGTAACGA	CGCCTGCAGA	AAGGTAAAAG	4260
GACTTCAGTG	CGGCACGAtT	GGCGTTGCAG	TGTGCGGTCT	CtCTGCGAGG	ATATCGCAGG	4320
CGCCTGCGAT	GGCGTCTTGA	GCGCTGGAGA	CGGCACGATC	AGAATCTGCa	GCAGGAGCGA	4380
cGAgCGCTGC	GGCAGCGCGC	TCGATTCTTG	CCTGCGTGCC	GCACTGCGTT	TCTATCAAAC	4440
GCGCAAgCGG	CTCGAGTCCT	TTTTCGATCG	CCTGCATGCC	GCGTGTCTTT	TTCTTTTTTTT	4500
TGAACGGAGC	CCAGAGGTCC	TCGAGTGCTG	CAAGGGTAGG	AGCGCTCCTG	AGGTGCTCGT	4560
AGAGCGTgGG	GGTGAGCATG	CCTTCTTTGA	AGACGGCGCG	TATAATCTCG	AGTCTGCGTG	4620
TTTCGCGTGC	AAGGTGGGTG	TGGAAGAGGC	GTTCGAGTGC	GCGGATGAGC	ACCTCATCGA	4680
GGCAGTGATG	CGCTTCCTTC	CGGTAGCGCG	CAATGAAAGG	AACCGTGCAG	CCTTCTTTGA	4740

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GGAGGGAACG CACGGCAGTA ACCTGCGCGG TCGGGATGTG CAGTTCGCgc GcTACGCGTT	4800
CTGCGAGCTC GTCCTCTTGC ACGCTGAGTG CGTCCACAAA GTCTTGGTCT AAAGTCATGA	4860
GGGGGAGTGT AACGCGTTTG GCTCTTTTGA GAGAAGCGCC GGCCTGCAAC CGGCTCCGGC	4920
GCGGACCCTG GCGTGGCACC GGCCAGAGAA GGGCGAGTGG AGAATAGGGG AGTCGAACCC	4980
CTGACCTCTT GATTGCGAAC CAAACGCTCT ACCAGCTGAG CTAATTCCCC AGGACTGCTG	5040
GCTCCAGCTA TACACCAAAT ATGCGCGTCC TGCAAGGGTG TTTcCTGCGG GTGTGATGCC	5100
CCTCGTGAC CCTGTTCCCT GCGCGACTGC GCGCGGTGT AGCGCTCTAG GCGCGTCGGG	5160
GGGTGTGTGA GAATAGGCCG CATGAGCTAT TCGTGGAAG TGCGCGCGCT GTGcTGCGCA	5220
GGACTGTGTG TAGGTGCGGG GCTTCGTGCC CAGGAGGGCA GCGGAATTCG CGTGCGCGGT	5280
ATGCCGGAAC ACGCGCAGGT GACCGTAAAC GGATATCTGT GCGCAACACC AGAGGAAATG	5340
GTGCTCACCC CTGGTGAAGT TGAGGTAACC GTCTGTGCCT TTGGATATAC CAAAAGACG	5400
CTCCAGGTAG TGGTTGAGGA AgGCTCGTTC ACGGTGGTGG ATGGCCGTCT GGATACGGCG	5460
CGTTTGAGC TCACGGATGT GACTGCGCAG AGGGCGCACT TTAATCCGCG GGATCCGGCG	5520
GgACTGAACA CGGAgTACGT CACgTTCCGG GTGACAAAAT CTGCAAAGTG TACGGTAACG	5580
gTAAAGGATG CCGAAGGAAA GGTGGTGTGC GAGGAGCCGG TGGAGTTAGT TGAGCTGGGG	5640
TTGAACGTGG GGGGAATATT CGGGGGCAGT AATAAGAACA GCGAGGATGT TAGCGTTAGC	5700
GCAAAGGTAG CGTTCAAGG GAACGTTACG AGCGACCCGG CTATGGGCCA GCTCTATGCC	5760
TCAGCGCTGT GTTTGTACCG CATCGTGAC AACAACGATA GCAGCGGCGC AAACAAGTGC	5820
TTCATGCGGA AGGGTTTGAC GTTTGCGACC ACCTGTGCGT ACGGCATTAA GGGATTACCC	5880
GTGCGCTCT CCGGAGAACT GGGTGCCAGT TCAGAGACGG GGATAAAAAA GCCGGACTTC	5940
TCAACCGATG TCGGCCTGTC GCTCAAGTAC CAAAACAAAA TATGCTCCAT TGCCACGTAC	6000
AGCAAGTGCG GAACCACCAC GGGGAGCAAT AGTGACGGAG CGAACAGTGT GGCGGGTGTG	6060
TCcGGTTATG CGTGCTGCCT GCAAGTCTCG TGATGGGCTT GGAGAACAAT ACGCTTCAA	6120
GGTAACCTCT ACGAGGGCTG GGnAnTACGC GCTTCCATTG GGTACGTTAT CAACACGAAG	6180
CTGAGAGTCG GCGGACCATA GCGGGGCAGG GTACCAGCCT GCTGCGATCG CGCGGGCAAG	6240
TGCCGCCGTC AnCGTGCGCG GTCTGCGGGT ACGTCATACC AAACCAGCGC GCGCTGCTGG	6300
GGTAGCAGCG CACCGTTCCT TTTCCCTGTG CAATGAGGCT GTTTACCGCC GCGGGCAAAA	6360
GGTATTCCCG CTCGTGCTGC GCGCGCgCb TctCTTGAC GAATGTCTGC CAGCACGCTG	6420
CGAGGTGTTC GAACACGCGC GGAtGAAGCC AAAAAAGTTC ATAGACGCTA CTCCTGCCC	6480

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GGTGAGTGTG CAGGGCGCGC GTGCCGCTGT GGCGGGcAGT CTTCCGCGCG CTGTGnGrTA 6540  
 ATGACCCGTC TGcCGCCGTG CGCGTGCCAG CCGATGTGCG TGTGTTCTGTG TATGGCACGC 6600  
 ACCAGGCGTC CTGCGGCGGG GACTGCGGGG GTGGGGGGAG AGACTGCGGC GTCAcGTcCG 6660  
 CAAAGGTGCA GATACCGCGC GAAACGCCAC CGGTTTCGCT GAGCgTGTGC ACAAGGGGgT 6720  
 AGCCGACCAT GGCGTGGCGT GTCGAGTCCA GCCCCTGCGC GGCAAGGTGC GCGGCAAGcg 6780  
 TTTTGTAcgC GTCGcnTCCG TAGTAGTCAT CAGCGTTGAT AACCgCAAAC GGTGCAGTCA 6840  
 GCTGTGTGCG TGCgCAagCA AGCGCGTGGC CCGTnCCCCC ACGGCGTGCG CGCGACAGGA 6900  
 TGCgNCAGAG CGGCGCCGTG TGC 6923

## (2) INFORMATION FOR SEQ ID NO: 117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCTTACA ACCAATCTCC ACAAAGACG GATATACGCG CGCGAGATCG TCAAGCTCGG 60  
 TGGGGCACAC AAAGgTGAAG TCGGCCGGGT AAAaCmTAAA CACCGCCCAr cTACCCTTAA 120  
 TGGATGCGTT AGAGACCTCC GTAAACTTCC CCCCgACATA CGCAGGAmGc TTAAAGTCTA 180  
 TAACCCTCTT GCCTATGAGA CTCTCCaTAG cAACCTCCCA AACGTTcGCA CTCTAGCGCA 240  
 AACTATAGGA AACAAACGGG GAAAAGTAAA GTCTTTTACA CGTATCCCCC GGGTCACCAC 300  
 ACCATCACGC AGTACGTTCA GAAACAAGGC GAACGCTGGC TTTTTCCTCT TGTGTAACTA 360  
 CCTTCTTCGT AATGCATAGC TCCTTTTTC CTTTCAGAGA CGGTGCCTCA AACATAGCAT 420  
 CAAGCATTA TCTTTCCACA ATAGAGCGCA AACCcCGCGC CCCCgTTTTT TGATCAATTG 480  
 CTGCTGAGC TATTGCGTCC AAAGCGTCCT CATCAAAGAC aAGACGCACG kCATCCAACG 540  
 CGAATAACGC TTCAAAGTGA CGGACAATAG CATTTTCGCG TCGTACCAAG ATATTGCGCA 600  
 GATCCTCTTT AGAAAGAGCA TCCAAGGCGA CCGTACCCG CAGACGGCCG ATAATCTCTG 660  
 GGATTAATCC AAATTTcACC AAATCATCCG GAATGACGTC CTCGTGCATC AGTTGCAGAC 720  
 CTCGCTCCTT TACCGTTTTT ACATCTGCTC CAAAGCCAAC CGGATTCTTA CACAcTCTCG 780  
 TACcGACAAT ACCATCTAAC CCAACGAACG .cACCACCACA GATGAACAAA ATGTTcGATG 840  
 TATCCACCCT GAGCATGTct TGGTTTGGAT GmTTGCGACC CCCtGCGGAG GCACcGATGC 900

729

TATCGTTCCC TCAaTTATTT TCAAAAGCGC cTGCTGAACC CtTCACCCGA CACATCACGC	960
GTAATAGACA CGTTCTCGCT CTTACGCGAA ATCTTATCGA TTTCATCAAT GAAGATAATC	1020
CCCCGTTCTG CGAGGGCAAC ATCTCCGTTT GCATTCTGAA CGAGCTTTAA TAAGATATTC	1080
TCTACGTCCT CACCCACATA ACCGGCCTCG GTGAGCGTAG TAGCATCTGc tATCGCAAAG	1140
GGGACCTTCA TTTTCTGAGA AAGTGTCTTA GCCAACAGCG TTTTGCCTGA ACCTGTCGGC	1200
CCAATAAGCA GCACGTTAGA TTTTCAATC AATACCGAAT CAATATCCAA AGACCTACCT	1260
GCCACCCGTT TGTAAGTGGT GTACACCGCA ACCGATAGCA CCCGCTTGGC CAAATCCTGC	1320
CCAATAACGT ACTGATCAAG GTAAGCTTTC AACTCTAAAG GAGTTGGAAT CTCTCTTTG	1380
GTCATGAGCG CAAGTGCCGA CGGCTTGCGA TCACGCAAGT ATTCTGCACA CCGCTCCACA	1440
CAATAATTGC AAATAGAAAC CCCATGACCG GTCACAATCC GGCCTCGCTC ATCTTCTTTT	1500
TTTCCACAGA AAGAGCAGCC CAATACCAGA TCCCCCTTAG ACCTGAGCAT GCTTCTCCT	1560
CTTCATTACC GTATCTACGA TACCATACGA ACACGCCTGC TCCGCGGAAA GGAAGAAATC	1620
TCGCTCCATA TCCTCCCGCA CCTGCTCCTC TGACTGCCCA GTGTGCAAcG CGAAATACGC	1680
AATCGTCAGC GTCTTTAGGC GCAGGATCTC CTGCGCCTgG GATGCACACA TCACTTGCCT	1740
GCCCCGTGAC GCCACCCAC GGTGATGGA TCATCACCCG AGAAGACGGA AGCGCAAAAC	1800
GCTTGCCAGG CGCACCTCCT GCCAGTAACA CTGCTGCCAT ACTCGAAGCC TGTCTAAGC	1860
AAATGGTCTG CACCTCAGGG CAAATGTGCT GCATCGTATC GTACACTGCA AGCCCTGcAG	1920
TAACCGCCCC GCCAGGACTA TTAATGTACA GGCTGATATC CTTATCTGGA TTCTGAGACT	1980
CTAGAAAAAG TAAcTGCGCT ACAACTAAAT CCGCCACCGC GTCAGTGATC TCCCCGTCTA	2040
CGAAAATAAT ACGGTCCTTC AACAAGCGGG AAAAAATGTC ATAGctCCGC TCTCCACCCC	2100
CCGACTGTTC AATCACGTAG GGAACCAGAT TATGCATACG TTCACGCACG GGACTGCTCC	2160
TGAAGAAAGT CAGTCAAAGA CTGCTCCGGC CCACACTCAG TCACACATCG TCCGAGCAAT	2220
TTCTGGCACA GCTTCCGTTT TCGTATTCCT TCACACAGCG CACGCCGTTT TTCCTCCCCT	2280
GCATAATACT CGCGTACCCG CTCCTCTTTG GAACCTGTTT TGGACGCAAT GCGTACGTAC	2340
TCCGTCTCAA TTTCTCAGC AGAAACAGAC ACCTGCTCCT GCTTAAGAAG GAGCTCAACA	2400
ATCACACGCT GCTTCAGGTG CTCTTCCACC TCCGGACGCC ACTGCTGAAA AAACCTGCAGC	2460
TTATTCTGCG GGGTGCCCGA CAGGCTCACC CCAAACCTGAC GCATCACCAA CGCCCAACGA	2520
GACTCCATCT CCCCCACAAC CAAAGATTCC GGCAGAGAAA AAGGATTCTC CCGCACCAAT	2580
ATACGCAACA GCTGCCGCCT CTTATACTCG TGCAGCGCTG CCTCCAAcGC TTCCGCGAGG	2640



TTTTGCCGCa	aCTCCGTGTC	AGATCGTCAA	GTGTGCGAAA	AGCATCGCTC	ACATCTTGCG	2700
CAAGcTCATC	ATCAAGACTC	GGCAACTGAC	GCTGCTTGAG	CGCCTTAAGC	GTTACCCTCA	2760
CCTGAGCGGC	TTCGTCCTTC	AGCATACCGG	CCCTTTTAGC	AAAGAGACAC	CGCTGTCCTA	2820
ATTTCATACC	CAATATATCT	TGCCCAAGCG	CAAAGGGACC	TTCTCCACC	CCAAGCGTAA	2880
AGACAACGCC	GGCGCGCTCA	GTACCCGGAC	GAACGGCACC	TGAATCGTCA	ACCTCGTGAT	2940
AATCGACGGT	GGCAATGTCC	CCTACCTCTG	CACACGAATC	TGCACCCTTA	TCAGTAACCA	3000
GCGCATTGCG	CTCCTGAATA	CGCGTTAACT	CTCGAGAGAC	GTCTCTTCT	GTGACCGACA	3060
CAGTGGGCAC	GGACAGCGAA	AAGCCCGATG	TGTTGCGTAG	TTcAACGGAA	GGAAATACGT	3120
CGTATATGAC	AGCAAAaGAG	AAaTCCTCGT	CAGGATCGAA	CACTGGCTTT	TTCTTAAGCG	3180
AAGGACGGGA	GATAGGAAGA	GGCTGACTGT	CCTGCGACGC	CTGGGCAAAC	CCCTCCTCCA	3240
GAGCTTTTTTC	CATGAGGGCC	GCCGCTGCAT	CTTGCCGAAT	AGCACTTCCA	TACTTCCGCT	3300
CAAGCACTGC	AAGAGGAACT	TTCCCTTGC	GGAAACCAGG	AAGCCGCGCA	CGCTCAAGAT	3360
ATTCTCAAC	AAAACGCTGA	TAATGcCGct	GCGCATCCTC	GCGCGCGACG	ACCACCTCTA	3420
GCTCAACCTG	AGATTGTGCA	AGCGCGGTGA	ATTTTTTTTG	AAGTTCCACA	AGCCCAGATC	3480
CTTAGGAAGA	AATACCTACG	TCCGCAACGC	cTCGCACGGT	CCAAGCAGGa	TGCAGCAAaG	3540
CGCTGaAAAA	GCGGGAAACG	GGGATCGAAC	CCGCGaCTTC	CACtTGGCAA	GGTGGCGCTC	3600
TACCACTGAG	CTATTCCCGc	ACAGGCGCct	GCGAGAGGAG	GGACTTGAAC	CCTCATGCCA	3660
GAGGCACTAG	ATCCTAAGTC	TAGCGTGTCT	GCCGATTCCA	CCACTCTCGC	ACGGAAGAsA	3720
TsCGGCAAGC	AAAAACTCGC	CCAACAGGAT	GCAGACACCC	AACCGCCCCT	GAGCCATGcA	3780
GGCTTCGAAC	CTGCGACCCA	CAGATTAAGA	GTCTGTTGCT	CTACCAACTG	AGCTAATGGC	3840
CCGTCTCCG	ACACCCTCCC	CCCAGGATCA	CATATCATGC	AAAAAGGATC	AAGATGAATC	3900
GTATCGTCGC	GTCCACGCA	CCTCCTCTTT	TCGCTCAACA	TTTCCTTCAA	TCAGTCCAAA	3960
CCTCTAGGAA	GATATCCAAG	TCGCCGAACA	CAACAGGGGC	GTAGTAGGGG	ATTGACTGTG	4020
CAGTCACTGG	GTCCGTCGGG	TTCAACCCTAC	AAGGAACACT	CCGTTTGCCG	TACTCGTTCC	4080
GCATAGGCCC	TGTCTTTAGG	TATAAACTCC	CTGCCCCATA	CGCCGGCACC	CCTTTTTTGC	4140
AGGAACGGTT	TCCTAAACGA	GCTATCCGTG	CTACCCTGGC	AGCCGACCAG	GGAGGGCGCG	4200
TATGGATCAG	CATACACGTA	CACGCGATCT	TGTTTCTGCA	TTTTTTGGGC	GC'TTCACTT	4260
TGATGTCCAG	GGACCTTCCG	TCCGCACGGT	TGTCGACGTG	TTGCGCGCAG	ATATGGTGCG	4320
CGGCTTAGAG	GAAGAGGCGC	AGCTTCCTCC	CCGTATGGGG	AGTGCACTTG	CGATGATTCC	4380

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CACTTGGGTG	GCGCCCCCCC	GTGTATCCCC	CTGCAACCGA	CGCGTGATAG	TTATCGACGC	4440
TGGAGGAACC	AACTTTCGCT	CGTGCCCTCGT	ACGCTTCGGC	GACAGTGGCA	CACCTCACAT	4500
CGAGAATTTA	GAAAAACGTC	CCATGCCCCG	TACCACCCGT	GAGTACTCAA	GGACAGAGTT	4560
TTTTGGAGAA	ATTGCAGACA	ACCTGGCACG	TCTGAAAGGT	GCAGCGGACT	GCATTGGCTT	4620
TTGTTTCTCT	TACCCATATC	GTATCAGACT	GACGGTGACG	GTGAGGTTAT	TCAGTTTGCG	4680
AAGGAAATCA	AAGCTGCTGA	GGTCATCGGC	ACGTGTGTCG	GTGCTGGTTT	GACAGAAGCG	4740
CTAAGTGCTC	GGAAC TGCC	TGAAC TCCGT	TCTCTCAAAA	TGCTCAATGA	CGCAACGAGT	4800
GCGCTGCTTG	CAGgTTTTTT	TGCGGCACCA	GAGGGGTGTT	CGTTCAGTTC	ATACGTAGgT	4860
TTTATTTCTG	GCACTGGAAT	GAATCTGCG	TATCTGGAGC	CAGACCCTAT	TCCTAAAATT	4920
CCTGCGCATC	ACACACCTCA	GGTGGTAGTG	TGCGAATCGG	GAAAAAGCAA	CAAAGTACCG	4980
CGCAGTGCTCT	TTGACGAATT	ATTCACTCAA	ACTACTGCCG	AGCCGATAT	TGCACACCTA	5040
GAGAAGATGT	CCTCGGGCAC	CTACCTCGGT	CCCCTTGCTT	CCGTTGTCGT	GCGGCTTGCG	5100
GCACAAGAAG	GTCTTTTCTC	ACACGCAGTA	CACGCTGcAC	TCAGTACGGT	TTCTTTTACA	5160
CTCGTGGATA	TGGATCGTTT	TTTATTTGCT	CCCTCTGTGT	CCACCACCAC	GTTGGGCGCG	5220
TTGCTCGCAC	CGGGCACCGA	CACAGACCGA	GAGATTCTCT	TTCTTTTGCT	CGATGCGGTA	5280
kTTGCACGTG	CAGCACGCAT	CGCTGCGGGA	GTAATCGCCG	CCTCAGTATT	AAAAAGCGGT	5340
GCTGGGTATG	ATCCGCTTCG	TCCCGTGTGC	GTGCTCGCAG	AAGGCACCAC	GTTCCAACGC	5400
ACCTACCGCC	TACGCACCCG	GGTTACTTCC	CACCTGCAAG	CCTTTTTGAC	TGAGGAGCGC	5460
GGTGTGTATT	TCGATATCAT	TTCACTTGAA	AACGCCGTAA	CGCTCGGCTC	TGCACTCGGA	5520
GGACTCAGTT	CGTAGGCATA	TGCCTAAACG	GACTGATGAT	CCTGTGAGAG	ATAGCGCCGT	5580
GCAGTGCTTC	CTGTCATCTT	CTCGTCGGCC	GCGTGTGGCT	GAGCGGCCGT	GCTCGCCTTC	5640
TGGTGCGAAC	GCGCTCTCCC	TGTCTCTAGG	GGAGTAACTT	CCACGCCGAG	TGTATCTTCT	5700
CAATCTTGTA	CACGAGTAGT	GCCTTCCCTC	CATGGTTCAT	GATTACATCC	ACTCGGGTCG	5760
GGCTCTCGAA	GACAATGAG	TCCACCCGCA	CGTTTTGCCG	CGACGGCACG	AACACGTGTA	5820
TAAAATAATC	GCGTAGtGCC	GCAAACGAAC	ACCTTCTTTT	GGCAGGGCGT	CCGAGCTCTG	5880
CTGCAATATG	TCAGGCATTG	AGTACGCGCG	CCGATATGCG	TCGGAAAGAT	ACACAAGCCA	5940
CTTGTGATAG	TCACGTTTCG	CAGTGATACG	ATTCAAATGC	GCCACCACAT	CTTGCAATTC	6000
TGCCTTTGTA	CGCTCATAGT	CTGAGCGCGT	GATGCGCACG	GTGCCGAAGT	GGCGACAACG	6060
CCCGCACGCT	CCTGCGGACT	GTGAACATTC	ACCTTTCCAT	CGTTCTGCAC	CCACTTCTGG	6120

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ACGCGGGGCT GTGTGCATGA AACACTGCCC CACAATACAC TTCCGATTAA GTAGCATACT 6180  
 TTTCCTCTTG CAAATGCGCT CCTCACTACA CGCCCACCAG CGTACACAGA GTAGGATCGT 6240  
 TGAAGAGCTT TGCGTACCCC TGTGCCGACA AGCCCAACTT ATCCTCCAGG TACGGATTTG 6300  
 CACCATGATC CATCAATAGC CGAATTAATA CATGATCTTT CCTACCCACT GCCAACACCA 6360  
 GCGCCGTTTG ACCATTTGAA CCTCGCACGT TTGGATCTGC TCCTGCATGC AAGAGCAGAC 6420  
 GCGCAACAGT TCGGTTCCCA ATTTGAGCTG CTTCCATCAG CGCAGAATAC GCGCGATCGT 6480  
 CAGATAACTG ATCTACTGGc gCACCgCGCG CAATAAGTTG CGCTGCCATC TCATCCTGAC 6540  
 CCTCCCGCAC TGCCAAAGAC AACACAGsGT ACCGCGTGCG TCTTTCAACG CAGCGCTAAA 6600  
 TCCTGCATCC AAAAAGAGAT TGACAATATC AATATTCCCA TCCATGACTG TCGCGATGAA 6660  
 ATTTTCTTCA AAACATGGAT AACCgCGCTC TAACAGCGCA GTGCGTGCGA CACGCTTCTT 6720  
 TTTCTGCCTT ACAAATCTcT CGTGCTCGAC ACGAAAGAAA TCCTcAAACG TCTCCTCCTC 6780  
 AAGTAAAAAG ACCAAGTCGC GAAATACATG GATATCCCTG ACCTCCGTTG TTGTAGCCAA 6840  
 GAGCAGCAGC TGCATACCAC GCCCACAAGC AACTCCAGAA AAGAGnATAA AAGCCGGATC 6900  
 GCGCATGGGC TCATGCGGTA CAAAAAAAAC ACATGCGTTG CATCCTGTAC CAACGCCAAA 6960  
 GGGTAACTGG CACGGTGGAT GTGGTC 6986

## (2) INFORMATION FOR SEQ ID NO: 118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACTGTCTGCC ACGCTACACA CACTCACACA TCAGTATCTT AAATACGAAG AGTGTTCAAA 60  
 ACAGCTTGCA CAAAAGACGC AAGAAAGCGC AAAGCTTATA ACTCTTTCAG ATGAACTGAA 120  
 TGGGATAAAC CAAAAAAA TACAATTTGA CGCATGGGCA CTCATTCTT TTCTGCACGA 180  
 AATTACTGCC TACGCAAACA TACGTTTGCA AAAATGAGT GAAGGACGTT ACCATCTGAG 240  
 GGTAGCTGAC TCGCACGTCA ATGCACGAGG ATATCAAGGA CTTGCGCTGC TCGTTGCAGA 300  
 TGCGTACACT GGGAGCGTGC GCCTTCGGCA ACACTTTCAG GAGGCGAAAC CTTTATGGCC 360  
 TCTATCAGTC TTGCACTTGG TCTTGCAAGT TCTATCCAAA CCCGATCGGG AGGTATTGTG 420  
 CTTGACTCGC TGTTCATAGA TGAAGGATTT GGAAGTTTGG ATGAGGCAAG TTTAGATAAG 480

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GCAATTGGCA TCTTAGATGA AATCAGAGAG GGAAGTCGCA TGATAGGCAT CATTTCTCAT	540
GTTTCATGAAT TGCGCACGCG CATCCCTCAC AAAATTCTGA TAAAAAAAC AAACGCAGGA	600
TCACACGTAA TGCAGGGGGA TGCAGAATGA AAACGAGCGC GCTCTTTCTT GATTTTACG	660
AATTGACTAT GGCGCAGGGA TACTTTTTTC ACAAGCCGCA CGAGTGTGCG tGTTTGAAGT	720
ATTCTTTCGT AAACACCCCT TCGCGGGAGG GTACTCCATT TTTGCAGGAC TCGATCCGCT	780
CCTGACGGCA ATAGAGCAGT TCCGCTTCAG TGGAGAAGAT ATCGATTATT TGCGCACCTT	840
GCACTTATTT CATGATGACT TTTTGTCTTA CCTTGCTTCC TTCCGCTTTT CAGGAGATAT	900
ACACGCGCTA GAAGAAGGTT CAGTAATATT TCCTCACGAA CCGATCATCC GCGTGCACGC	960
GCGCTTGTT GAAGCACTTC TGCTTGAAGG ATTGATACTC AACACCATTA ATTTCCAAAG	1020
CCTCATCGCA ACAAAGACTG CACGGATGTG GCGCGCGTCA GGTGAAGGTG TTCTTATGGA	1080
GTTTGCCCTC AGAAGAGCAC AGGGCTATGA CGGCGCGTTG AGCgCCACaC GCGCTGcTGC	1140
AATAGGTGGC GCAACAGGGA CAAGCAATAC ACTTGCTGCA AAGCTcTACG GTATTCCGGCC	1200
AATGGGAACT ATGGcGCACG CgTGGGTGAT GTCTTTtGAC AGTGAAGAAG AGGcCTTCGA	1260
ACGCTATGCT GCACTCTATG GAAGCGCGTC CGTATTCCCTC ATCGATACGT ACCATACCCT	1320
GGG	1323

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TACTnCTACT TCCATCCCCT CCAGAACTCC TCCCgGATAT TCctTCATCA GTACATGGAA	60
TGCTCCCCTA CCGCCTTGCA CCAAAAATGC AAGACCCGTA GCTTCGGTAT ACCGCTTAGC	120
CCCgATACAT TATCTGCGCA TGCCTACTCG ACCAGTGAGC TATTACGCAC TCTTTCAaGG	180
AATGGCTGCT TCTAAGCCaA CCTCCTGGCT GTCCAGGTAC CCACACTTCA TTTCACACTC	240
AAGCGGTATT TCGGGACCTT AGCTGACGGT CTGGGCTGTT TCCCTCTCGA CTACGAACCT	300
TGTCGCACGC AGTCTCACTC CCACACGTTG ACTGCCGGCA TTCAGAGTTT GATTGGGTTT	360
GGTAGGCGAT GAAACCCCTT AGCCCATCCA GTGCTTTACC TCCGACAGTT TTGTATAAGG	420
CTGTCCCTAA AGGCATTTTCG GGGAGAACCA GCTATCTCCA GGTtTGTTTA GCCTTTCACT	480

CCTAGTCACA AGTCATCCAT ACCTTTTTTA ACAGATTATA GTTCGGTCCT CCACAAGGCT	540
TCACCCCTGT TTCAACCTGC TCATAACTAG ATCACCCCTGG CTTCGGGTCT ACGACGTACA	600
ACTCACCACG CCCTTTTAAG ACTCGGTTTC CCTCCGGCTC CAGGACTCCT ATCCCTTAAC	660
CTTGCTGCAC ACCGTAATC GCAGGCTCAT TCTACAAAAG GCACGCTACC ACCCTCACAG	720
GGTGTAACAT CTTGTTGGTT TACGGTTTCA GGTTCATTTT CACTCCCTC ACCGGGGTTC	780
TTTTCATCTT TCCCTCACGG TACTTGTTCA CTATCGGTAG TTGTCGAGTA TTTAGCCTTA	840
GATCGTGGTC GACCCAGATT CCGACAGGAT TCCTCGTGTC CCGCCGTACT CAGGTACCGC	900
ACCAGCAGGT CCGCCCCATT CCGCATACGG GGATTTTACC CTCTCTGTCA GGC'TTTCCCA	960
AAACCTTTCT GCTATAGGCC GGATTATTTT ACCCACCGAA CGCAAGCCCG CGCGGCCCTA	1020
CAACCCCTGT TAGACACAGG TTTAGGCTCC TCCAATTTTG CTCGCCACTA CTTTCGGAAT	1080
CTCTCTTGAT TTCTTTTCCC AAGTTACTTA GATGGTTTCAG TTCACCCAGT TTCGCCTTAC	1140
CCTCCCTATT CATTCAGGAA GGCAATGACA AGGCTTTACC TGTCGGGTTA CCCCATTCCG	1200
TCATCCCCGG ATCACAGGAC ATGTGCTCCT CCCCAGAGCT TTTTCGCAGCT TATCACGACC	1260
TTTCATGCCT GACAACTCCA AGACATCCAC CGTAAACCAC TATTCGCTTG ACCATATTAT	1320
CCATCCCTTC TCAACTTCAC ACCCCACCCT AATACTCTCA AAAATCACCT ACCACCTACT	1380
CC'TTACCCCA TAAACAAAAC AAaGGGACAT AAaGAATAAT AGTGGGCTTT CCCTGGAGAT	1440
AgGGGACTCG AACCCTTGAC tACGACCTGC AAAGCCGTCG CTCTAGCCAG TTGAGCTATA	1500
CCCCCTTTTC AAAAGGGAAG GGGAGAGACT GCCGTGCAGG AGCAGAAAAA CCtTaAGtGG	1560
CTTCCGCCAC ACGnCGAACA CGGCACCATG CCATGCCCAT ACCCTTTcTC TTAGAAAGGA	1620
GGTGmyCCAG CCGCACCTTC CGGTACGGCT ACCTTGTTTAC GACTTCACCC TCCTTACCAA	1680
ACATACTTCG GCACCGCCCT CctTGCGGGT TAGGCTAGTG ACTTCGGGTA TCTCCAATC	1740
GGATGGTGTG ACGGGCGGTG TGTACAAGGC CCGGGAACAC ATTACCCGCA CCATGCTGAT	1800
GTGCGATTAC TAGCGATTCC AACTTCATGA AGTCGAGTTT CAGACTTCAA TCCGGACTAC	1860
GATTGCCTTT TTGCGGTTTG CTCCACTTCA CAACCTCGCA TCGCTCTGTA GCAACCATTG	1920
TAGCACGTGT GTAGCCCCGG ACATAAGGGC CATGATGACT TGACGTCATC CCCACCTTCC	1980
TCCGGTTTGT CACCGGCAGT TCCGCCAGAG TCCCCAACAC CACTTGCTGG CAACTGGCAG	2040
TAGGGGTGTC GCTCGTTGCG GGACTTAACC CAACACcTCA CGGCACGAGC TGACGACAGC	2100
CATGCAGCAC CTGTCAAGAG GCGTATcGct ACGCCACCGC ATTTCTACGG CGCTCCTCTT	2160
GATGTCAAAC CCGGGTAAGG TTCCTCGCGT ATCATCGAAT TAAACCACAT GCTCCACCGC	2220

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TTGTGCGGGC	CCCCGTCAAT	TCCTTTGAGT	TTCACCTTTG	CGAGCATACT	CCCCAGGCGG	2280
TACACTTAAT	GCGTTCGCGT	CGGCGCCGAG	ACTCATGCCC	CAACACCTAG	TGTACATCGT	2340
TTACTGTGTG	GA CTACCAGG	GTATCTAATC	CTGTTGCTC	CCCACACtTC	GCACCTCAGC	2400
GTCAATCATC	GGCCAGAAAC	CCGCTTCGCC	ACCGGTGTTT	TTCCAAATAT	CTACAGATTC	2460
CACCCCTACA	CTTGGAATTC	CGGTTTCCCC	TCCGTGATTC	TAGACCAGCA	GTACCCAGTG	2520
CAGTTCCCAA	GTTGAGCTCG	GGGATTTTAC	ACCAGGCTTA	CCAGTCCGCC	TGCATGCCCT	2580
TTACGCCCAA	TAATTCGGAA	CAACGCTCGC	CCCTTACGTG	TTACCGCGGC	TGCTGGCACG	2640
TAATTAGCCG	GGGCTTATTC	GCACGACTAC	CGTCATCAAA	CGGGCATTCC	CTCCCGTCCT	2700
CATTCTTCGT	CGGCAAAAGA	ACTTTACAAT	CTTTCGACCT	TCTCATCCAC	GCGGTGTCGC	2760
TCCGTTACAG	TTTCGCCCAT	TGCGGAATAT	TCTTAGCTGC	TGCCTCCCGT	AGGAGTCTGG	2820
GCCGTATCTC	AGTCCCAGTG	TGTCCGGTCA	CCCTCTCAGG	TCGATACCC	ATCGACGCCT	2880
TGGTAGGCCA	TTACCCCAAC	AACAAGCTAA	TGGGTGCGAG	GCTCATnTCT	GAGCGAGGCC	2940
GCAGCCCCCT	TCCTCTCAAA	GA CTACGTCC	AAAAGAGCGT	ATTCGGTATT	ACCCCTATT	3000
TCTAGAGGCT	ATCCCCATCT	CAAAGGCAGA	TTACCCACGC	GTTACTCACC	AGTCCGCCAC	3060
TCTAGAGAAA	ACGAAA					3076

## (2) INFORMATION FOR SEQ ID NO: 120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CnGATGTGCG	TAAACGCCTG	GAGACGCTCA	AGAACACGCA	ACGTCAAAAG	GGCAGAACGC	60
CGCGCCGCAC	GgTCGAAAAC	TCTTTATAAC	TCATAGAGAC	ATCCTGCTCA	GCACCCGCAC	120
CGTCGGATAT	ACAGCGTATA	ATAACAAAGG	GGACGCCATT	AACTGACGCT	ACATGCGCAA	180
AGGCTGCCCC	CTCCATTTCC	ACACCATGCG	CACCAAATTC	GCGTATAATG	CGTGCACGTG	240
TTTGCGCATC	TGACACGAAA	AGATCCCCCTG	AGGCGACGCG	CCCTTCGACT	AAACGAGAAA	300
CGCGAGAAGG	CGGATCCCCC	GAGCCAGAGA	GCGCACAAGC	ACCCTCGGTC	CACTCCGGAT	360
CCCGTGTGCA	GAGATCAAAG	GCTTCCCGCA	CCAAATACCG	CAATGCCGTG	TTGCGAGTCC	420
ACTCTACAGA	ATCCATGCGC	GGAATACGCC	CTTCTGGTA	ACCAAAGCG	GTAAGCTCTA	480

736

CATCATGCTG CACTGCATCG ACAGAACTA GCACATCAAA AACACACAAG CGTCATCGA	540
GAGCACCTGC AATTCTCTGTA TTGATAAGCA CACGCGCACC AACTCCGAA ATGAGTAGTT	600
GAGTGCAAAG CGCTGCATTC ACTTTCCCAA CACCGCCGCA CACATACACC ACCTGAAGCG	660
CACCCACCGA CACAACATAG AACGTGAGCC CTGCCCCGCTC TGTACCTACT CCCCCGAGAC	720
ACTCACGTAC GCGCGCAACC TCCTCTCCCA GTGCAGCAAA AACGCCGACC GTCACGCACC	780
CTCCCCGTGA AAAACACGAA AACGCGCACT CGCAACCCAG GCACGGAAAA AAGCTGTCCC	840
TTGAAGGTCA GGAAAAAGCC CCGACCACAA GGCACACCGA TAAATGAACG GAATATAGCA	900
GGGAGAGGAC TCGAACCTCC GGCTCCGGG TTATGAGCCC GACGAGCTGC CAACTGCTCC	960
ACCCTGCGGT GACGCACAGA GCGTACCACG ACTAGAGCCC GAAGTCAAGC CACAAAGCAG	1020
GACGCTCCGC CCCAGCTTGA AGCGGAGCCT TACAATCATA CATACGACCA GAGGATACGA	1080
CACGCAGTTT A	1091

## (2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19186 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ACGACCTCGC CTGCAAAATC GCTATCCTTT CCCCATCTTT ATAGGTGAAT AGACCCGGCC	60
AGGGAGTAAA GGCCCGAATC TTGCGCTCCA ACACAAcTGC AGGATTAcTC CAGTCCGCCA	120
aTCCCaTCTC CyTACAGAGC TTACCACAAA aTGTTCCTg CGAgTGaTCC TGtGCTGCAG	180
GGGCGAGCGT GTGCCGCTCA ACACCGACTA AAACATCATC CACAAGATCG GCAGCCACCA	240
AAGACAAACG AGAAAGAAGC GCGCCAGTAG TCTCTGTACC GTCGAGCTGA ACACGGGAtG	300
CGCAAGAATG TCCCCTGCAT CCATCTCCTC ACCAATGTAC TGGAGCGTCA CACCCGTCTC	360
GCAGTCCCCC GCTAAAATCG CCGCAGGGAC CGGTGTACTC CCTCGCCAAC GCGGCAACAA	420
CGAAGGATGA ACGTTAATAG CACCGCGCGG GAAAAGCGCA AGGAACCGAG GGCCAAAAAT	480
CTTACCGTAG GCAAAACACA CCAGCACGTC CGGACGCAAA GCCTCCACCG CGTCATAAAA	540
GCGCGATCC AAACGCCCCG GAACGAAAAG AGACGCAGAC TCAGGAAGAA CCCAGACGC	600
TTTTAAGCGA AAAAATTCCC TTGCAACCGc AGAATGGaCA AGCTTcCCCC aGCGTcCGaC	660
AGCAGCAGGA GGATTcGTcA AAACCCCCAC AACCCGaTGA GCGcACGCCA CCCGGCGCAA	720

737

AGAAGGCACG GcACACTCTG GAGTTCCCGC GAAGAAGACC CTcACCATGG GCTAACGAAT	780
CGTCCCGCGc AGCGCgnCAT ACCGACGAAG GGCATCATCC CTCCGCTTTT CGTCAATGCG	840
ATCCAAAAAA AGAATACCGT CAAGATGATC GTACTCGTGC TGGATCACTC TTGCCAGAAT	900
ACCATCTGCA TCAACGGCAC AACGTTTACC ATTCTCGTCG AGGTACTGCA CACTCACCCG	960
ACGCGGACGC AACACCCCTT CATAAATGTG AGGAATGCTC AAACAGCCTT CCTCGTAGGA	1020
AGATTGCTCT TCAGACGCGG CAGTGATCTG GGGATTGATA AAAGCGCGGA CGTGGTGCTC	1080
AACATCTACT ACAAACACGC GGACGGTACG CCCTACTGCG GCGCCGCAAG CCCACACCG	1140
CCTGCCCCAC GCATCACACG AAACATACCC GAGATGAACG CGCGCAGCTG CTCGTCCACC	1200
TCCGAAACCG GCTCGGAAAC CGTTGTCAGG CACGGCTCAC CTAAAACTT AAGCTCCACC	1260
GCCTCTTCCC GCTCTTACCC AAGAGAAACT CATACCCGCC TAGTACAGCC TTGAGTCGCT	1320
GACCTTGCGC CCCTTCTTCA TCAGtTGCGC CGCAACGCCT TCTTCTTGCG ATTcAGAAGC	1380
GTGGAAGGCT TCTCATAAAA TTCTTTTTTC TTCCACTCGC GAATAATACC TTCCTTCTCC	1440
ACCTGGCGCT TGAAGCGCTT AATTGCCTTC TCTAAATTCT CAGAATCATC CACCGTTATG	1500
TGAGCCACCG ACCCTCCCCT GAAAAAACA CAGCCTACCA GGGGTAGnTA GCGCAAAAGA	1560
CGTCCCCTGT CAATCGTTTC TTCCGAAAGC ACTCCTGCCT CCCCTGCACG CACACCTtAC	1620
GTGTCTTGCT TATGCAACCG CTGACCTTCC TAACGTGCGT CTACTTGTGG TACAGTGCAG	1680
CGCTGTGCGT AGAAGTCAAA ATTGTCCGCA CCGACCTCCT TTCGAGTGCA TCCGTGGGAC	1740
GCTAGCCTAC CCTGCACAGG CGTCCACCCC TCCTGGGAAG AGGCCCCGACC TGCCGTGAAC	1800
ATTACCGGAA GCCGCGTTGC GGTCTTTATC TCCTCCCTGA CCGCTGTGCT TCTGCTGCTC	1860
ACCGTTCAGT GCGCGCGGTA TATGCTCATG CGTGGAACG AGACAAAGGA ACTGAACACA	1920
CTCACTGAAC GCGGCGCGAT CTTGGACCGA AATGGCCGGT TTCTTGCCGT TGAACCACC	1980
GTCTACAACC TCAGTGTTAA CAAAAATCTT GTCTCAGACC CACGCACTGC AGCCACGTG	2040
TTAGCACAGG TCCTTGACCT TTCAGAACAA GATATTGAAG AAAAATTCCG CACCGCGCGC	2100
GCTCACTTCT TTTACCTCAA GAAAAAATG AGTGAAcGG AAAAGAACCt TGTCGCTCAC	2160
GCTCTTAAGG AGCACTCCCT GAAAgGATTT CGCCTAGAGG CAGTGCGCAA CCGCATCTAT	2220
CCAGAAAGTA GCCTAGCGTC CACGGTCATC GGATACGTAG GTGATGACGG AAGGGGACTG	2280
AGCGGTATCG AGTACAcTG CAGGATGTTT TTTCTCCTGC CCCGTACCAC ACCGGGTATA	2340
CGGGCAAGGG GCATACTGTC ACCCTCTCGA TCGACCGAAC CATCCAGTAC ATGATGGAAA	2400
AAATCGCAGA TACTACGCTC CGGCGTACCC AGGCAGAAG ACTCATGTTC CTTGCGGTGG	2460



AGGCAAAGAC AGGTCAGATT CTATCCTACG TCAGCAAGCC GTCTGCTAAC CTTTCACACT	2520
TTTCCCAAAG TACCCCTGCC GAACGCTTCG ATCGCCCCGC CCTTTTCATC TATGAGCCTG	2580
GCTCTGTGTT CAAAATTTTT TCCATCGCTG CACTGTTAGA ACTCGGGGTA ACTTACACCC	2640
ACGACACGCT CCACTGCGAC GGTTCCCTCT CCTTTACCTC CCCCTTTTTA AAACCAGGTC	2700
AAAAAGGCCA TCTCATCCGC TGcCTGCGCC CACACGGcAC CATCAGCGcT GaAGATATCA	2760
TCCGGcTTTC GTGTAATGaC GGcATGGcAC AAATTGcTga ACGTGCCGAC AACCACAGCT	2820
TTGAGCAACT ATTGCGCGCT TTTGGATTTG GCGCGAAAAC AGAAATTGAG TTGCCGGGGG	2880
AAACCGTCGG TCTCTTCTCT CCCTCAGAAC GCTGGTCCCA CCGCAGCAAG CACACCATCG	2940
CAATCGGCCA GGAAATTGGC GTCTCTGCCT TGCAGtTGTG GCTGCCGcTA CCGCGCTCGC	3000
CAACGAGGGC GTACCGCTCG GCCTCTCCCT CCTCCATGAG GTCACTACCG CCGAAGtACC	3060
GTGGTGTACC GGCACAAAAA GAAACCCAAA ACACGCGTTA TCTCCGCACT AAATGCGCAA	3120
AAGGTGTTGC GATACATGCG CACCGCCGCA GAACTTGGA CCGGGAAAAA GGCGCTCGTA	3180
GACGGGGTGC CGATCGCAGT CAAAACAGGC ACTGCGCAAA TGGCGCACAG AAATGGTCGT	3240
GGGTACAGCG ACACCGACTA CCTTGCAAGT TGCATCGGCC TTTTCCCCGC GCACGATCCA	3300
GAAATTATCT TATACATTGC CATCATCCnt CCTATCGGAC AAGCCTATGG AGAGCTCATT	3360
GCAGCGCCTG TCATCTCTCA AGCGGCAAAC GAGATTATCG ACTACCGCGG TATGGTCCGT	3420
GCCAACGCCC CGTTAATCCA ACATAGCGGT CTCATCCATA CGTCAGAACG GACACCTCCA	3480
CGGTTAGGAA CCCATATGCC AGACCTCACC GGTCAACCTA AACGTTTACT CCTGGATATT	3540
GCAAAACGCA CCGACGTGCA CCTTGTCcTT ACAGGAGAAG GTTATGTGTA CGAGCAGCAT	3600
CCGCCTGCGG GCACACCTCT GACAAAAGGA ATGACCATTG AACTCAAACCT CAAATAAAAA	3660
GCGAGATCCC GCGCGTTTCC CGGCCGGTGT TGCGCAAGGC TGCAGTACCA CACGCGCAGG	3720
GGATCTGAAA CACAGAAGAA AGCATCCCTT TGAGAAGTTT TTTGCGCAAA ACAGCGCTCT	3780
TTTTGCCCAG CGGTTTCCAG ATCTTGACAG TGCCTGACA CTTCCAAACG AGCAGCTCCT	3840
GCAACGCATC CCTCCTGATT ACCTCCTTGC AGCGGCCCAT GACGGAGACG CAACGCTTGC	3900
AGTACGGGGC ACCTATCTCC ACTCAAAATA TCGGCCGCGG CAAGAGGCTG CACGTCTTAT	3960
CAGCCAGGAT TTTTTCACGC ACGCGATTGC AAAAGGCGGC TATGTAGGTG CAGGTTTAGG	4020
TCTTGCTAT GTAGCAGAAC TGTACGCGCA nAGCCACCCT ACGCACACGG TAGTGCTTAT	4080
CGAGCCAGAT ATATTCGTGT TCCTGCTTTT TTTAGCCATA GAcTyTCAC TCCCCTCcTC	4140
CGACACGAAC GTCTAAAAaT ACTGCCTGCa CAGACGGTAC CGGATGTGTT GCAGTTCyTG	4200

CGCGCCACGG	GGGATGTGTC	TCTCCCCCTG	TTCCATTCT	TACCAGCCCA	GGAGCTAAAC	4260
ACCGCGTGGT	TTCACGATTT	TACCCAGGCG	CACCGGCACG	CAACTGCACA	GGCAGAAACG	4320
AATAAGCAAA	CGCTGCAACG	GTTCCGGTCCG	CTTTGGATAC	GCAACACTAT	AAAAAATGCC	4380
GCACAGCTGT	GTGTGCGCAC	GCCCCGTAAAT	GCGtGCGCAA	tGCGCGGCAG	GGAGTACTGC	4440
ACTCATCATT	GCAGGTGGCC	CTGGGGTGGG	TGCGAGTATA	TCGTTCCTTC	CGTACCTAAA	4500
AAAAAAACAC	TGATTATTGC	GGTTGAaTAc	CGCGTTnTGg	CGTGTGCaGC	GCGCGCGTCA	4560
CCCCGGACGT	TGTGCTTCTG	TTTGAtCCAC	AATACTGGAA	CTATTTGCAC	GTAGCACGTG	4620
CGGTGGCGCC	CCATGCACTG	CTTATCACTG	ACATTTCTGT	GTTCCCTGCa	GTGTTTCGAC	4680
TCCCGTGGGA	GTACATTGTC	CTTGCaGGTT	CGGCATGCCC	TTTCGCTACA	TCCCTTGCGC	4740
ACCATGATGC	CTCCTGCTCT	CCTTCCCACG	CTCTTCTCT	CCCTTTTGTG	GCGCCCGATC	4800
TTCTCGCCTC	AGGTGGGTG	GTTGCTACAA	GTGCGTGGGA	ATGTGCCCCG	TACTTGGGAG	4860
CGACAACCAT	AGTGTACATA	GGGTGGGATC	TGGCATTTC	TGGAGCGCGC	ACGCACTTTC	4920
GCGGAGCGCT	GTTTGAGGAG	CGGGCACACC	TGCAATCGGG	TCGAGTGGCT	CCTGCCGAAA	4980
CTACCTCCTT	CTGTGCACTG	CACTCCCTGC	CCCTATATCC	TGTCCCGGCT	GCATCTGACC	5040
CCCATCCAGG	AAAGAACTCC	CCTGCTTnCC	CTACCGGGGA	GAACAAAGAG	CAAACGGTGC	5100
TAACCGaCGC	GCGTTTTTCA	CTGTACGCCG	TGTGGCTCGA	AGCACACCTT	GCGCGTTATA	5160
CGCACATTAA	AACGTATGCG	CTTGAGCCTG	CAGGAAGGAG	AGTTGCAGGC	ATCACGCCCT	5220
TGCGCTTTTC	CCAGCTTGTC	ACGTTACTCA	ACCGGTCGTC	AGCTGTGCCG	CACTGCCGGA	5280
CCATGTATAG	CCGCCGACGC	AGGCTATACT	CCCGGTATAG	AAACAGCAGC	GTGCAGGTCA	5340
ATTGCACCGA	TGCGGTGCGC	TGGAGGCGCA	CGATGAAGAG	TACACCTGTG	CACTGTCTCG	5400
GTCATTTTAC	GAAGAAAAAG	AAATCCGCAG	AAGGTGCACG	GAACCTATGG	CGTGCTCTCA	5460
GACGTGCGGA	TACGCGGTGC	GCTTCTCCCC	ATAACCTCGA	GCACGCACCT	GAGAGAACTC	5520
GTTCTTCCT	CAACGCGATG	CCACTGACAC	CCACAACGTA	TGAAAACAAA	ACACATGCAT	5580
TGTACACAGC	GCTGTGCACG	CTCCTCCCGA	CCGAGCCTAC	CTACCGCGCA	CGGGCACACG	5640
CACACCTCTT	TGAACCTCTC	ACCCGAACAC	TCAAGTTTTG	CGCCGCCTAT	ACCGAGGAGG	5700
AGGGGGAGTG	GCGCGAGGCC	tGACATCCGG	GGCCACTCAA	AGACGTGTGT	GGGGCgCaGG	5760
GGCaGGGCCC	GTGCGTTCCC	CCTTTCAGGG	AAAGAGCCAA	GCGCGTGCGT	CCTGCATCAG	5820
TTTTAGAAAC	ACCAAGACGT	CTACGTTTTG	CTTCTTGCGA	TTCTCGTAGT	CCGCCAGCG	5880
GCGGGGCGTG	TAGTGTGCAT	GGACGTCTGC	CCTCACCTGT	GCTGCATGCG	CACAGCCGCG	5940

740

CGCAATCAGC	TGGGCGTCGT	GCGCGGGGGC	GCGCCTAAGT	TTTTCAGGAA	GCACTTCTGA	6000
CAGAAGGTAT	GCACTGAGTA	CGCGAATCAA	CGGtGACGCT	TGGTGTGCAC	CAACGTGAGA	6060
AGATGCGCGT	GTGCCTGTTC	AAAGTCGCCG	CACAGGTGAC	ACGCGAATGC	GAGGTAAAAG	6120
CGAGTCCACG	GCTGGACGGG	CGCCTGTGTG	GCGGCAACGC	GCGTCATAAA	GGTACGCAGC	6180
TCCGAGTACT	TTCCCGCAAG	GAGCTTGCCA	ACGGCAAAGG	TGAGCGCGCA	CTTCATGATA	6240
TACCGAGGGC	TGCGCGTGCA	CAAAATGTTC	TAGTCGCTCA	AGTGCTTCAA	AGTCACTTAA	6300
AAGGATCAGT	GACTCTGAAA	GGAGAGACAC	CCTCCGCAAG	GCAACCCTAT	TGCGGGTGAA	6360
CACTTCCTCC	TCCAAAAGAG	CTGCCAATGC	CGACCAATCT	TCCGCATCCA	GGTATCGAAG	6420
CAGTCTCCTG	TTTTTAACAT	AGAGTGATT	TATCAGCAAA	AAGAGTAGGA	GAAAAATGAG	6480
AAAAAAAAATC	CCATACGCGC	GCACAGATTG	CCAGCCTGTA	CCCCGGACAG	GAGTGAGAAA	6540
CAGAACATAT	CCGGTACCCA	TACACAGCAG	CAGGAGTGCA	CCGTAAAAa	GCACTACTAA	6600
TGCTTTGATC	TTCATGGGAA	aTCTCCTATA	CTGCCTcCCC	GCCTGTGCGG	GGCGCCATTTC	6660
TACTATGGGG	GCGAGCGAAA	CGTGAATACG	TATGCAATTG	TAGATATACC	CGAGGAAACC	6720
CACTTCAGCG	ATGACGTGTA	TCTTGATGAC	ACTTTTTTTAG	TGCTGACCCC	CGCAGgTCTC	6780
TTTGACGAAG	CGCTAAAGAG	TCGACTGCAG	GAGTGGGACT	TCACCACGGT	GCACACCGGc	6840
GGACAACCTGC	TTTCTTCTGA	GACTACACTG	GAGTGTCTCT	TGCCTGCATC	CGGCGATCCA	6900
AACGCGAAGG	GTGCTCCCGG	ATCCGAGGCC	TTGCGTGAC	AACGAAGCCG	TTTTACGCA	6960
CTGAAGAAAC	AGTACAACGA	GTTTCAAATG	TTGTTGAGC	ACGTTTTTGA	TCAGTATCGT	7020
GCAAAGCAGa	GCCTGAACAC	GCGCGCGGTC	ATTGACCGTG	CGAAGATGCT	TTGCGAATTG	7080
GTAAAAAAGC	ATCGGcAAAC	GCTACTGCGC	GTCCTTCCCA	CCATTCCCTA	CCGGGAGCAC	7140
TACGCGCTTG	AGACACATGC	ACTCCGTTTC	ACGTTGTATG	CTGTTGTCTAT	TGGGTTACAG	7200
CTAAAAATGC	AACCGTTCAA	GATCATtGAG	CTCGCAACAT	CTTGCCCTGCT	TCACGAAATt	7260
GGCATGGCGC	GCGTTATCCC	GAAGCGTACA	CCACGGAGGG	GGAGTTAGAT	CCAAAAACGC	7320
AGAAGGCGAT	CTTTGCGCAC	CCTATTATCT	CCTACCATAT	CCTGCGTGAC	CACTCGCTCC	7380
CTCTGCCGGT	GTGTGTTGGG	GCACTTGAGC	ATCGCGAGCG	CGAAAATGGG	CTCGGCTACC	7440
CGCGCAGGCT	CGTGGGAGAA	AAGATTTCCC	TCTATGGCAA	gAtAAtCGCA	GTCgCtTGTT	7500
CtTACgAGGC	AGCAACCGCT	CCGCGCTCAT	ACAAGGAAAT	GAAAAACGCC	GCTGAGGGCA	7560
TCGTCGACCT	TGTGCGTAAC	GCGAACACCC	AGTACGATGC	AGTCATTTTC	CGCGCGCTTC	7620
TCTTTGCCCT	GTCGTTTTAT	CCTATCGGGA	CCCATGTGCA	CTTATCAAAC	GGGAAAATCG	7680

CGCAGtGGTG	GACGTTAACC	CCGACGACCC	ACGCTTCCCC	ATCGTGCAGG	TACACGGAGA	7740
AaTTCACCGC	AACGGCAAGC	CCATCATTCA	CAGCACGAGC	GCAGACGAAA	TTTTTATCAC	7800
GCGGGCCCTG	AGCGTAAAGG	AACAGCGTCT	TATCCTTCAG	GAAGGTGGCG	ACTGACCCTG	7860
CGCAGGGcAG	ATGCCCCCTC	CTGCTGCTGG	CTTAGACGCT	TTTTTAGCCC	CTCTAGGTCG	7920
TGTTTCGCAGC	GAATAACTTC	CTCAAACCTG	TCGCGCTCGA	TGGTTTCTCG	CTCCAAAAGg	7980
CGCGtTGCGA	TGTACTCAAG	GAGCTCTTTT	TTCTCCGTCA	AGAGTGCTAC	CACCGCGCGG	8040
TAGgTcCAGC	TAGAACGCGC	GCCACTTCCT	CATCAACGTA	CTGCTGTGTG	CACTCCGAAT	8100
ACTCGCGCGC	TAAC TGCGGC	TCCGCGAGAT	ACCCGGTTCC	GCGCGAGTA	AGTGCAAGgT	8160
TTGAAACTTT	TCGCTCATCC	CATAATCTGT	AATCATCTTG	CGGACAATGT	CTGTTGCGCG	8220
AGAAATATCG	TTCCCTGCAC	CAGTTGAAAC	TTCCCCAAAG	GCTACAAATT	cCGcTGCGnk	8280
TCCTGAAAGC	AGCACATCTA	CTTCTGCCAA	CAACTGCTGC	TCCGTAACAA	TATGCCGATC	8340
GTCTTCAGGA	ATGTGAAAAG	TATATCCAAG	CGCAGAGGTG	CCCCGGGGAA	TAATTGTAAT	8400
TTTGtGCACC	TTGTCTGCAC	CCTTCGTGAA	GGTACCTGCA	AGGcATGTCC	TGTCTCGTGA	8460
TACGCAATAA	TCCGCGCTC	TTCTTCTCGA	ATTACCCGAC	TTTTTTTCTG	CAATCCTATC	8520
ATTGTCTTTT	CGACCGCTTC	GTCCAAATCC	GTTTCAATCA	CCTGCGCACG	CCCAGACCGT	8580
ACCGCGAGCA	ACGTGCCTC	GTTCAACACG	TTTGCCAAAT	CAGCACCTGA	ATACCCACCG	8640
GTGATGCGCG	CCACTGCCTT	CAAATCCACT	TCTGGCGCTA	ACTTCACGTT	CTGCGCATGA	8700
ATACGCAGAA	TTGCCTCTCT	TCCCTTAAGA	TCGGGCCGAT	CTACGCAAAC	CTGTCGGTCA	8760
AAACGACCGG	GGCGTAGGAG	CGCAGGATCT	AACACATCGG	GGCGATTGGT	AGCAGCAAGC	8820
AAAATGAGAC	CGGTGGTGTT	ATCAAACCCA	TCCATTCTTA	CCAGAAGCTG	GTTAAGCGTT	8880
TGTTCCCGCT	CATCGTTGGA	ATGGATAGCG	TTCAGGCGGC	TTTTTCCAAT	TGCGTCAAGC	8940
TCATCGATAA	AAATAATCCC	TGGCGCCTTC	TCCCGCGCTT	GTTTGAATAA	ATCGCGCACA	9000
GCGGAGGcGC	CAATCCCCAC	AAACATTTTC	ATGAAGTCTG	AGCCACTGAT	GCGAAAAAAG	9060
GGCACTGACG	CCTCACCTGC	CACTGCGCGT	GCAAGCAACG	TCTTACCCGT	CCCTGGGGGA	9120
CCGACCAACA	GCACCCCGCG	GGGAATTTTC	CCCCGATTTT	CAGTATACTT	TTTAGGGAAC	9180
TTGAGAAAAT	CAACTACTTC	CATCAGCTCT	TCTTTTGCTT	CATCCACCCC	TGCAACGTCT	9240
GCAAAGCGTG	TGGTGACCTT	TCCTTCTTCC	ACCGCCgCAG	AGCGCGCGTG	TCCGGCTGAG	9300
AAAATACTGC	TCCCAGCCCC	GCTTACATTT	GAGGCCATCC	GCTTAAAGAA	AAAGCGCCAG	9360
ACAAAAAAGA	GGATGAGCAG	CGGAAAGAGA	TATTGAAATG	TCTCTATGAG	GTAATTGCgC	9420

TCGCGCGGCT TAATACTGTA GACCACCTGC CGCTCATCGA GCATGCTCAA AAAGGAATCG	9480
GAGAGGACAC CGATGGCATG ATAGGTAGGA GCCTCCCGCT CAGAGAGCAA CGAGAAACCC	9540
CGCGCAGAAG GCGCAGGGCG CGCGGAAGTG TACCCGACAA AGTAAGGGGA ACCGACAACA	9600
ACCTTTACGA TTTCCCCACT TGCAATGCGA TCTTTAAATT CCGAGAACGG GATGATGCGC	9660
AAAGCACGGG AAAACAAAA GTGGTTTGCA AGAGCAAGCA GCGCACAAAG AGCAAGGAGC	9720
ACGAGCGAGA GCACCTTACG CGAATTTCTG CGCGGAGGTC TTTCGCGTGA CGACGAAGGG	9780
CCTTTTTGAG GGGGGGGGA GAACTTAAAA AACCCGAATG GATCTGAAGA ATCATCTGAC	9840
TGTTTGTAGC GCGTATTCAT CTCAGTTAAG GCTCCCTTTT GCAGTGCGCG CGGGCACGCC	9900
GGCCCATGAT ACACGAAAAG AAGGTGAAAC GTCGACAGAC TGTGTGAGAG CCGTACGGcg	9960
CAgCTTAGCG ACGTCCGCTG GGGCGGTATG CACGGTGCTG CAAAAAACA CACGCGCGCG	10020
GCTATTGCTT ACCCTCATGC GCGCGTTCAC CGAAACTTCA CCTAATGACA CCTACCTATC	10080
ACCCGTACCC GGGCGACAAT CGCCCTTTTC TATACGCCGC GCTTCAGCGA CGTGAGCACC	10140
TGTCCCTTAT CCGGTACCGC GCAGAGCACG CGCAGGACCT GGCACCCTTG AGAGCGTTCT	10200
TGGCGCGCAT CGAGGCGCAC GCAACCGTCA TTGGTGCACG CACGCGTGGG GACACCCTTT	10260
TTATCCTTGC CGCATCGATG CCGTCTGATG CACTGCGCGA CGAAAAACAC GCATATGTGC	10320
GCACAATCTC CTGGGAACAG GCTCCTCAGA TACTTGAGAC GTTGGAGCGT CCGCCGCTCC	10380
CTCCTTATG CCCGCCCGTT CCTACTTCCT GTTCTTCTTC GCGTCTTATT CCCGACGTGC	10440
CGCACAACAC CAGGTCACAC GCGCAGGAGA GTTCCTACAC CTCTCGGCAT GCGCTTTTGA	10500
CGCTGCTCAT TGAGTGGCGC GCGCTCATGG TAGAGATGGA CTATTCAGTG AGAGCGCACA	10560
GGGTGCAGCG TAGTTCTGCT CCGTTGCATG AAAGACACGG CACTCTTCCC TCTGACGTAC	10620
TGCTCTTCCA AACACAGGGG GAGGTCTGCG CTCTCTGTGC CTTTCAGTTG CAGCACGTGC	10680
GCGCAGTAGG CGGGCAGCGT CATCTTATCA TTCATGAAGC GGCAGGAGGC GGAACATTG	10740
CATGCGAACG CATTTTCTCT CTCAAGGAGA TTGATTTTGC CACTGCAAAA TTTACTGAGC	10800
GSTATCCGTCG CGGGCTGTAC CAGGTTGCTG TGCATACGGC ACACGCAGAC TTTACGGTCA	10860
ACCTCATCGT TCCCTCACTC AGAGAGCAGG GCGGCGCCTA CTCCCTTGCA GAGTCTTCTG	10920
CCTTTCACAG GAGGGTAAGC GCGTAAACTG CAGATTACGC AAAACTAGCG GTTCTAGCCC	10980
GGAGGGtGAA GCGCGCCGTG TGCATCGGCA cGACCCCGCC AGAGAAGGCG GGCGCCCGTC	11040
TTCCCCGCGG TgGCGsGCTG CGCCCTGCTA CCCCCTCTGC TGTGGAGCGG GGCCTTGTCT	11100
TTTTCTGAG GGCTTGTTAC gcTGCGCGCC AGTCCCCGAG GAAGAAGGAA TTGCTATGAG	11160

TAGAGGTATT	TCTACCTTCA	GGAATATCGG	CATCAGCGCG	CACATAGATT	CTGGAAGAC	11220
AACCCTTTCT	GAGCGCATTC	TCTTTTACTG	TGATCGTATT	CACGCCATCC	ATGAGGTGCG	11280
TGGTAAAGAC	GGTGTGGCG	CCACCATGGA	CAACATGGAG	CTTGAGCGGG	aGcGCGGTAT	11340
TACCATCCAG	TCTGCCTCCA	CCCAGGTCCA	GTGGAAGGGA	CACACTATAA	ACGTCATTGA	11400
CACTCCCGGG	CACGTTGACT	TCACCATCGA	GGTGGAGCGC	TCCTTGCGCG	TTTTAGACGG	11460
TGCCGTCTC	GTA CTCTGTT	CGGTTGCAGG	CGTCCAGTCC	CAGTCCATCA	CTGTCGACCG	11520
GCaGcTCCGC	CGCTATCaCG	TGCCCCGTAT	CTCATTTATC	AATAAGTGTG	ATCGTACGGG	11580
TGCCAACCCt	TTCAAGGTCT	GCGCTCAGct	GCGCGAAAAG	CTCTCCCTTA	ACGCGCATCT	11640
TATGCAGTTA	CCCATTGGGC	TTGAAGACCG	TCTAGAGGGT	GTCATCGATT	TAATTTGCGT	11700
CAAAGCCCTT	TATTTGAGG	GAGAAAGTGG	CGCGCACGTG	CGTGAGGCGC	CCATTCCCGA	11760
ACAGTATCAG	GCAGATGTGA	AAAAGTACCG	GGATGAAC TC	ATCGATGCGG	CGTCTTTGTT	11820
TTCTGACGAG	CTTGCTGAGG	CCTACCTTGA	AGGAACTGAG	ACCGATCAAT	TGATTGAGC	11880
GGCAGTACGT	GCGGGCACCA	TTGCAGAAAA	GTTTGTCCCG	GTTTTTTGCG	GTTCTGCGTA	11940
CAAAAATAAA	GGTATTTCAGC	CAC TTTTGG A	CGCTATCACA	TACTACCTGC	CAGATCCTAC	12000
CGAGGTA ACT	AATACCGCGC	TCGATCTGGA	TAGAGCCGAG	GAGCCAGTTA	CCCTCTCCAC	12060
CGATGCAGAC	GCACCGGTAG	TTGCGCTCGG	GTTTAAACTA	GAGGATGGCA	AATACGGCCA	12120
ACTCACCTAT	GTGCGTGTAT	ATCAGGGGAC	TATCAAAAAA	GGGGCTGAGC	TTTTTAACGT	12180
CCGCGCGCGC	AAGAAATTCA	AGGTGGGCCG	TTTGGTACGG	ATGAACTCTA	ACCAGATGGA	12240
AGACATCAGT	GAGGGAACCC	CCGGAGACAT	TGTGGCGCTT	TTCGGCGTGG	ACTGCGCGTC	12300
GGGAGACACC	TTTTGCAGTG	GAGATCTGAA	TTACGCAATG	ACTTCGATGT	TTGTTCCAGA	12360
GCCGGTCATC	TCGCTTTCCA	TCACTCCTAA	GGACAAGCGG	TCCGCTGACC	AAGTTTCCAA	12420
GGCGCTGAAC	CGGTTACCA	AGGAAGATCC	TACCTTCCGC	AGCTTCGTAG	ATCCTGAGTC	12480
TAACCAA ACT	ATCATCCAGG	GGATGGGGGA	GTTGCACCTG	GATGTGTACA	TTGAGCGCAT	12540
GCGACGCGAG	TATAAGTGTG	AGGTGGAGAC	GGGCATGCCG	CAGtGGCGTA	TCGGGAGGCA	12600
ATTAGTGCGC	GCGCGGATTT	TA ACTACACC	CACAAAAAGC	AAACCGGCGG	TTCCGGGCAG	12660
TTCGGGCGTG	TGGCCGGCTT	TATAGAGCCC	ATCGCCGGGC	AGGACTATGA	GTTTGTAGAT	12720
CAAATCAAGG	GAGGAGTAAT	CCCAAATGAG	TTTATCCCTT	CGTGTGACAA	AGGCTTTTCGC	12780
ACAGCGGTaA	AGAAAGGAAC	TCTTATTGGT	TTTCCGATTG	TGGGGGTGCG	CGTTACCATT	12840
AACGATGGGC	AGTCTCACCC	GGTTGACTCC	TCAGACATGG	CGTTCAGGC	GGCAGCGATT	12900

GGTGCCTTTC	GTGAAGCGTA	CAATGGGGCA	AAGCCAGTAG	TCTTAGAGCC	AATCATGCGA	12960
GTGTCCGTGG	AAGGGCCCCA	GGAGTTCCAA	GGCAGTGTCT	TTGGGTAAAT	TAACCAGCGG	13020
CGGGGAGTGG	TTGTATCGTC	AGCGGACGAT	GAACAATTTT	CCCGCGTGGA	CGCGgAGGTC	13080
CCGCTGAGCG	AGATGTTTCG	GTTCTCCACC	GTGCTACGTT	CTTCCACACA	AGGTAAGGCT	13140
GAGTATTCTA	TGGAGTTTGC	TAAATACGGC	AAGGCACCGC	AAGGTGTGac	GGACTCGCTC	13200
ATAAAGGAAT	ACCAAGAGAA	ACGAAAAGCA	GAACAAAGGT	AAGCGTAACG	TGCTAGGCGG	13260
CGCGTCCTTC	TCGACGCGGT	GGCGAAGTCT	TGAATAAGGG	GGCTTTCTGG	TGTacCCTCC	13320
CGGGCCGAAC	GGTACTCTCC	TCACATGAGC	CGAGGAGGTA	TCACGTGGGA	GGTTAACATC	13380
ATGAATGCTC	ATACGCTTGT	GTACTCCGGC	GTAGCACTTG	CCTGCGCGGC	TATGCTCGGC	13440
TCCTGTGCCT	CGGGCGCCAA	GGAGGAAGCT	GAAAAGAAGG	ctGCAGAGCA	GC GTGCGCTT	13500
CTGGTCGAGA	GTGCGCATGC	TGACCGTAGG	CTTATGGAGG	CGCGTATCGG	CGCGCAAGAG	13560
TCTGGCGCAG	ACACCCAGCA	CCCCGAACTT	TTCTCCCAGA	TTCAGGACGT	TGAGCGCCAG	13620
TCTACCGACG	CCAAGATTGA	AGGGGACCTC	AAGAAAGCTG	CCGGTGTGCG	CTCAGAAGCT	13680
GCGGATAAGT	ACGAGATTCT	CAGGAACCGA	GTTGAAGTTG	CTGACCTACA	ATCTAAGATC	13740
CAGACTCACC	AGctTGCGCA	GTACGACGGG	GACAGCGCGA	ACGCTGCGGA	AGAATCGTGG	13800
AAGAAGGCAC	TTGAATTATA	CGAGACCGAT	AGCGCGCAGT	GTCTGCAATC	CACCGTCGAA	13860
GCGCTCGAGT	CGTATCGGAA	AGTCGCGCAT	GAGGGATTTCG	GCCGCTTACT	ACCCGATATG	13920
AAGGCACGTG	CGGGTGCTGC	AAAGACGGAC	GTTGGCGGTC	TTAAGGTAGC	CGTCGAGTTG	13980
CGTCCACAGC	TGAAGAAGC	TGACAGCCAA	TACCAAGAAG	CACGTGAAGC	TGAAGAGGTA	14040
AATGCACGTG	CCAAAGCTTT	TAGCGGGTAC	CACCGTGCCC	TCGAGATCTA	CACAGAAGTG	14100
GGGAAGGTTG	TACGCCTGAA	GAAGACCGAG	GCGGAAAAGG	CGCTGCaGTC	TGCAAAAACA	14160
AAGCAAAAGG	CGTCCTCTGA	CCTTGCGCGG	AGTGCGGATA	AGAGTGCCCC	aCTTCctGAA	14220
AACGCTCAGG	GTTTCTCAAA	GGAGCCGATT	GAGGTAGAGC	CGCTTCCAAA	CGACAGGCTT	14280
AACACAACGC	AGGCAGATGA	GTCTGCGCCG	ATCCCCATAT	CTGACACCTC	TTCACCTTCT	14340
CGCGTGCACT	CTCGGGGTGT	TGAAGACGGA	GGACGTTCTC	CAAAATCCTC	TATGAACGAA	14400
GAAGGAGCCT	CTCGATGAAG	ACACGTAATT	TCTCGCTCGT	ATCCGCGTTG	TACGTACTGC	14460
TGGGTGTTCC	TCTGTTTGTG	TCTGCCGCTT	CCTACGACGA	CAATGAATTT	TCTCGCAAGA	14520
GTCTGCGTA	CTCGGAGCTT	GCAGAGAAGA	CATACGATGC	GGGAGAGTAT	GACGTCTCTG	14580
CAGAGTACGC	CCGGCTCGCT	GAGGATTTTG	CGCAAAAATC	CTCGGTCTAC	ATCAAGGAAA	14640

CTATGGCGCG CACCACTGCC GAGGACGCTA TGAACgTGC GCGCACCCGC CACGCGTGGG	14700
CGAAAAATGA GCGCATCGAT CGCGCCTATC CGACCGAGTA TTTGCTCGCT AGCGAGGCTA	14760
TCAAGACCGG AGGcTCGCTT TTGACAGCAA GCAGTACGAC GTAGCGCTCA CGTGGGCGCG	14820
TAAGGCGTTG GACGCACTCA AAAACGTAAA GCCTGAAAGT CAGTTGCTTG CAAAGGCCGC	14880
GAAGGAGGag GCTGCGCGCA AGGCCGCCGA GGCACGAAAA CTCGAAGAAC AAAGAATTGC	14940
AGCCCAGAAA GCGCAGGAAG AACGTAAGCG TCGGGAGGAG GAAGCTGCGC GCAAGGCCGC	15000
CGAGGCACGA AAACCTGAAG AACAAAGAAT TGCAGCCCAG AAAGCGCAGG AAGAACGTAA	15060
GCGTGCGGAG GAGGAAGCTG CGCGCAAGGC CGCCGAGGAA GCAGCGCGAA AaGGCGGAGG	15120
AACTCGAGAA GGGTCGTGTG CTACCTGCGC AATACAAGGT GACTACGTGG TCCATTGACC	15180
GGGAATGTTT CTGGAATATT GCCAAAAACC CCGCCGTTTA TGGCAACCCC TTCCTCTGGA	15240
AGAAGTTGTA TGAGGCGAAC AAGGACAAAA TTCCTCAGTC CAAAAACCCC AATTGGGTAG	15300
AGCCTGAGAC AGTCCTGGTC ATCCCCAGTC TCAAGGGAGA GGAGCGCGAG GGTCTGTATG	15360
AGCCCAACGT GAAATACCGT CCTCTGCCGT AACGGATAGA CAAGAGCGTA TACGCTTTTT	15420
CCCCTTTTCC ACAAGGGTGC AAGGGGCGTG GTTGGGAGCC CATAGAGAAA GaGCTyCCCA	15480
GAGCGCTGGA ACGCTACGGT GTCCaGCGCT CTTTGTGTGT TTTGTCTCT ACAAGAAAGT	15540
TCCACTTTTT GCTACACTTC CTTTCTATGG ACGTGTCCTT TGAAGAGCTT GGTTTGAATG	15600
AACAATgCTT GCAGCGGTGC GACTCAAGGG GTTTCGGTGC CCAACTCCCA TCCAGGCTGC	15660
TGCCATTCCC CACTGTTGG CAGGGGATGC GAATATCATC GCAAAGCCC GAACCGGGAC	15720
TGGAAAAACG GyCCCTTCGG CCTCCCCCTT ATCCAAGAAC TGGGAAGCCC GTGCGAACAC	15780
CCAGGGGCCT TAGTGCTTGT TCCTACAAGG GAGCTCGTGC GCAGGTCGCA AGCGAACTGA	15840
GCTCCCTGAG GATACAAAA ATACCTCGGA TTCACACCGT GTACGGTGGG GTCTCCATCG	15900
CGGAGCAGCT GCGTAATCTC GAACAGGGTG GAGAGATAAT AGTAGGAACG ACCGGGCGCG	15960
TCATCGATCA TATTGAGCGC GGTCTCTCG AGCTGTCTTA TCTGCGCTAC TTCATATTAG	16020
ACGAAGCGGA TGAGATGCTA AACATGGGTT TCGTTGAGGA TATAGAGTCT ATCTTCTCTC	16080
ATGCAAATAA AGACGCACGC GTCCTTATGT TTTCTGCCAC TATGCCCAGG CAGATCCTTT	16140
CTATTGCCTC TACCTTCATG GGAAGCTACG AGGTTGTTGA AGAAGTCACT CCAGAAGAGG	16200
CGCGCCCGCT CATTGAACAA TTTATGTGGG TTGTAAGGGA CGCTGACAAA ATCGAgGCGC	16260
TTGTGCGCCT TATTGATGTG AGCGACAAC TTTACGGTCT GGTGTTCTGT CAAACCAAGG	16320
CGGACGCCGA cACTGTTGCG AAATCTCTAG ACGAACGCCA TTACCATGTT GCTGCACTTC	16380



ACGGAGATAT	TCCGCAAAGC	CAGCGAGAAA	AAATTCCTCGA	GCGCTTTCGT	ACAAAACGAG	16440
CGCGTATCCT	CGTCGCCACT	GATGTTGCCG	CTCGCGGCAT	TGACATCGAA	GGAATTACGC	16500
ACGTGGTGAA	CTACTCCATT	CCTCATGATA	GCGCTACTTA	CACGCACCGc	GTcGGcAGAA	16560
CTGGACGCGC	AGGATCACAG	GGTATCGCTA	TCAGTTTTGT	ACGCCCACAC	GAGACACGAC	16620
GGATGGAGTA	TCTGAGTAAA	CACCTGTAATG	GCGAATTGAA	AGCTAGTACG	GTACCTTTGG	16680
TGGAGCACAT	CCTTACTCAA	AAGGAGGGGC	GTATTTTCTC	GTCCCTCAAG	ACTCATCTTT	16740
GCCAATTACT	CTCTGAAGGG	GTGCACGGAA	CCTTTTACCG	TTTTGCGCAc	GGCTGCTCCA	16800
AGAAGACCTT	AAAGCTCGCG	TGGCAGAAGC	CCTGGGTaCT	TCCGCCGACG	TTCTTCAGGA	16860
ACCGAACGTG	TCGCTTGTCG	CCGCGCTCCT	GCAAATCCAC	TACGGTACTG	CGCTGGACCC	16920
CAGGCAKTAC	CGGGATATTA	AAACGATTAC	GCCAGAGACG	GCCCGCGCAC	GTCCCCATGA	16980
mGCGGAAAAG	GCGTATGTGC	GCATTGAGTA	CGGAAAAAAA	AGCTACCTCA	CTCGGAAACG	17040
TGTTGTGCAG	TTTATCTGTG	CCCTGGTAAA	AATCCCCGGT	CATCTTGTAG	ATCGCGTTGA	17100
CATAACCGAA	CGTTkCGCGT	TTGCcGCATa	CCCCGACGCG	CAGgaGGAaG	CAGTTCGCTT	17160
ATCCAAGAAG	CGCAAGGACC	TGCCGCGCGT	TTCTTTCGTT	GGGCACGCCA	GTcGCCTAAG	17220
AAATACCGCT	ACCCCTGCAG	AAAAGTCTAC	CTATCCAAGG	CGCCTCCCTT	CCGGAGAAGG	17280
CCTAAGGGAG	CAGATCTCAA	GGAGAACCTC	TTCTCTTAAG	AAGGCTTCTG	GGAAACCGGA	17340
GGATTCTCTT	CCCCCTCCCC	AAGAACATCG	CCTTGATTGA	TGCAGCGGCT	CACTGCGCCA	17400
CTACAGCATT	CGTGCAAGCC	AGCGCGAGAT	ACTAAGGGCA	TAGTTACCGA	CGGCTTCTAT	17460
ACCACGCACG	ATGTCCATAT	ACAGGAGcTC	CGCCTTTACA	TCTGCACCCT	GCTCAAGACG	17520
TCTGCGCACA	AGTCCtTTTA	GATGGGCCCC	CTTGCTTTTCG	ATAGAGTGCG	TCATTTGGTT	17580
TACGTGCAAC	ACCTGCTTAT	CTTCCaGTGG	ACGGTTCaAG	TGCGAATACA	CAAAGTCAAC	17640
GCACTCATCC	ACCATGCCgA	CGTACGGGAC	TAACCTCTCG	ATATCATCAC	GCTTGAGCGG	17700
TACATTTCCC	TTGATGCTCT	TATGGAAGTA	CAACCCTATA	CCACACAAAT	GGTCAGTAAT	17760
ATTTTCAATA	TCGTCTGCAA	TGGAaaACAT	TAATTGCACG	TTATGTTTTG	CTTTCTCGCT	17820
CAAAGAAAGA	TGCGATGTTT	TAATCAGAAA	GCGCGAAAGC	TGTTCCTGCA	TTTGATCTGC	17880
ATAATCCTCT	TCCTTTGTCA	GGCGTGTTAC	GATCTCATCA	GTAAGAAAGCA	TACACGTTCC	17940
CTGAATGGAC	TTACGGATAG	TAACAAGCAT	ACCCTGTGCT	ATTGAAAACA	TTTTTTTCAG	18000
TTCAATTtCC	GCACGAAAAA	TATGTGCCTC	AGCGCTCTCT	TTTACCGCAG	TTTCTTGAAA	18060
AACAAGCTGA	TACCTwTCTG	GAGCGTCGTC	ATACCGAGGA	CGAATTAACC	ACTCTACAAA	18120

747

CGCTGCAAGG TGCTTAGTGA AGGGAAACAC AATAATAGTG TTGACGATGT TAAACATACT 18180  
GTGAAAGAGC GCAAGCCGCA CTGTGATGTT ATCAAAACCC GAATTCTTTG GAGTCAAAAC 18240  
ACACAAGAGT GCCAAAACCTG GATGAAAAAA CATCAAAAAA ACCAATGCAC CAAACACaTT 18300  
AAACAGCACG TGGAcTGC GG CAGtCTCCGT GCGTTCAATT TACTCCCAAT GGCTGCAATT 18360  
GCAGCATCAA TGGTAGAGCC CACATTACTT CCTAATACGC TTGCTGCAGC GAACTCCACT 18420  
CCGaTGACAC CACCGAACGC CATAGTCAAC ACGATCGCAG TGGTTGCAGA CGAGGAGTGC 18480  
AAGATGACCG TTAACACAAA GCCTGATAGG AGTCCTACAA AAACACTGAG CGCACGATCC 18540  
TCAACTGCAA TTTTAAGGAA GGAAAGCTCT TCTACAGAAA GTGGAGGAAT GAGCGAAGAG 18600  
AGCAAACCAA GCCCCGTAAA GAGAAGACCA AAGCCCATGA TGCTCTCGCC CAAATGTCCT 18660  
TTATGCAAGT GTTTAAAAAA AGTCAGAAAA TAGCCAATCC CAAAGGCGGG GACAGCGATT 18720  
GACGCAAGCT TAAACTGAAA ACCCACAAGC GCAACAATCC AAGCAGTAAC AGTGGTACCG 18780  
ATATTGCGAC CAAGAATTAC GCCGATTGAC TCGGTCAAAG AAAGCACTCC CGCGTTAATA 18840  
AAAGAAATCG TCATAACCGT CGTAGCCCCT GACGACTGCA CAATAGCGGT AACTGCCATG 18900  
CCGGTTAGCA CCGCGAAGAA ACAGTTACTG GTCATCACTT GGAGaTTTT GTGGAGGCTT 18960  
TCTCCAGTAC CCTTTTGAT ACCGTCACTC ATCAGCTTCA TACCAAAGAG CATGAAGCCA 19020  
AGGCTTCCGA TACCCTGCAA AAGGACAGCC ACAAGGTGCA TCGGCGCCCA CCATAGCAAA 19080  
AACAGGGGAT ACGTATCAAT TGTCCGAAGC GGGACACTGC GCCGTACGGA CGTATGTTTA 19140  
TTAGTCAATC TCTCTTTTCT CAAATAGTCT CGCCGTGACA TCGCTT 19186

## (2) INFORMATION FOR SEQ ID NO: 122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGGTATGTGG TGCGCGATTC ACGTAAACGA AATGTTTCTT TTCGCAGAAC AGATGCTAAA 60  
TAGCTGGCGC ACAGCGATAC ACGCCATAGG GCAACTCTTT TTGCGCACGA GTGCGCACGT 120  
GCCGGTGACA CCCATTCAATC TGTTAGATCC TGCTCACTAC CTGGAACGCA TTCCCATCGT 180  
GTTGTGCGTG CACGCGCTCT GTGGCGTTGC AGGAGGCACG CTATGCCTAT CGTTGGCGGT 240  
ATGCATCATT CCTGCGCTCC GTGCGGGCCG CGTGCGTCCC CTTGACCTCA TGCGCAAGGT 300

748

GTGATAGGAT	CCCCCAGTT	TTTTTGATTT	CTTACATCCG	GCTCGCAGAC	GGATGGGTAC	360
CATCTTTTAG	AAGAGCACGC	GGCCGGTGCG	GTAGGGGCTA	TGGAAGAACG	CAAGAACTAT	420
ATGGATCGGC	TTGCCGAAGC	ACTTACGCGG	CGCAAGGTGC	AGCTCGATCG	GGACATCCTA	480
CCAAAGGCGC	TGGAGCAGTA	CCGTGTCCAG	GTCACAGCGG	TAAAGGCAAT	TCGCAGTAAT	540
TTGCTGCAAA	AAGGTTTCTT	GCACGATGAC	GCGTACAAGT	ACGACAGCAA	GATGACTGAG	600
ATTGAGTTGC	CAGAAACTTc	CCctACGGGG	AAAATGAGAA	GCCGATGGTC	ATTGGTTCTC	660
GCCTTTCGCA	CTATCAGACT	ATGCTCGGTT	TTTTGGACAA	CTACTACCGG	TTCGATTCGG	720
AGTTTCTAAT	CCCGAAACGT	ATTGCAAAGC	TCGTTGCGCT	CAACGGTACg	TTCATGTGGA	780
AAGATTTTAC	TGCTACCACC	AAAGACGCGA	ACACACGTGG	GCTATTTGAC	ATAGTGCAAT	840
CTTTCTATGG	CGCTGCTGAT	CCTATTTCTGA	TAGGACTGGT	GAGGGATTCTG	TTGCAGTACC	900
TAGTAAAAGC	CCATGAGGTA	ATCAGCACAG	CACTTAAGTC	CCTTTCGGTG	TTTCATCGCG	960
AGCGCTACAA	ATTGCTTATT	CGCCAGCATG	CTCTGGATGG	CTTGGACGAG	ACAACGGTGG	1020
ACGTCAACAA	CCCAGAGGTT	GCGCTTGACG	CGATGAAAAA	GAACTTTTCA	GAAAATGCAA	1080
AAGGCCATCC	GTTCTACAGC	GAGTTGGCAA	CCGTGGTTTT	GAGAGAAGAC	TTCTCTGCCA	1140
ACGCAGAAAA	GCTGCGGGCT	GCAATCCTCC	GCGAGTTTGA	AGAATCTTCT	GCACCCAAAA	1200
GATGcCGCGG	TGCTATGCGC	AATCCACACG	CCGTACTACT	TTCTGGTTTC	AGATCGCTTG	1260
GAGCTACTTC	TAGCCACTTT	CATACTGCTC	TGGAAAAGAT	TCGCTTCAAT	GAGGAGCTCG	1320
TGACTCAGTC	TGAGGCGGCC	TTCTTTTCAA	AGGTAGTGTT	AGCCTTTCTC	AAAGCTTTCA	1380
ACATTCAGAC	GCGTTCAAAG	GACGTTGAAA	TTGTCGTCTG	CGACCCGGCA	ACACAGATAC	1440
AGAAAAAGGA	ATGCGTAAAC	GTTGAGCTCT	TTCAAAAAGA	GCTGGCCCGG	TGTGTCAAAC	1500
TGTATCGGGG	TTTTGTGTCT	CCAGACACTC	CGATTCATGA	AAAGTTAATG	GCGCTCAAGG	1560
ACGAGCAGct	CTTCGAGCTC	CTTTTTTAAAC	ACGTAGCAGA	GGCGCATACG	CTGGTTAAAC	1620
AGCTTGCAAG	TCTTGATGAG	TACTACAAGA	CAGTGAGGTC	TGATGTGCGC	GCGAAAATTA	1680
AAGGGGTCAA	GATTGAAGTT	ACAACTATCA	CCACTTCTGT	AACCAAGGCA	AATAAGTGCC	1740
GCGCAGAATA	TGCCTCGCAA	CTAGAGGAGC	AAAAACATAT	GAAGCGTTTA	GGGGTAGCCC	1800
GTGCGTAGAA	TGCGGCTCTC	GCGCCGCGGc	ATTCTCACGG	TAGTAGGTAC	CCTTCTTCTC	1860
CTACCTCTCT	TTCTTCCGA	AAAAAAAAG	ACTCACGCGC	CGCTCCCTCG	ATCTGAAAGA	1920
AAAGAGTTTG	TGGTGTCTCT	TTCTCCGTAT	AGGCCTGTGC	TACACCCGCA	CGTGGCATCG	1980
CGCGTGGACG	AAGCACAGCT	GCTCACAGCC	CTATATGAGG	GACTTGTCAC	CTATGATCCG	2040

TACGATCTCC ACCCAATCCC GGCCTCGCA CAACACTGGT CGGTAAGCAC CGATGGGTTG	2100
ACGTGGACGT TCTATTTACG AGATCAGATT TTCTTTCAAA ACGGCGACCC TATCACTGCA	2160
GAGACGTTCC AGCAATCCTG GCTCAATTTG TTAAATCCTG AATGGAATGT GCCGTATGCG	2220
TCTTTTTTGG ATGCAGTTGA GGGGGCACGT GCGTACCGCA GCGGCACTAC GGCTGACTCT	2280
CACACGGTTG GGATTCCTCGT AGAGGGGTCA GACAAAAAGA CACTCGTGGT CAAGCTCGCG	2340
TACCCAGCAG GACACTTCAT TCAGATGCTC TGTCAACACG CATTTGCCGC AGTCCACCCC	2400
ACCCAATCTG CAAGCGTCGG CACGCTGCAC GCGCGTACGG CAAGCGCCTC AGCACACAAG	2460
CCGTTCATC CTATCGCAAG CCGTCCTTTT GAATTACAAC AAATGCAAGC AGATCGCGTG	2520
GTGTTGCGTG TTAACACCCG CTAATGGGAC AGGGaCGCGC TTGCCCTCCA CGCCATCGTG	2580
GCGCTgcATT GCACAAGACC CTGCAGCGCG CGATGCGGGG TTTAACGATG GGAGCATCCA	2640
TTGGATTAGT GGAGCGCTGG AGCACAGTTC TTTGCAGGAT GCAGCTACAC TTCAGATCGT	2700
ACCGCTTCTG GCAACAGAGT ATCTGTGTTT TAAAACGGCA CATGAGCCGA CGTGCAAgCC	2760
ACGcTGCgCA AGGCACTGCT TTTAGCTACT CCGGTGGAGG AGCTTACCGC GCGCTATTTA	2820
TTTCCCGCAC GAACGCTCGT AACTCCGTTT ACCGGCTACC CCGTACCGCC TGTAAGTACAT	2880
GAATACAATC CTGCGCGCGC ACGCTnTtTT AGCAGAAGCG AAGATAGGTG GGAAGACAGC	2940
CCGTACTCCT CTTAAAATTC TCGTTTCCGA CACCGAGGCG TGCCGGGCAC TCGCACTTGA	3000
ACTTCAGAAG GCCTGGACAG CCCTCGCACT TGCAGTGGAA ATCTGGGCAG TCGGGCCTGA	3060
AACGTACCGG GAATATGTGC AGGATGAAAA ATACCACGTG AGAATCGTGT CTTGGGTTGC	3120
GGACTTTGCA GATCCGATGG CGTTTCTGGA GCTGTTTAGA AAGGGATCAA AGACACACTC	3180
AACCGGATGG ACCCATGAGG AATTGAGGC ACTGCTGACA CGCGCAGGAG CAGAACCGCA	3240
CGTGCTTCGT CGTTGGGAAC TTCTTGCGCA GGCAGAACGT ATCCTCTTAC AGGAAGCAGT	3300
TGTGCTTCcG CTTTCGCGTT TGCATGCACT GCACGCGGTA CAGCGGCGCA CCGTGCGCGG	3360
CTGGTATGCA AATGTGCTCG ATGTGCATCC ATTTAAGTTT ATCTCGTTAC AAGAAGAAAT	3420
AAAGGTCAAC CTAGACTCAT AGAGGGGCTG CAACCCGTGC ACACCCAGGT GTACCTTGCA	3480
ACGTAGATGT ACCGGCGTGT ACAATGCCCT CTGCATACAC AGAGGGGATT ATGGGGTATC	3540
CGTTTCGCGC TCTAGAGAAA AAATGGCAGG CCTATTGGCG CGACAAGCgs GTCTTTTG TG	3600
TGTCCGAGGA TGAGCGCTTC CCTCCTGAGC GCGGTGCGTA CGTGTGGAC ATGTTTCCCT	3660
ATCCTTCAGC GCAGGGACTT CACGTCGGAC ATCCAGAAGG CTACACTGCA ACTGATATTT	3720
ACTGCCGCTA CTTGCGCATG GGTGGTTACA ACGTGCTCCA CCCTATGGGT TTTGATGCCT	3780

750

TCGGACTTCC GGCAGAAAAC TTTGCACTCA AACTGGTAC TCATCCGCGC GTCTCCACCT	3840
CCGCCAACTG CGACACCTTT CGCAGACAGA TCCAGTCGTT TGGTTTTTCC TACGATTGGG	3900
AACGTGAAAT ATCTACCGCA GATCCAGAAT ACTATCGCTG GACTCAGTGG CTGTTCCCTCA	3960
AACTTTATGA AAAAGGATTA GCCTATGAAG CAACCGCGCC CATCAATTGG TGTCCCAGCT	4020
GCAAAACAGG CCTTGCAAAC GAAGAAGTAA GAGACGCGTG CTGCGAGCGC TGTGGTGCTG	4080
AGGTGACGCG GCGTGGTGTC CGCCAGTGA TGGTGCGTAT TACAGCGTAT GCCGAGCGTC	4140
TCCTTTCAGA TTTAGATGAA CTTGACTGGC CTGAGTCAGT TAAACAAATG CAGCGTAATT	4200
GGATTGGAAA AAGCTGCGGC GCGGAAATG ACTTTCCCGT AGATGCGCCT GCGTGTTCAG	4260
TGCACGATAA GCTACCACAG ACAATTTCGCG TGTACACCAC GCGTGCGGAC ACGCTTTTGT	4320
GAGTAACGTA CCTGGTACTT GCTCCCGAGC ATGAAGCGGT AACGGCGCTC ACTACACACG	4380
CACAACGCGC AGCGGTACAG GCGTACGTGC AACGTGCAGC AAAAAAGAAC GATCTCGAAC	4440
GCACTGATTT AGCGAAGGAA AAGACCGGTG TTTTCACCGG CGCGTACGTG CGCAATCCAA	4500
TCAATGATAT GCGCATACCG GTGTGGGTAG GTGATTATGT GCTCGTTTCC TACGGCACGG	4560
GGGCAGTGAT GGCAGTTCCT GCACATGATC AGCGCGACTG GGATTTTGCC ACTCGGTTTG	4620
GCTTACCCAA GTTAACCGTG GTGTCTGCAG ACTACACTGC AACAGTTCCT AATAGCAACT	4680
CCCCTCAAGG CGCGGTACTC CAAAGATGCG TCTCAGACGA GGGTTTTGTC GTCAACTCTG	4740
GAGCTTTCAA TGGTCTTGCT AGTGCCGACG CGCGAGAACG TATTGTTGCC CATCTTGAAA	4800
TGCGTGGCGC AGGTGCACGG CGCGTCACCT ATCGCCTACG CGACTGGGTG TTCAGCCGTC	4860
AGCGCTATTG GGGAGAACCC ATCCCTCTTG TGCAGTGTCC T	4901

(2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CCCACCTGTC TCACCGGCCT GAACGCCGCG GTCGAAGCAC GCGTGATACA TCCCCCTCAC	60
CTACATCCGT TACAGAAATA ACGGAGGGTA CGAACTGAAT GGAGCTGTGC CCCCTGGGAC	120
TATCAATATG CCAATTTTGG GGAAGGCGTG GTGCAGCTAT CGCATCCCCC TCGGTTCCCA	180
CGCCTGGCTT GCACCACACA CATCCGTGst CGGCACAACC AATCGCTTTA ACATTATTAA	240

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CCCCGCGGGC AACCTGTTGA ATGAACGAGC GCTCCAGTAC CAGGTGGGAC TGACGTTTCAG	300
TCCCTTcGAG AAGGTGGAGC TCAGCGCCCA GTGGGAACAG GGCGTGCTTG CTGACGCTCC	360
TTACATGGGC ATTGCCGAGA GCATCTGGTC CGAACGCCAC TTCGGCACCC TTGTCTGCGG	420
AATGAAAGTG ACATGGTAAA AACGCGTGCT GTTCGATTCC ACCTCCCCTA TCAAACCCCG	480
TTTTTGCTCGT CTTGCCTTTG CAGTTGCAAA ATTTTGCTCTC GGATGAGGGC TGCCTCTTCA	540
AATCGTAACT CACGCGCACA AACCTTCATG TGTAGGCGCA ACGCCTGTAc CATTTTTTTTG	600
CGTGCAGCAT GTGTGCGCAC GTCTGCGTCT GCTGCGCGCA ACAGGGGTGC GACCTGTACa	660
cGCGCAGtCT TTTTTTACTT CCTGCTCACG GACCAGAATA TCTTCAATAG ACTTTTTTAAT	720
CGTACGGGGT GTAATCCCAT GAGCACGATT ATACGCCATC TGAATCTTTC TCCGTCGAGC	780
AGTTTCCTCT ATTGCTTCAC GCATCGCATC GCTGATTGCA TCCGCGTACA TTACCACAGT	840
TCCGCGAGCA TTACGTGCTG CTCGACCAAT AATTTGGATG AGACTCGTCG TCGAACGTAA	900
AAAACCGACT ATATTGGCAT CAAAATAGC AATGAATGCC ACCTCGGGCA AATCAATACC	960
TTCTCGTAAT AAATTTATTC CAACTAATAC CTCACATTCC CCCGCACGCA GACTCGTGAG	1020
AATTTCTACG CGTTCAATAG TTTCAATTTC CGAATGAACA TACTTTGTCC TTATTCCAG	1080
TCCATTGAAA TAATCTGTTA AATCTTCAGC CATTTTTTTTT GTCAATGTTA GCACCAAAtA	1140
CGTTTCGTCC gCGcACTACA AGCTTTTACC CGcTGaCATA TATCTTCTAT TTGTCCATCC	1200
GTTTTTCTCA CTTTCGATGCA TGGATCTAAA AGTCCAGTGG GACGAATCAG TTGTTCAACT	1260
ATTTGCACAG ACTGTGTGCG TTCCTTCACC CCAGGAGTTG CAGAAATAAA AACTGCTTGA	1320
TTTAACAATG CCTCAAATTC CGAATCTTTC AGTGGACGGT TATCTCGTGC ACACGGCAAG	1380
CGAAAGCCAA AATCGATGAG ATTCTGTTTA CGCACCCGAT CTCCTTCATA CATTGCACCA	1440
AGCTGCGGAA GTGTTACGTG ACTTTTCATCA ACAAAGAGCA CAAAATCCTT TGGAAAATAA	1500
TGAAGAAGCG TCACCGGCGG TTCACCAGAT TTTCTACCTG CAATCGGCGC AGAATAATTT	1560
TCTATACCGT GGCAATACCC CATCTCTCCG AGCATTTCAA GATCGTATTC TGTGCGCGTT	1620
TTTAAACGTG CCGCTTCTGC AAGCTTATTC TCTTGAGTTA ATTGTACCAA CCGTTCATCG	1680
AGTTCTTGTC TAATACGGTC CATGGCGCGA GGGATTGCAT CCTCTTTAAG TACAAAATGC	1740
TTTGCAGGGT AAACGGTAAG TTCTTCAAAT TCCCTTAGAA CAGCACCGCT TACAGGATGA	1800
ATGCGACGGA TACGAACAAC TCGATCCCAA TCGCACTCGA TACGATAAAA TTCTTCTAAA	1860
TACGCAGGGA AAATTTCAAT AACGTCTCCC CGAACTCGGA AGCGACCGCA CTCGAGCACC	1920
GCGTCGTTAC GCTCGTATTG CAGAGATACA AGTTGCCGCT TGAGATCTTC AAGATCAAGA	1980

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CACTGGTTGA CTTCCACGTG GATACGCAGA TCACGCCAGG ATTCAGGCAA CCCAAGACCG 2040  
TAAATACACG AAACAGTTGC GACTACAATA ACATCACGAC GTTCCATGAG ACTAAACGTT 2100  
GCAGATAAAC GCATTCTATT TATCTCTGcA TTGATAGAAG CATCTTTCTC AATGTAGAGA 2160  
TCACGAGCAG GGACATACGA TTCAGGCTGA TAATAATCGT AGTACGACAC AAAATACTCC 2220  
ACCGCATTGT CTGGGAAAAA ACCTTTAAAT TCCCCGG 2257

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TACTCATCGG CGTCGCGCnT TCnTACTCCT TGGGCATTGA CTA CTCTTCAAC TACCCCGTCT 60  
GATACCATGA CCATTACATC CCCAGGACAC AACGTACGCT CATGAATCTG TATAGGGGGC 120  
AGATCCACAA TGCCAATAAC TGGACAATTC GAATGAAGAT GATACACTTC GTGCGCCTCT 180  
CCCGCCTGGG TAAAGACAAG GGGACTTTCC ATCGATGCGT TAATGTAGCG AATATTCATA 240  
CCCGCTGTGT CAATTAATCC CAAGAATAAG GTCGTGTACT TATCGTGGAG ATGCATACGC 300  
TTTACTGCCC GGTCCACCGC ATACAAAATC TCAGGAAGAT TCTTTTGTG TTCCACGATG 360  
CGAATCGTAC TGAGCACAAC ACCCATAACT AACGACGCGG CCAAACCTTT GCCAGAAACA 420  
TCTCCAATTA CAAATAAAAA CAGGTGTTCA TCAATTGAAA TAACGTCGTA ATAATCCCCA 480  
GATACATTAA CCAGTGGCTG ATAGAATGCC CCGACGCATA TTTCTTGGT ATGTGGGAGC 540  
GCCTTAGGCA AAAGTGC GCG CTGTACACGC GCCATCATTG CCCATTCTG GGATACATGG 600  
GAGTACAACA ACAAAGTGCT CATGTTCTC TTTGATTTA AATACTCTT AACTCTTTG 660  
AACAGAGCG ATATAACTTC GCGCTCAACA GCACGGATAA AACGACATAC TATAAAAAGA 720  
CGCAGCTCTC CACTGGAAAG ACATACCCCA CGAGCCCGAC GTCGGTCAGA CATAAGACAC 780  
AGATCATCAT CAAAAAATA TATACCGTCT GACCAAGTGCC ACGTGTAGTC CATAGAAAAC 840  
TTATGAAGCA CAAGATCATA CGTGCGTGTG TCTGAAACAA ATCGTGGCAG CACTGTTGTA 900  
AATAACACGn TTA CTTATCG TATCCATTAA GAGCACTGCG CAATCGGAGC GATATTCAAG 960  
CACCTCCTGG AAGGCAGCAA CAAGTTGTTT AT 992

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GTGCAGGATC CGTCTCTTGT TCACGAAGAA CTCAGACACG GTTGGCGTAT CTGCAGATCG	60
CCTATGCTCC ACGGGGATAT ATTAAAAAAC ACGCGCACGC TAGAAaCctC GCCGCATATA	120
AACgGCGGTC AAgAtTTGTC CAATACGCGA TTAAGCACAA TTACACCACT GAGTCAAAAA	180
GCAGTATCAG GATAGACAGG GGAACAGGTA TGCCTGATAC GGTAATATTT AAAAAATAA	240
AGGTCAATGA CAAAAGCTG GCTTCCTTTG TAAGGGAGCT CATGTCTCAC CAGGTAGATC	300
AACTCACGGT TTTACAGAAA ACGGAGGAAA TCTACGGTAT GCTCGTGGAC CTA CTGATCT	360
AGCACTAAGG AAAC TTATCA TGATACCTAA ACTGAGCCCA AATGCTGACC CCTGCACAGC	420
GTGTGCTTCC ACCCTGCCT TTCCGCCGCA GCCCATGGAG GAGGAAGGAG AGTTTTTATA	480
TCAGTTGCGT CTTGAGTACT CCCGCGAAGT GTTATATGnC GTTTTCACGC GGnTACGCGT	540
GCACACTTTT GnTnGGTACC CACGCGTTAT GGCAACGACA TTGCTCGGTG CGTAGGGCGT	600
ATACGTACAC CGGTACAAAC CGATATCGCG AGTGTGGTAC GTGTTGCATC AGACCAAGAT	660
TTGTGCACAT GGCACATACA TAGGGAAAAG GAACGTGCTG CGGAAATGAT TTTTCGGGAT	720
CGCATTGAGC ACTATCAACT TGaGATGaAA TGTATTTGCT GTCAC TATCC TTTAGAAgAA	780
gCACsCsTGG TaTTTTCTATA CAgTGCGCCA GCACGTkTTG ATTTCaGAGA ATTAGTTAGA	840
GACTTAGGAG CTACATTTGG TACGAGAGTC GAACTGCGAC AGATAAATGA ACGGAAGAA	900
GCGCGGATAG TAGGCGGAAT TGA CTGCTGC GGGCGCGCGC TATGTTGTTG CTCAGTGTTT	960
AGCAGGTTGC GTCCAGTCTC GGTAAAAATG GTAAAGGAAA AAAATCTATT ATTTTCGTTCA	1020
ACCCAGATGA TGGGTCGTTG CGGACGATTG CGCTGTTGTT TGACGTTTGA GGAATGATCG	1080
TTACACACGT AGCCTGTGTG GCGCACCTAA GTCGCTGCAC CCACTCGTAA CACCACACTC	1140
ACATGTGCAG TGTGTTGCGG TGTACAACCG ATGTGAGCGT GGTGGGGTTT GTTAGCAAGG	1200
GGACGTTGAT CTGTTCTGTC TGCTGAkTGT CTTTGTCCCG TCGTATAGAA CACACTCGCA	1260
GGTTTCCCTG CCCAATACCA TTACTTAGCC CACCTCCTCT AGGAAATTTT CGTAAATGCA	1320
GAACGTTTGG TAATACTTGA TTTTTTATAA GTCTCCATTG AATATAGGAA ACGAGTATAC	1380
CCGTTAAAAG CATAGCATTG CTCGACATTA TCTATTGTTT TACGCAAGAG GATGCAGAAT	1440



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GAAGAGTCTT GAATATTATC GATCACAGCC AAAAGCAGAT GTGCACACGC ATCTGAATTT	1500
GAGTATGAAA TACGAACGAT ATAAGCAATG GTCAGGAGTA GTCATTCCAA ACTTTCCACG	1560
TAAAATGCGC GGGCTCGACG AAATGCATGA AATTATTGGT GAGTACACGC GTCCTCAGTG	1620
TAAAAGTGGC CAAGACGTGT TGAATTTGTT TACCATGTCC ATAGAGGATG CCATTGCAGA	1680
CAATGTCGTC GTAATGGAGA CATCAGTTGA TATTGGCTTT ATCACCATT ATGAAGAAAA	1740
TTTGGATCAT TTCTTATGTG ATTTAAGCGA TCTGCATCGA CGCTACAAGC GCAATGTTAC	1800
CCTTCACTTT GAGCTCGGTA TCTCCAAAAT ACGAGAGCGC AGyTnCGTAG AACAGTGGGC	1860
TGAGCCCATG ATGCGAAGCG GTATCTTTGA AAATATTGAC CTCTACGGTC CAGAGATTTT	1920
CGAAGGAATC GAAGATTTCA TCTATATTTT TAAACTGGCC GAGAAGTATC ACTTAAAAAA	1980
GAAAGCCAC GTAGGCGAGT TCTCTGATGC GCAATCGGTA CGGCACTTTG TCGAAATATT	2040
TAACCTGGAC GAAGTCCAAC ATGGCATCGG AGCCGCTACT GACGAGAACG TTTTGCGGTT	2100
TCTAGCTGAA AGAAAAGTTC GCTGTAACGT ATGTCCAACC AGTAATGTCA TGCTCAACGT	2160
CGGTGGAATG CCCTAGAAAA ACATCCTATA AAAAAAATGA TGGATGnCAG GGGTCCGTGT	2220
TGGGTTAGGA ACTGACGATC TTCTCTTTTT TGGAAAAACA AATAGCGAAC AATTGTTTGA	2280
TATGGTTTCC T	2291

## (2) INFORMATION FOR SEQ ID NO: 126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CCGCCAGTCC ACCGGTGnCA CCCTTCAACG CCGGTTAGGG AAAGCGTGCG GCACGCCAGC	60
GAGCGCAGCG CATGCTGGAG CkCATTCCAA GAATGGAGTA TGCCACGCAC AGGCTCCTGG	120
GTACGAGCGT GCATTTCTTG AGCcGctGTT GACACACGGC CGAGTGTAac GGAGCACTGT	180
GCCTTGTGCT AGTCCCTGAG CGAGAAGGAT GCAGCAGGAG AGGGCAAGGG AGGAGAACAG	240
GAAGGAGCAC CGGTAGTAGT TGATGGGGTT AATTTTTTTC CGTTATGATC GCTGCTATAT	300
GTTGTCGGTG TTGTCGTATC TTCACGTGTA CTTTGGGCCG TTTCGTCTGT TGCAATCTTA	360
TGCGGTGTTG ATGGGGATTG CCCTGTATGC GGGATTCTTT TTTACGTATG GGGTGTGCC	420
CAGTGCGTAT CGCTTTTTGC CCCAAGACAG GGGGCGTGCG TTTGCGCCGT GTGCACAGGA	480

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AGCAGCGGGT AAACCCACAG GGGCAGGAGT GATTTTTGTG TCCGTCCTTG TGTGTAGT	540
GTACCTGCTT ATGCGTCCGA GTTTTGTGCA TCGCTTATA TTGCTGCTGA CGTGGGGGGT	600
GATGCTCACC GGATACTTAG ACGATTGCGC GCAGGTGTGC TGGGGGAGT ATCGCAAAGG	660
CGCGTTGGAC TTTTGTGTTG CCGTGTGAC AGCAGCGCTG TTGGGTCATT TTTATTTTCA	720
CGATCAGGTG TTCTGGTGGT TTCCTTTTTT TTCAGATCCG GTGTTGCTCT CTCCTTTTTT	780
ATTTTTTGCC GGTTCGGTGG TGATTTTGTG GATGTCAATT AACGCAACCA ATTGCACAGA	840
CGGGGTTGAC GGGCTTTCGG GAGCGTTGGT GTTGATGGCG CTTCTTTCGA TGGGTACGAT	900
TTTTTACTTT TTGTTGGGAA ATGTGCGTGC GGCGCAGTAC CTAAGGTGC CGTTGTAGT	960
GGATGGTGC CAATGGGCAC TGATGAGTTT TGCACTTGCC GGGGCGCTGA TGGGGTATGT	1020
GTGGCGTAAT GCACACCCTA GTACGGTGTG GATGGGAGAC GCAGGCTCCC GTGCGCTGGG	1080
GTTTTTCATT GGGGTGTTGG TGTGTGATCT GGGCAATCCA TTTTGTCTGT TGATGACAAG	1140
CGGTGTTATT TTGGTGAATG GGGGTACGGG GCTTCTAAAA GTGGTGTGTG TGCGTTTTTT	1200
TCATGTGCGG ATCCTGAGCC GGGTGCCTTT TCCGCTCCAT GATCACATGC GTGAGAATTG	1260
GCACTGGTCT ACGGCGCAGG TATTGCTGAG GTTTATGATT TTACAGGGAC TGCTCACGAT	1320
TGGTCTTTTG GGGGTTTTGT TCAAACGCG GTAGAGGGAG GGCACCCCTT GCGGGGCACG	1380
CCGGGCCGAG CGAGGGCGAC GGTGCGGAGT ATCCGGCGCC TTGACGTGCG TTTATTTCTT	1440
TTGCTAGCCT GCCCCTAATT GCTTTCGTT TCCGGAATGA TGGTAGAGGA GACAGGGCGG	1500
AAGGCGTGGG GTGTGTATGG TGCCGGTGAG AAGGTTTCATA GCGGTGTGTG CGGTGACGGC	1560
GTGTGCCGGG CCGTGTTTTT GCGTTCAAGC GTTTATCTCT TCTCGGATCG GGTATGGGCG	1620
CTTTGGGATA TATGGGAACG AGATAAAGGA CTCCTACTAC AAACATGTTT CGATGACGGG	1680
ACTAGGGGTT GACGTGGTAA CGTCTTCAGG CGTTGCGATG GTGTTCAATG TGGAGAAATG	1740
KTGACGCAG CTCATGTTTC GCGCGCAGGC GCTGCTGGGG TACGCGTTT AGGTGGCAG	1800
GTTCCGCTTT ACACCTGCCA TTGGCGGCAG TTTCTTTGCG TCGCACGACC ACGCCGAGG	1860
GGTGGCTCTG TCGCTTGACT TTCAGTATTT CTTTAATGAT TGGGTCGGGT TGGACCTGAA	1920
CATAGGCGCG GGGGTGGATG TTCCGGTGAA CAGTAACCTG CGTTACCTGA TCGGGGTGGG	1980
GACGCCGGAG TTAGCGAAGA TTCTCATCAC GCATACAGTG ACGCATGGAC TGGCTAATCG	2040
CTGGATATCA GGTCCCCACT GGTGGAATTC TCTTTCTTCG TGGGTCGGGA ATACCGCGGG	2100
AAAAGTGGCT GGATTTGTAG CGCGTTTGAT AGCAAATTAT CTGCTGAAAG GCTCACAGTA	2160
CAGCATGTT	2169

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## (2) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TACCACCAGC AAACGCCGTG AGGTCAGTCC TTCCCGGCAA ATTTCAAAAA AGAGCGCAGG	60
GAGCCTGTAC ACATTGAGTG CCAACACCCA CAGCCCAGAG AAAACATAAC CCACAGCCAT	120
CACTGGTACT ATCACCGAAC TGACAACACT AATGCGCGCG ACCCCCCCAA AGATAACAAA	180
CGCAAGGAGA AAAGACAGCA ACACCGCTAG GATCTGGACC CACAGAGAAG AATCCTTTCC	240
GTAGTAAGAG AGAGTAGAGA CAATATTATA AGCCTGTAGT GCATTGAACC CGTACGCGTA	300
TGCAAAGACA AGACACAGCG CAAAAGCAC CCCCATGGAG CGACTTTTCA GACCCATTTT	360
GATGTAATAG GCGGGACCAC CTCGAAAACC ACACGCAGTA CGCGTTTTGT ATGCTTGGGC	420
GAGCGTACTT TCGACAAAGG CACTTGCAGC GCCAAAAAG GCACTCACCC ACATCCAAAA	480
CACTGCCCCCT TTTCTTCCAA AGGCGATAGC GTwAGcAACG CCGACAATGT TCCCAGCCCC	540
CACACGGCTC GCAGTGAAA TCATAAGCGC TTGAAATGAT GAAACTcCTT TCCCCCTCTT	600
TTCAGCCAGC GCTGCAAACG CrGGtTCAGA AGACTAAGTT GAACACAGCC AGTC'TTTATG	660
GTaAAAAGAn ACCGCAGACG ACAAGCCAAC CGA	693

## (2) INFORMATION FOR SEQ ID NO: 128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCACTTCACA TCTTTTCATC AAATTACCGC ATAATACGAT CAACCCTCTT TCCAAATACG	60
GACACCAATT GCCTGCAAAC GCTCCACTaG ACGTTCATAT CCACGCTCAA TTTGATACAC	120
GTTACGGATT ATACTTACCC CGCGCGCACA ACACGCTGCA ACACCATCGC CATTCCCGCA	180
CGCACATCAG GAGATACCAG GTCACTCCCA TGCAATGCAC TCGGACCTGA AACAAGCGCC	240
CGATGCGGGT CACACAGGAT GATACGCGCA CCCATGGTAA TTAAGTTGTC CACAAAAAAC	300

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ATACGCGACT CAAACATTTT CTCATGAATC AATATAACCC CTTGACTTG AGTCGCCACC	360
ACTGTCATAA TGCTAGTCAG ATCCGGCGGA AATGCAGGCC ACGGGCCATC ATCTATTTTA	420
GGAATCATAC CGCCAAAATC GTAATTTACC CGCAGATCCT GCGACGCaGA GACGCTTACC	480
GCGTGCTCTT GCTCGCTCCA AATTACTCCA AGTTTTTTTAA ACGCAAAACC TAGTGGACGT	540
AGATCACGTA CGTTCACATC CGAAATCGTC AATGCTCCAC GCGTTACTAC CGCAAGCCCA	600
ATAAGCGAAC CTACTTCCAT GAAATCAGCC CCAAGTGTAT ATGTGGTACC ATGCAACGCG	660
CTCACCCCT CAATTGTTAA AACATTCGAT CCGATGCCAG AGACGCGCGC ACCCATCGCA	720
TTCAACAAAT GGCATAGATC TTGCACATGC GGTTCGCTCG CCGcGTTTCGT GATTACCGTA	780
ACCCCTCGG CAAGAACTGA AGCCATAAGC ACATTCTCTG TCGCCGTCAC AGATGCCTCG	840
TCTAAGAAGA CATCACATCC CACCAGCTTA TTTGCAGAGA AAGTAAACAC CCCATCTAAA	900
CGAACTTGTG CGCCAAGTGC GGCAAgCGCA AGAAAATGCG TATCAAGTCT CCTGCGCCCA	960
ATAACATCAC CACCAGGTGt GGAAGCACT GCTTTTCTAC CACGCGCAAG AAGTGGCCCT	1020
GCAAAAAGAA TGGAAGCACG CACTTTCTGC GCAGCTtCGC ACGGCACTTC GCACGTCTGT	1080
AACTGAGGAA GATGTAACAT GTACTCATGA TTACCACGCC TTTCAACACT CCCACCAAAC	1140
GCACGAAAGA TAGTTAACAT CACCGCCACA TCCTCAATGT CGGGCACATT TTGCAGTAAC	1200
ACTGGCTCTT GTGTGAGAAC TGCCGCCGCA ATACAGGGAA GCGCTGCATT CTTATTTCCA	1260
CACACGCGAA TACAACCTGA AACGGGAAAC CCACCTTCAA CACGATAGCA ACTCATGCTC	1320
TCACCCCTTT GCGCACACAT TCCTGTAGAA CACCGATCAA CATACAACTT AATTGCACGA	1380
ATACCGCAAA AGTACGGCCC CATCCTGTGT ACTTACTTAG GCGTCAGCaA ACGCTTGACC	1440
TACATGCTCG AGTGTCCACG AGGGCAGACA CAACATACCG ATCGAGTACA CGGCGTATCT	1500
TAAAACGCAA TCCTTCAATT ACCAACTCAT CCCCTACCGT AGGAGACGTC CAAAACGTTC	1560
CAGGAGTAAA CCTCCACCG TGTGGTACAc GCGCGACTGC AAACGCGTAC CTAACACTTC	1620
GTTAAAATAT TCAAGAGGAA CCGTTCCTGA ACATAAAATC TCATGAGTAC CGACGCTTTT	1680
CATCTGAAAA TCAACACGAG GTTTTGACAT TCGCTGcACC ATTGACCCAT GCACTGTGTA	1740
TCCTTCTACT CCTTCGAAA CTCCAGCAAG TGAACCAAAA ATTACCTCCA TAATGTCTGT	1800
CATGGTTACT AATCCTTCCC CATCGCCCCG CTCGTCTACC ACTAACGCCA TCTGcTGCTT	1860
TGATACCGAG AGCATATCTA AACTGAAAA AAGGTCAGCT ACATTCCGTA CACAACACAA	1920
CTCCTGTGCC AAATCACCCA CCCGATGCAC CGCAGCTCTG GTGTTGCTA CACATGCCGA	1980
CACCATCTGA TCTGATGACT GCGAGGGTAA TACTTTACTT TCTCCAAAAA TATCCCAGTA	2040

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GTGTACGAAA	CCCCAGACGA	TCCCCGCAGC	ATCATGCACG	AGCAACTGAG	AAAAGGAACA	2100
GGTACGAAAA	GCATCCCACA	CATGAGATAG	TGGTGTGTCC	TGAAAACTG	ACACAAAGTG	2160
TGTGTGCGGT	ACCATAACGT	GTGCAAGCGG	TATGCGTTTA	AACTGTAAAG	CGCGCTGGAA	2220
CAATTGATTT	TCGGTTGACG	AAATCACCCC	TTCTCGTGCC	CCAACTGCAA	TAAGCGTTTT	2280
AATTTCTTCT	CGCGAAAGAC	ACGTCGTATG	ACGCGGcAAA	AAAATACCCT	CCAGCACATG	2340
CATCAATGCT	GACGACACAC	ACGCGCAGGG	GTACAGCAAC	CAGTAACTCA	ATTGCAAAAA	2400
AGGCGCAATC	CACATCAAGA	ATCCCAGTGA	GTACCGTGCA	CCCAGCGCCT	TCGGGAACAT	2460
TTCTCCACAA	AGAATAATCA	CGCACGTCAC	CGCAACCACT	GCCTTCCACA	CCGACTGTGC	2520
ACCCCAACAAC	TCCATAGAGC	CTAACGTCAC	CACGCTAGAG	AGCACCATAT	TCAGTGCAGT	2580
GT'TTTGCACA	ATAACTGTGG	TAATCAGCTG	TTTCGCGCCG	GCCAGAAGCC	AGCATAAGCG	2640
TTGTGTACAA	CGTGTACTGT	GCCgCTTAAG	CTTACGTTCA	TCGTCTTGGT	TCACCGACGA	2700
CAACGCGCTT	TCTGAACCTG	CACATAGGGC	CGAGCACACA	AGTAAGAACA	TGAGTTCCAA	2760
TCCTACCAGA	AAAGGGTATG	CCACGCGCGC	TTCCCTACTA	TCCTTGAAAC	TCAAACCGAA	2820
CACGTACGAT	TCTGCGCACA	TGCAGTTGTA	GCACCACACA	ACGCCAAGAA	CCGAATACAA	2880
CCGTGGTGCC	AGGATCAGGA	ATACACCCTG	TATACTCCAT	GATAAGACCT	GCAAGGgTCT	2940
CACTGGTACA	CGAAGAAAAA	TCGGTGCCGA	GTAGATCATT	TATCTCATCC	AAGCGCAgcG	3000
ATCCAGGAAA	TATATACGCC	CGTACCCCCG	CACGCGTAAC	cTGCGGACCT	GTTGAATTCA	3060
CAGGGAATTC	ATGCGCACTG	CTCTTAAAAA	ATGCTTG GTA	TATATTGTGC	TTTGTACAA	3120
GACCTGCCGT	CCCGCCATAT	TCATCAAGCA	CAATGGCGAC	TGCGCGTGAG	TGTGCGCGCA	3180
ATTTGTGCTG	CACATATGCA	AGTCGTGTAC	ATTGGAAGAC	AAAAACCGGC	GCGCTCACAT	3240
GTTGCATCAG	TGTTCCGCAC	TCTTCTAAAT	CTCGTCCGTC	TACCTCTTCT	GAGCACAAGA	3300
ATTTCTTCAC	ATCGAAAATA	CCAATTATCC	AATCAACACT	CCGTTTCATAC	ACTGGAACAC	3360
GCGAAACGCG	CATCTTCTGT	GCACAGGCAA	TTGCCTCCGC	CAGAGAACTC	GCGCGCGGAA	3420
CTGCAATCAA	TTGCGCACGA	CAGGTCATAA	TATCTCGCGC	AGTAAGGGAT	GCAGAATGCA	3480
AAATACGTTG	ATACAATGCG	CGTTCGCGGG	AAGTCACAGT	GCCATCCGCC	TCTCCAGCGT	3540
ACAGTACGGT	GTGCAGGTCG	TCATCCGTAA	CACGCAGCGA	GGGAGTGTGG	CACGCGACAC	3600
GCGCAAGACG	CAAGAGCGCA	CTCCGCGCCA	TACAGAACAC	CTGTACAAAA	GGAGTAAGCA	3660
TCAAAGCGCT	CCACTGCAAG	AATCGCGCAG	TATGCAGTGC	CAtGCGTTTCG	GCCGGCACAA	3720
GGCAAGTGAC	TTCGGAATAA	TTTCTCCAAA	AAGAAAGTGA	AGCACCGTTC	CTGCACCGAT	3780

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GCTCCACCCC	ACTGCGTGGA	TGCCAAAGAG	GGCACGTGCA	AAAAGCGCAA	TGACTGCAGA	3840
CAACGCACTG	CTCGCCAGGG	TGTTCCCGAT	AACCACAGCA	GCAAGATAGA	AGTTTTTCCG	3900
TCGAAGGATA	CGCATTGCCA	CTCGAGCGCG	AgCATGACGT	TTTTCGTACA	GGTAGCGAAG	3960
TCTTAAGGTA	TTTAGCGCAC	AGAACGCTGT	TTCCGCAGCA	GAGAACAACA	TGGAAAGCAC	4020
CAGCAGCACT	ACCAACACAC	CGAACGCAGC	GGAAACGGAA	AGAACACTCA	CACGTAATTC	4080
CCCCGAAGGc	tAAAACACCA	GAACCGAAGA	GACAACGCCA	TACATCCTTG	GACCCCTCCC	4140
CGCTGGGGGG	GGGCACCTTT	TAAGGTGCTC	ACGCCCTTGT	GTCAAGAGCA	CACCCCTCCAC	4200
TACAATGAAc	TGCGTGTCG	GAGACGCGC	GGAGTCCTCT	TTCTATGAAT	AGAACCGAAT	4260
CTCCTCGTGG	CTTAATCAAA	GCCACCGTAC	GTGAACAAGA	CCGAGGCCGA	ACCGTTTATA	4320
AAAAGATTGC	CCAGTTCCTC	TCCCTCATTG	GAGAAGAGCA	GGCGGCGCTG	GTGCTCAAGC	4380
AACTTGAGCC	TGCACAGATT	GAGGCGGTGG	TTGCCGAGCT	CCTGACACTC	AAACCCCTCA	4440
GTCCAGAAGA	AGCGCGTGAG	ATcTACGGGA	GTTTTCTGCC	CTCTGCGCTC	GTGTGTCGCC	4500
TGTTACCGGT	GGATGCGTnT	GCGCAGTCGA	TGCTTTCCAA	AGCGTTTGGG	GAAGAAAAGG	4560
CCGATCTTAT	CTTGAAGCGG	GCGGTGCCAG	CGGCACAGCC	GAAACCTTTT	GAGTTTTTGG	4620
TGCGCTTGAA	GCCTCCCAAC	TTCTCCCCCT	CCTGGAAGGA	GAACCTACCTG	CCACCAAAAC	4680
ACTCATCCTC	TCGCAGCTGC	CTCCAGAAAG	CtGCGCACTA	TTTGAGTAAT	ATCAGcACAG	4740
AGGAGAAGAA	GGACTTGATC	GTTGCGCTTG	CAAAGTTAAA	GCACGTTAAC	CCTCAGGTGC	4800
TGCAAGTCAT	GAGTGACTCC	TTGCACAAAA	AGTTT			4835

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGCTTTCCCT	GCGTTATAGG	AGGTAACGAT	TGCACCGCCT	GTTCAAATTT	TTCCACACA	60
CCTGGTGGTG	ACTGCGATCG	CATCTGTGCG	GCGAGTTCAT	TGCGTGCTTT	CGCAGCAGCA	120
ACAAGTAACC	CAAGCGCGTG	CATGAGCGCG	GTGTCAAAAC	GATTACAACC	ACGCTGTGCC	180
GCAAGCGTTT	CAGCGAGGGA	CTCCCTCGCG	GCACCTTCT	TGTACGGTGT	CCCAGCATCG	240
AAGGCACACA	CGATCTTGAA	TCCTGCTCCC	GGGAAAGCG	TCAAACGCGC	GCCTACATTC	300

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CACAGCACAG TATCTTTGTT TTGATGATGC GTCTGATCAG GTCCAGTTCT GTACCCTGcA	360
GAAAGAGTAG CACAACCTGc TGcCTCAAGC CTGaCCTGTT CCCGCCCTT TCGGGCGTAT	420
ACGAGCGTGA ACTCAGTACC AAGGCCATAT TTA CTGTGCG GGTCCGCTGG CATGCGCCGA	480
CTATTGGTGC CCTTTCCTTT CACCTTAGAG GTGACAGAAG GAGCACTTTT CCATATACCG	540
TTTCGACGAAA AGGAAAGGGC ACAGTTGAAT GTAATGCCAC TGTTCGAAAAT ATTCCGTGCC	600
TGATATGCGA TTTTTCGCGC AACCCACCA AACCTGGAG CGTATTGAC GCTCCTTGAC	660
TCATAACTAG TAGTAATAAA GGGGGTCCAC AACTGCGCAA AATTAGAGGG AAAACGGGA	720
TCTTTTCTTA CAGAAAAAGA GACATCGTAG AGGTGGAGTG TGGCCTCAAG GGAAAAATCG	780
CTTCTTCCTG ACTTTAAGAA AGGAGAACGC GTCGTCATAC TTGGATCCGC AGTTCCCGAC	840
CCTAAAGCAC TTTCAAAATC CACCTTCAAT CCCTTGAGAG AAAGCTCAAC CCATATGGGA	900
TCCTCACCTG AAAAGCTCGT ATACGTGGCG CCTTTCCTGG GCAACAAGGG AAAAGCAAGC	960
TTCCAGCTGC TCTTCGTGCG AAACCCATGT CGTATGCTTT TACCCGCTGT AACTGGAGAG	1020
GCACCTTCTG CATCAAAGAC GACACCCAG CTAAGTTCAG CAGAAcCGCT GAACGCGGCG	1080
GAGGACGAAA AGGCGCGTGA AACCCCGTCC AAAACCGCAC CATGAAGGAA AAACACCCCA	1140
CACCCTAACG CAAAACGCGC ATATACGGAT ATACAGGCGC CCATAGGGCA GCCATTATGA	1200
CCCTTTCATA AACACGATCA ACATTTTTTC CCGTCAGCGG TAATTTTTTTT CACTACTTCA	1260
CTCAGTTTTT GCACAAATGG CACAACACCA CGCCCGTTT CTTCTATACG CCTCCCCAGA	1320
AAGTGACTCT TCTTCCCACC CACGAATATC TAATGTACAC CAACATACAT TACAGATACT	1380
GCTAGATCTG ACACATGACA TCGTTGTACT AAATGTGGT GAAAACACGG TACACTACTG	1440
TATGCATGCG TCTAGTGTTA GGCTCGTGCA TTTTATACT TTTACTCCGA GGGCGCGCTA	1500
CCGTATCGCG TCTGCACGCG AGCCCGGCCG TCACCATTTT GGGGAGTACT CGTCTTACTT	1560
GGGGCATTAA CTTAGGCGCG AAGGCGAACT TCGTGCTACC CGTAGCACCG CTTGGGGCAA	1620
CCGGCACTGT GCGAGAGAAC CCAATCATC GCTTCCGTCA TCGCAGACAC GGTTTTAGGA	1680
GTTCCAGTAC TCTCTTTTTT TCGCTGACGC TTTGTCCACC GAAAACTCGG TCGAATCTGC	1740
ATAAAAGCAG CGGTGTGTAT GCAGAAATCC TGTAAAGGAA CCTAGAGTGT GCGCTCCCC	1800
TCGGTTCCTT ATCTGGTGAG GCTTTAGGCG AACTCACGCC CACAGAAAA CAAAGCTTCT	1860
CCGTAGAAGC GACCCTTCGC TTCTACGGCG CATATCTCAC TATTGGAAAA AATCCGACCT	1920
TTTCTAAAAA TTTTGCCAAA TTGTGGCCCC CGTTCATCAC CACACGATAC AAGGAAGCAG	1980
ACACCCAATA CGCCCTGGC TTTGGGGGTT ATGGAGGGAA GATTGGTTAC CGCGTAGAAG	2040

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ACGTCGGGAA TTCCGGGCTA GGTTTTGA CT TTGGGTTCCCT TTCCTTCGCT TCAAACGGCG 2100  
 ACTGGAGCAC GAGCGGGACT AGCCATAGCA AATATGGGTT TGGTAGTGAC CTCTCTATGG 2160  
 TACAAGAGAA ACAAGAAGCT GTTTTAACT GTGGAAC TCG CCGGTAATGC TACCCTCCAG 2220  
 GAGGGTTATG CCACGTTAGC TCCAACATTT TCGGGAGCAC CCAACAACAA ACGGGCATCC 2280  
 CACGCGCTCT TATGGAGTGT GGGAGGGCGT CTTCGATCA TGCCTGGTGC AGGATTCCGC 2340  
 TTCATTTTAG CTACG 2355

## (2) INFORMATION FOR SEQ ID NO: 130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CGGGCGCGTC GAGTAGTCGG GTGCAGGAGG GATCTGCAGC GAATGACCAT TTTCAGGACG 60  
 AATCGACCAC GGCAGAACTC CTTTAGTCAG TGGCCGCCAG CGCGTGAAA TAGATGTGGA 120  
 TGGATGAGTC TCCCGTCCCT GTGCAAGAGT TTAAACTTTC TCAGTTTGAG GGTCTTTGG 180  
 ACCCTCTGCT GTTCTCATC AAAAAGAACG AGCTGAGCAT TTACGATATT CCTATTTGCG 240  
 AAATTACTGC TCAGTATCTG CAGTACGTGG ATCAAACCGT CTCGCCCGAT CTCCGTGGTC 300  
 TGACGGAGTT TTACGCAATG GCTGCGGTTT TTCTGTACAT TAAAAGCTGC ATGCTCCTCC 360  
 CAATGGAAC AGATCTAGAT GGTGAGGATA TCGAGGATCC TCGGCAGTCG CTGGTGAGC 420  
 ACCTTATCGA ATATCAAAAA TACAAGCAAC TTGCAAGCT GATGGAGCTG TATGAGTGTG 480  
 AAGACATGTG GTGCGTTGAG CGAAAAAGA CGCAGCATCT GTTTTGTCT CCAGCAGAAG 540  
 TGCTCTCCT ACACGGTGAC GTTCGTGATT TGCTGATGCT CTTTATTCGG TTAGTGAGAA 600  
 AGACGCCTCA GTGGATTATG GATTTGTACG AAGAAGTTTC GGTAAATGAG AAGCTGACAT 660  
 TGCTTTCGGA ATTGCTTGGG GTTCGGGGC GGTGTGTATT TACTGAGCTT ATTAAGCA 718

## (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CAACTGTGCA CCGCCGnTA nAATAAGTGG ACTCGCACA CGCCAACAGT GTGGATATGC	60
GTGCGAAATC TGTTCGCGTC TAAATAACGC TCCCTGTTTC TGCACACGTG CAATAATAGC	120
CTTATCAGCA GCTTTTACAA AAAGCCCCTG ATAATCTGCA ACCTCTGCGG TAAAGCGACA	180
CTCTGCATCA AGAGGACACT GAATCGAAAT ACCCGCATCC TTAAATACTT CATAATCATC	240
CTCTCCGAAC GCAGGTGCGA CGTGTACAAC ACCAGTGCCG TCTTCAGTAG AAACAAAATC	300
CGCAACTCGC GTACAGAACA ATCCCTCCTC TGAATCTCCT TGTACAGAAG GATCCGGTCC	360
CTGCCCCAAC ACAGGATAAG AAAAAAGCGG CCGATAGCGA ATCCCCGCAA GATGTTTACC	420
TCTTTTTC CACACTACGC GGTAnAGnAC GAATCTGGAT AaTAGAaTTC AgACGAGAAC	480
GAGCCAAAAT ATAGTGCTCA TCATTGCGCT CTATTAGCAC GTACAAAATT TGTGGTCCCa	540
GCGCAAgcGC TGctTGccGG AgCGTCCAGG CGTGGTGGTC CATGCAAGAA AGCACGTATG	600
CGCAGGAAGT GATGCACTTC CCCAAGACGC TGCCGCACAA AACTCCCGTG CAGCAGGACT	660
ACCAGGAACA ACAGATGTAC ACTCAAAACG CACAGTAATG GCAGGATCAG ACACATCCTG	720
ATATCCACCT AAATTCAATT CGTGATTAGA AAAGcTGTCG CACACCGTGG ACAGTACGGG	780
AGTATTTTAT AACCTTCATA CAGCAGTTTT CGTGCCATA GTGCGCCACA ACCCACCACA	840
CGGACTCCAT GTAGCAGACA TCCATGGTTT TATAGTCATT ATCGAAGTCA ACCCAGCGCC	900
CAAGACGCGT GAGTGTGCGC TGCCACTCCT TCACATATCG CAGCACACTG GAGCGACATG	960
CCGCGTTAAA CGCGCTGACA CCATACGACT CAACATCACT TTTTGAATTC AAATTGAGCT	1020
CTTGCTCAAT CAGGTGTTCA ATGGGCAGAC CATGACAATC CCATCCAAAG CGACGCGGCA	1080
CGTACGCACC ACGCATTGTC TGATAGCGCG GAATAATATC CTTAATCGTG CTGGGCACAA	1140
AGTGACCAA ATGTGGCAGT CCAGTTGCAA AAGGGGACC GTCAAAGAAA ACATAAGACT	1200
TCCCTGCGC ACGCTGCGCC ACAGACTGCT CAAACACCCG GCGTTCCCGC CAAAAGGCGA	1260
GAATACGCCG CTCTGCGCG AAAAAATCAA CCTTTGGGTC CACAGGCGTA TACATACAAC	1320
CTCCGTTGCT CAGAATCGCA TAAGGAGCGT AAGGCATTAT ATCATTTTCG TCCTTCCTTT	1380
TCCCATACG TCTTATGACC GCGCCACAC CTTTCCCCAC CTGCACCAGA TACCCACGT	1440
GTGCGTAATC GCACGTGCTC TGCCAATTAC TGCATTGAGT ATTACGTATG CAATAATGCC	1500
CCACATTACA CCTTCTGCAA TCGAATACGA AAAAGGCATC ATCAGAACTG CGACGAAGGC	1560
AGGAAACCCT TCCCACATC TTGAAATCC ACATTGCTTT CCATGCAGCT CGTTACCGTA	1620
ACAGTGCAGG GAGCGATGGT AGCCGACATT GCAGTTGCAG TGAGAACCGC ACCCATCCA	1680

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TTCTCTGTATG CGAGCGTATT GCAGGATTTCG CCGCAAGCAC GTAAGCCAGT GCGAGAAACG 1740  
AGGTATCAAA AAATGAGCGC ATTCTTATGC ACATGATTCA AAATGACTAA ACCTCATAGT 1800  
AAATGAGGCG CCACCACGGG ATGCAGAACG CACATCGGTA GAAAAACCAA ACATTTTCTT 1860  
CATCGGAGCC TGTGCATGCA CAAGCTCCCG TCCGTGTTTT GAATCCATGC CCAGAATTAT 1920  
TCCCCCCCCG TGTATGATCA CATTTCATCAC ATCTCCTAC 1959

## (2) INFORMATION FOR SEQ ID NO: 132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

GTTCCGTCAG CAATTTTCAGT ACGCGGTGA GGTATTGGGC GAAAAGGTTT TCTCGAAGCA 60  
GGAGACCGAA GACAGCAGGG GAAGAAAAA GTGGGAGTAC GAGACTGACC CAAGCGTTAC 120  
TAAGATGGTG CGTGCCTCTG CGTCATTTCA GGATTTGGA GAGGACGGG AGATTAAGTT 180  
TGAAGCAGTC GAGGGTGCAG TAGCGTTGGC GGATCGCGC AGTTCCTTCA TGGTTGACAG 240  
CGAGGAATAC AAGATTACGA ACGTAAAGGT TCACGGTATG AAGTTTGTCC CAGTTGCGGT 300  
TCCTCATGAA TAAAAGGGA TTGCAAAGGA GAAGTTTCAC TTCGTGGAAG ACTCCCGCGT 360  
TACGGAGAAT ACCAACGGCC TTAAGACAAT GCTCACTGAG GATAGTTTTT CTGCACGTAA 420  
GGTAAGCAGC ATGGAGAGCC CGCACGACCT TGTGGTAGAC ACGGTGGGTA CCGGTTACCA 480  
CAGCCGTTTT GTTCGGACG CAGAGGCTTC TGTGAtGCTG AAAAGGGCTG ATGGCTCTGA 540  
GCTGTGCAC CGTGAGTTCA TCGACTATGT GATGAACTTc AACACGGTCC GCTACGACTA 600  
CTACGGTGAT GACGCGAGCT ACACCAATCT GATGGCGAGT TATGGcACCA AGCACTCTGC 660  
TGACTCctGG TGGAAGACAG GAAGAGTGCC CCgCATTTTCG TGTGGTATCA ACTATGGGTT 720  
CG 722

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGACGAACAC TCCAACCCCA AATGACACCT TCTCCGGAAG ATTACCCAAC TCAACCAAAT	60
TCCGACAACC TTCAAACAGA CCATCTGCAA GATTCTTCAC TCCAACCTGGA AGACGAACCG	120
ACGCTAATTC CGCGCAGTCT CGAAAGGCC CAGATCCAAT TTCCTTCACG GAATTAGGTA	180
AAACCACGTC TACAAGGCTT CCACACGAAG AAAACACATC CTGCCCAATC ACCTGCAGCG	240
ATCTCGGAAA CACAATTCCCT GCCAGACTCA CACACTTGTG AAATGCATGA TGACGAATCT	300
CTCGCAAGCC GTCCGGAAGT TCAATACGAG CGAGTTTGTG ACACCCATGC AAATGGCATG	360
GCTGGCCCCA TnCATGGCGC ACCGAAACTA GGCAACGnAC ACCCGACACC AGCGGAAACG	420
GCACCCATAA AACGCCTTGG TAGCCACCTC GGACAACCGG CAGCCCATCA ATCTGACTGG	480
GCAGTACCAC TGCAATGCCC TTGCCAGAT ACCGCGTGaT AATTATCCCA TCACGGTCGG	540
GAGTCAGACC GTACTGaAAA AACTTCGCCG GCGTCTCTTT CACCTCCgCA CGAGAGACAG	600
CATTCTGCTT CGCagAGACA GGATGCGATA CCAGTACGCC CAAACCGATA CACCACATAG	660
CAAAAACGAC TACTTGTTTT GGCATTATTT CGTCCTCCTT TTAAATCAA CACGAGCCAA	720
AAACTAACAC TCACTTCAAT GGATACGCGT CCCACACAAG CGGTGCGCAA sATGgACGAA	780
CCCCCTTGAA AAGGTCAACT TTTAAAAAAT TAAGCACTCC CGCAGATATG CGCACCGTCT	840
CCTACAGGGA CTCCATACCT CGCCGGTAAA ACTAAGACCG TGAGCCCTCA CCAACGCAAG	900
ACAGTTGCAC AGCAGTATGT ACAACTGCGC GCAGACCCGC TCGATAGCAG GTAACCTAAG	960
TGCGCTGAAA cCACTCGAAG ATGCTGCTCA TCAATTGCCA CAGTTCTTAT TCCGCACTGT	1020
TCGAGCAGAT ATTGGCGCAG TGTTCCTGCA GAAAAACCTA TGCAACGGAT ACAGGTAAAA	1080
TAACCAGAAT TACACGGCAA AAACTCAACA CGCAGCGGTA CCGCAGCCCC ACACTCCGTT	1140
GTGCTCCAGG TAAGATCAG TACCACGCGC TGCACCTCTC GGTAGCGTGC ACACATCAAC	1200
TGAAAAAATT GGTGTCTCTC ACGTGCCGTG GCTGAACCCA ACCCAGCAGG CTCATCCTCT	1260
TCAGCCAACA GACGCAGCGC AAGGTTCTGC GTAAGGTGGC AGTACATGAA AGTGATGCAC	1320
GGATCATCCC CATGACTTTT TTTTCAAAG CCTGGTACTG GGAAACACCA AGAGCGAGTC	1380
CTGCACAGCT TAGAAAACCC ACGCGTAATC CCCATGCGTA CTCTTCCTTC GTTAACCCAT	1440
CTATCTTTAA CGCGCAGATA TTCTTGTCG CTTGCGcAAA GcGGGCAAAA AAAGAGCCAC	1500
GCATCAAAGA CGCCTCATAC TCGAACCCGC TATACGCATC GTCACAAATC ACCAGTACCG	1560
CACACCCTGc GTCaTaTTAA GCATACACCA CCTCGTATAA TTGCTGTGCC TCCTCTTCCG	1620
TGGGGGTATA ACTGACGGAT TATGGGGGAA ATTCAAAAT AACCTTATCA CCCCATCCGA	1680

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AGCCTGTGCG TCCAGCGCTT CCTTGACGCG GCTCAAATCA AAGCGCCCCG CTCGAAAAAG 1740
AGAAAAGGGA ACCGGcGTTG CCGCACAAACG CACTGCTAGC ATGAGATCAT AATTTTCCCA 1800
GCGCGGTGCC GGCACCAAAA CCGTCTGTCC TGCACCCACA AATAAGTCCA TAGCACAGGA 1860
CAACGCTGCC GTAAGTCCCG GCAACACGAT AGGAAGCGAC ATCTTTGGAA AACTGCCGC 1920
ACAAGAATGC TCTCCCTGCT CTGCTGCACT CTGCATTGCT GCAACGTCCG GTTCATCCGG 1980
ACACAACACA GGATCACGCG CACACAAACG cCGCGCCCag cGCTCGCGGA GCgCAGGAAT 2040
ACCTGCAGTC GGCGCGTAGG AACTATTTTC AGAAGAAGAA AGATCAGGAA CAAGCGCATG 2100
CAACGTATCA CGAAGCACCG GCACCCCATG ACGCAGAACC ATGCCAACCG CCCCATTCAT 2160
ATCAGGCGCA GCATCCGCGC CTCTGCATTC TGTGCAACAA TCCCGTGGGG AAAATACGCG 2220
CGCAAACCAA GAGGAGATAA CAGCGCGTGC ACCACCGTTC CTCAAGAGC AGCGTTTAAC 2280
GCACGCGCGC CTTCAGAGAG GTCCATGT 2308

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## (2) INFORMATION FOR SEQ ID NO: 134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

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CTTTGACCAC TCGGGAAACT CCCCAAACGA ACAAGCCAAC TTAGGGATTG GAACCCTAGA 60
CCTCGAGATT ACAAATCACG CGCTCTAGAC CGACTGAGCT AAGTTGGCGA TGACTACGCG 120
CCCCGGACTG TACGCGCGAA CCCACGGCTT TGTCAAGCCG CTCTCACTGC ACTAAGAAAA 180
ACTACACGCG CAGAACAGCA GAGCACGTAC AATGCGGACT CTATACCTTG AATTCTCCA 240
CCTCATCTGC AAGACTGCTG ATGCTCTGct TGCTACGCTG TGTATCTCA TTAACCTCGT 300
GTatGCGTTA TTGATCTCGA TGGCACCAGC TGCCATCTCA TTCATACTTC TGGCAATTTT 360
ACTAGTTAAG TCGTCCAAGC GCTGCATCTC GCGTGCAATA ACCTCGCCCC CTTTGAGCAT 420
ATCCGCAGAC CCCTCCTTCA CGTCTAcGGT GCGGGCATTG ATGCTCTTAA TCGCAGCTAG 480
GACtCACGGC TTCCATCCGA CTGCTCTTTC ATCGCCTCTG TCAGCGACCG GTCATTGTA 540
CGCACCTGAT CGGACAAACG GAAGaTGGTA TCAAAC TGCT CCTCAACCGC TTTGAAGAC 600
GTGGAAAGCG TATCTATTTT CACACTGAGC GTCTTGAGCG TCTCAGTAAT GGTCTTTCTT 660
TGGGTGCTAG ACTCTTCCGC AAGCTTACGG ATCTCATCCG CAACCACCGC AAAACCCTTT 720

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CCTGCCTCGC	CCGCATGCGC	CGCCTCGATA	GCGGCGTTCA	TTGCAAGCAG	GTTCGTCTGA	780
CTTGCAATGT	GCTGAATAAC	ACTGCTCGCC	TCAAGCAAGC	TTCCCGATTG	CTsrcTGaTC	840
TTTTGCGTAA	TACCGCTAGa	GCTAACCAGC	GTGTACGCC	CATCAGCGGT	GGCAATAGCA	900
AGACTGTGCA	CCGCCTCATC	ACTCCGTTCA	AGTGTCTGCG	TAATAGACAC	AATGTTGGCA	960
ACCATTTGCT	CAACTGAGGA	GGAAGACTGT	GCGACGTTCA	CCGCCTGCGT	CTCAATGCTA	1020
CTGTTcAGCC	CCTTAATTGT	CTTGATGATA	CTTCCACCGT	GTCCGTGGCC	TCAnACACCC	1080
CACTCACCTG	CAATTCAACT	CGGTGCTTGA	CACCATCGAT	ATTGGCGGTA	ATCTCGTTTA	1140
CCGCACTGGC	TGTTTCAGTC	ATGTTACTGG	CAAACCTGTC	CCCGATGCGC	CGCATATCGT	1200
CAGAGCTCGA	CCCCACCGTG	GCGATACAAA	GCGAAT			1236

## (2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CCTTGGTGTT	GATTTTTTTTA	TATGTGGCGC	nTCGTTTTCG	GTGGTTCTTT	GCGCTTGGAG	60
CGATAGTCGC	GCTCGTGcAT	GATGCGTGCA	TTATGGTGTC	ATTCATGGTG	TGGTTTGGTT	120
TGGAGTTTAA	TCTGCGAGTA	TCGCGCGGAT	TCTGACGATT	ATCGGGTACT	CGATCAACGA	180
CACGGTGGTA	GTTTTTGATC	GGGTGAGACA	GACCATTCTC	CTGGATCCTA	TCGCGTCAGT	240
GACGACAGTA	CTTGACCGAT	CGCAAACAGA	CATGCTCACG	CGCACTGTAG	TGACAACGGt	300
GACGACGCTG	CTTGcAGcGC	TGATGTTGTA	TGTGTTTACC	GAGGGAGGCA	GTCGGGATTT	360
CTCACTCGCG	CTAATGGTGG	GGATGGTCAG	CGGCGTGAC	TCGACCATTT	ACATCGCCGG	420
TGGCTGTATC	GCCCTGATCA	GCCGGGGGAA	GAGCGGAGGT	CAGCTGCTCG	GACTCTGAAA	480
CCCCGCACGC	GCGGCTGTGT	GTAGGAAAGG	AAAGGAGAGA	GGAAGAGAG	GGGACTCGgC	540
GCTGCCGACT	TTGCTATTTT	TTCTTTACAA	TCGTTTTTCT	TTCCCCGCGG	GTGTGcAGGC	600
TGCGCGCTTG	CCTAAGGTGG	AGCCGTTCTT	TTTTGTTCCT	TTCCAGAAAG	TCAAGTGACC	660
TGTTAAAACC	TTGCAGAAAT	TTCTGCATCT	CTTCTTCAAA	CACCACAACC	GCGTGCCGGT	720
CAAACCCGGC	ACCGTCGACG	TTTTTGCTTT	CTACTACCTG	CAGAAATACA	TCTCCGACCC	780
TATTTTCCTT	CACATTGAAA	AAGTAGGTCC	GATTTTCCGC	TTGCACCTCT	GTAGTAAACA	840

GCTCACC GCG TATCCCCATG CTGTACCTTC CTTCTGCTTA TGAAGTCGTA TCCGCACACG 900  
AAAGCGCACA GCGATCTGCC TCGCGCACCA TGTCCGCGTG CAGCTGCAAA AGCGCAGyTy 960  
CCCCGCCTC GTCATTACCT TTCAGATCCG CAGAAATTCT AAATATTGGT TCTGTCTTTG 1020  
AACC GCGCAT CCACACGAAC GCCACCGCTT CTTGGTGCTC GTTGTAAAAT TGGATTTTCA 1080  
ATCCTCCGTC AGCCGACCGG CTAAATCCC CCGCCGCGTC CTGCTGCTCC CTCCCGCGGT 1140  
ACAATATCGG GCGGTACGAA CAAATGCCGA AGCGTTTTTT TAACGTGTCT TTCTCCTGCG 1200  
CCCACCTGCG TTCAAATACC CGCTGaTATG CGCTCTTGAG GAGTGCATGG TCAGTCGTTC 1260  
GTATCTGcAA GAGCGCGCGC GTATCGTGCG TTGGTGTAGT CGTGACGCA GgTAGGCTGG 1320  
CAAATAGATC CGATATCGTG AAGGCATGCT GCGCGCGTTC TGTTTGGTGT GAGTGCGCGC 1380  
ACCACCAGGC AAAGAGTCCT GGCTGTTTCC CATCCCCCG CAGGAGCAAG AGCTTTAAGA 1440  
GTGCAAAAAC AGTATGCAAA GGATCACGTA CTGCCGCCGG ATGGAGAATG CTGCCCCCGT 1500  
TTGATCCTTC CCCTAGAATG CGCACGCagT AGCCTTCTTT CCGTAGAAGG TGTGCCTTCT 1560  
CAATGAGGTG CGCCTCTCCT ACCTCCGTGC GAAAAACGTG CACGTCTAAG AgCTGCGCGA 1620  
TAGCTTCTAC ACGCAGCGAG GTGGGACCAT TGGTAACCAG CGCGATAGGC GCGCGCGGT 1680  
GTGGCTGCAT ACGGAGGTTG CGACTGAGTT CACAGATCTC CGACACAACC GAAAGAGCAA 1740  
AGACTGCCTG TTCGTGCGGA ATGACAGCGC GATTAAGGGT TTGGTCGTAA TAGACAATAT 1800  
TTCCCCGATC TCCGTCACAA TCTGGCACAA AGCCGAAGGc AATGGAGCGT TCTTCTGGGG 1860  
ATGAACCTCG CGTGGCTGCC TCGGTCAGTG CCTGCGCGCA CGCGgTAAGA GAGGACCCTT 1920  
CAGGA ACTAT GCGATGGCGA ATATCCCCTG GCGTTTTCGGC GATACTAAAA AGGGCGACAC 1980  
CGAGTGATTC TAGGAGGCGC CTATCTATGG AAGCTGCACG CGCACTTCCA TTGAAATCAA 2040  
TGAGGATAGA CAGGGGTGTT CCCTGTTTCG TGTAGGCGGC ACGCTGCTGG GTAAAGCGAT 2100  
GGAAAAAGGC ACGGTGCTCA GTTTCTTTAG GGGAATTTGC GATCACTTCC CTTATGAAGA 2160  
GATCATAGCT GTGCAGGCTT TCTTGTTTGT GTGTTTTGTT GTACAGCAGC GGTTCGAGTA 2220  
TAGAGGCGTT GAGCGTGGCA CAATGCTCTC GTATTTTCTG GAAAGAGGCG GGCTGTAAAC 2280  
ACTGTGCGAC GAAgTCTTCG CTCAGCTGTT GTGCCTGAGT AGGACTGAGC ACGCCGCCGT 2340  
CATTTAGGCC AAATTTAAAG CCATTGTATT CGATAGGATT GTGACTTGCG GAGATGTAGA 2400  
GGAAAGCGTC GTAGTTCCTC GCGTAGCTTG CAATTTCTGGG TATTGGTCCG ACTCCGACAC 2460  
AACGCAGCGA ACAGCCTTCC AGATGGAGGA TAGCGGTGCA GATAGAACTG ATAATCTCTC 2520  
CAkTAGGGCG CGAGTCGCGC GCGATGACAA CACGTGGTTT TGGGACCTTT TTTTCAAGA 2580

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ATCGGGCGTA GCTGAGTGCT ACCTGTGCGC TGAGTACAGC GTCAGCCTTT TGCCTGAGGG	2640
TGACGGTGCG CTCAGGGGTA AAAGCGTAGG GGA AACCTT GCGCCACCTT GAGGGTGACC	2700
GGGTGAGTGA TAGATGAAGC GCTGCGCaGG CTGCGGCAAG GTGAGGGAGG TGATGAGTGA	2760
GTTGAGCAGG GACATGCGCG GAGGATAGGG CGCGGGTGAA GGAAGTGCAA GGGAGGTGGT	2820
GGTCTTGACA GGATGAAATC AGGTGTGGTC GGGTGTAGGG GCGGGGGAGA GGTAGGAATG	2880
GGAGTAGTGG AATGGGTAGG TGAGTGGATG CACGCGGTGG TGTGGAGCTT TCCGATGGTG	2940
GTGCTGTTGC TGGGGACGGG GTGCTACGTG ACGGTGTGTA TGAAGTTTTT TCCTGTGGTG	3000
CGGCTGTGGT ATGTATTAAG ACAAACTATT GGGGGTCGCG GAGGTAAGAA GGGCGGCAGT	3060
GGTGAGGTGA GTGCGTTCCG TCGGTGTCC CACTgCtTGC AGCGACGTTG GGGTCTGGAA	3120
ATATTGTAGG GGTTCGCACG GCGATTGCGA TTGGGGGGCC TGGGGCGATA TTTTGGATAT	3180
GGGTGACGGG GATATTCGGG ATGGGAACGA AtTCGtGGAA GTGGTGTGG CGGTGTACTA	3240
TCGGCGTCAG ACTGGTGATG GCGTTTTTGT GGGGGGGCCG ATGTATTATC TGAAAGACGG	3300
AGTGGGAGTT CCAGGGGCTG GGGTACTTGC GAGTTTGTTT TGCATATTCA GTGTTATCGC	3360
GTCTTTTGGG ATAGGAAATA TGACGCAKCG AAcTCGGTGG CTCTAGTGTT CGAAGATGTG	3420
TTTTGTGTGG ACGTGCGGGT GACCGGGGCA GTGCTGATGG TCTTGGTAGG CTTAGTGAGC	3480
GTGGGTGGGT TAAAAAGTAT CAGTTGGGTG ACTGGGGTAA TGGTGCCTGs GATGGCGATT	3540
TTGTATGTAT GTGTGGGCGT ATGCTGgTGT GTTGCAATAC GCGACAgCTG GTGCCAGTGT	3600
GCTGGGATAT CGTGTCGGG GCGTTTGCCG GGACTGCAGC AGTTGGGGGG TTTGCAGGGA	3660
GTGTGGTGCG TCAAGCGATA GCGGnTAGGT ATTAGCCGGG GGGTAGCGGT GAACGAGGCA	3720
GGGCTTGGA CTGCTCCTAT TGCGCATGCG GCGGCTATTA CAGACCATCC AGTGnCGACA	3780
GGGGCTTGTG GGGTATCTTT GAAGTTATTT GTGGGGACAA TGGTGGTATC TTCGGTGACG	3840
GCATTTGCGA TACTGC	3856

## (2) INFORMATION FOR SEQ ID NO: 136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGACCTAGAG CGTAnACTGC TGGAGGGACC GCTCCGTCCA TTATACGGAC GATGGAGGGA	60
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AAAGGCAATG TTCTGCCCCG CAGTTGCGTC CGGTGCACGT GGAGGGTCAG TGACGAAAGA	120
AGAAGCAATC GAGGTGGACG GAGTGGTTAA GGAAGCGCTG CCGAACACCA CCTTTAGAGT	180
GCAATTGCAG AATGGGCACG AGATCCTTGC GSTATCTTTCA GGTCGGATGC GCAACACTAC	240
ATCCGTATCG TGCCCCGAGA CTCGGTGAAG GTCGCGCTCT CACCCTACGA CCTCTCCCGC	300
GGCAGAATTA TGTTTTCGTGA GCGTTAGATT CCTCTCTCGC AGgAGAGAGG TGCTTGCTCC	360
TCTTTAGCAG CGGGGTTGCT CATCCTTCAA GGAGGATTGA GAGTCCTGCC CTCAGGGTGT	420
GCACTCCGCG CGCCAGGCAG GACACGCTGA ATGCGATCCC GAAGAAGCCA AATACTAAAA	480
AGAAGCGTAC CCGaATAGAG CCAGGAGGAC GAGCGCCGCT CCCTGAATGA GAAGGCGCGC	540
CCCGTCTTTC CTGGAGCCCG TGC GCGCGGT AGGACCCGCC GGATCGGGCG GAGGTCTGCA	600
CTGCTCCAAT AACTCCACCC ATTTCCAgGA AAACCACCgA AGAAAGTGTA CCATCCCTCG	660
AAGTGTTCGG TTTCCCGCGC GTGCCCTCTC CAGGGACCGT GCGTGTGTGT GTAGCGGGTG	720
CGCGCTCCTG CCTTGTCGTC CGTACCTGGA GGTCCAAGCG CCAAAGCCCT CTGaGGCGTc	780
GCGTcCTGcA CGcGaGGaCC AAAATGcGcC ACCTGcGcGT TcGGcATcGT aGCGTGCGCG	840
TGATGCACGG TCAGAGAGGA CGGCGTAACt GcGTTGaTCC TTTTAAACTG GTCTCCGcA	900
CACGCGTCGC CCGGATTTTT ATCCGGATGA TACTTAAGCG CCTGCGCGCG AAAAGCTTTC	960
TTAATGTGTT CCTCAGAAGC ATCGGCAGCA ACGCCCAGTA TGGCGTAATG GTCAGGAACA	1020
GTGCGCTCGC TCATCGTTTA CCAATGGTG GTCCCCACGA ACTCTTGCTT GTTCAGGATG	1080
CGCTCCAAAT TCGGTAAGTC ACGCCCTGTT GCGCAAATGA CCTGAATTCC CGACTTTTTT	1140
GCCCGGACAC TAGCGACTGG GTCAAAGGGG ACATGGCTGC CCGGTACCCA CTCCTTGTCG	1200
ACAAGGAGGA GGAAATCATC CCAGGAGAGG GATGTGAGCG CCTTCGCATC CTTGTCTGAA	1260
CGAGGATCCC CCGTGTAAC ATGCGCAACG TCGGAAAGGT TAATAACCGT CTTTGCAGAA	1320
TAACGCTCTG CAAGGAGCAC AGCGTCGGTG TCGGTGAAAA AACC CGGTTT CCAACCAGCA	1380
GCAACGAGCA CCTGACCTGA AAAAACGTTT GCCGAGTCG GGTCATACAC GACCGGATTT	1440
GGACAAAGGA TTCCAAAAAG GGATTTGAGC AGCTGCGCGT TCAAACGCGT AgCCATGaTG	1500
CCAATCCAGT CAAGTTCAAC GTGTTGCGCC GTGGCATACA GCTCCCTGTC TTCTTGATTA	1560
TCGCCCTCGT GCGCAGGTTT CGCACAGGCC GGAGAAGACA GGCTCCGGCG TAgcGCACgA	1620
TAGGCGTTTT GATAAGTGCG CGCAGGTGCA CCACCGCCTG AAACGACAAT GAGCTTCCGT	1680
GAGGCGTCTT CGTATAGGTA CCGTTGAACG GAACGAACGA ACCGCCGAG AAGCTCTATG	1740
TCGGGCGTCT CAGGCGCAAC GATGGAACCT CCAAGTGACA GAACGGTGAC CATGAAACCC	1800



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TCTCGCCGGC ATCGTAACGC AAAGAGACCC TTTGGATCCA GGCCTGTGT GTATCTGGCA	1860
TTGCGTCCCA GCGTGACGG GCGATGGAG TGTCTACAC GGGCGACACA GACTCCTAGT	1920
TCTTGATTC TGTGCAAAA CCGACGTAAA AACTGTATCT CCGTAGTCTA GTGAGTGTTT	1980
TCTGTGCATG AGTTGCTCCC GTACGACCGG TGCTTTACGC GCGGTCCCC TTGTGTTCCG	2040
TTCCGTCTCTG GTGCTTGCGG TGTGGGTGT TTCTGCGTA CAAGCCGCCG ATGTGGCGCA	2100
CAATGCGGAT GTACCTTCCC GCTCGTGAA GCGCTCGAG CGTTCCGTT TTTTGTGTA	2160
TCCAAGCCG CTCGACCTTT CTAGTGACTT TCATGCGAAG GCCTGAAGG GGGAGGCACT	2220
GGTTCCTAGC CTTTCAAGG GAAAGGTGAC GCTTTGAAC TTTTGGGCTA CGTGGTGTCC	2280
GGCTGTCTG GCGGAGATGC CGTCTATGGA TCGCATGCAG GCTCTTATGA GGGGAATGA	2340
CTTTCAGATT GTCGCGGTCA ACGTTGGTGA CTCGAGAAAA CAGGTGGAAA GTTTTATCGC	2400
GCGTGGAAAG CATACTTTC CTATCTATCT TGACGAGGAG GGGAGTTTG GGAGTGTTTT	2460
TGCTTCCCGT GGTCTGCCAA CTACTTATGT TGTGGACAAG GCAGGGCGCA TCGTGGCAGT	2520
GGTTGTGGG AGTGTGGAGT ATGACCAACC AGAGCTAGTG GCTCTCTTTA AGGAACGGC	2580
GCGTGAAGT TGTCCCCGGC GTTGTGGGT CTTTTTGGC CGGTTGCTT TCTTTCTCA	2640
GTCCCTGCGT CCTGCCGCTT ATTCCGGCGT ACGTCTCTTT CATTTCGGGA GAATCGCTCG	2700
GTTCTATCCG GCGGGGGCG GCGCGGCTCC AGGTTTTTCT CAGCAGTGT TTTTTGTAT	2760
TAGGACTGAC GACGGTTTTT GTGTTGTTTT CAATCGTATT TAGCGGAGGG GTGCAGCTTG	2820
CAGGTGCGGG TGTGCTCACT GTGCTCACGC GTGTAGCGGG CGTGGGGGTG ATACTCCTCG	2880
GCTTAAACAC AATCTTCGAC GTGGTTCCGT TTTTGCCTGT GGAAAGGCGT ATGCACACAA	2940
CGGTGCGACG GGTGGGTGTG TTTCTGCGT ATCTTTTTGG GTTGCTGTTC GCAACGGGAT	3000
GGACTCCGTG CGTGGGGCCG ATTCTCTCTT CTCTGTTGTT CTATGCGGCG AGTTCTGGGC	3060
AGCTGCTCCA CGCAGCAGGG CTCTGACCG TGTATGCACT GGGATTGGGA CTTCCCTTCG	3120
TGTTTGACAG GATCTTTTTT GGACGTGCGG AGCGGGTGT TCGTGGGTA AAGAGTCACA	3180
TGCACGCAGT AAAGCTCGCC TCCGGGATGT TGATCGTCTT TTTCGGACTG CTGATGCTAA	3240
CGTCGGGGTT GCAGGCACTC AGTCGGCTTT TTCTACGGGC AGGATTGCGG TTAGAGGAAT	3300
ACTCGACGCG GGAATAAACC CCTCTTCGGC AAATAGCGGC ACTTCTTGCG CATGGTTTTT	3360
GTACCAGGGG GTTTGAGCGC GAGCGGCTT GGGGCTGTGC GGGTGGGTAG CCATCACGTA	3420
AATAGTTTTT TGATGCGTGT GAAGGCCCGC GTGACCTCTT CCTCGCTTAT TTTTCCTTCC	3480
GGTGCATGGG CGCGCACCAG GTGTTTGGGA ATTTCTGCTCA GAAAGGGGA GCGGTGCGC	3540

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TCTTCCCTTT TTCCGCCGCG TTTCCTTGTG CGGCAGTGTG TCAGGTACAA CTTCCTCTTT	3600
GCGCGGGTAA TTGCAACGTA GAAAAGGCGT CGTTCTTCCT CGATGCTGTG AACCTCTTCT	3660
ATACTTCGTT CGTGTGGAAT GGTTCCTCGT TCCACGCCGG CGATAAACAC TACGGGAAAT	3720
TCCAGCCCCT TCGACGCATG AATTGTCATG AGCGACACAG CGCCCTCTGT TTCTTTTTGG	3780
ACGTATATCGC GTGCTAGCAA CGTAACGCGG TTTAGGTAGT CGTACAAGCT TCCGTGTTCT	3840
GAACTCTGTT CCCAGTGTTT GATGGATTCT ACTAAGTGTT CGATTGCAA GAATTTAAAA	3900
CGTGCGGCAT GTTCGTTTTT TTGGAATTCT TGGATGAGGT AATTAAAATA CTGAATGTCT	3960
TCAACAAATT TCGGTACCTT GTACGCAAGA TTTTTCCTCCG AAAGTAGATG GGTACGCGCC	4020
TGGGTAATGA GCTGGAGAAA ATTTTCCACA GCGGTACGAT GTGATTCTTT TAAATCGACT	4080
GCATGTGTTT TATTGATAAT TTGATTCAGT GCATTGAACA CGGAACATTG TTGTGTATTA	4140
GCAATGTCGG AGACTAGATG CAGTGTTTTT TTCCAATTC CTCGCCTCGG GGTATTAATG	4200
ATGCGTAATA GGTGACATC GTCGTCAGGA TTAGAAATTA CCCGCAGATA ACTGAGCACA	4260
TCCTTTATTT CTTCCTCTG AAAAAAGCTC ATGCCGCTG AGACACGGTA TGGAATATTT	4320
TCTTGCAAAA ATACGCTTTC AATTATGCGC ATAAACTAT TCGTGCGGAG TAGGACTCCA	4380
AACTACTGA AAGAATAGGA TGCGGTATT TGTCTGCGA GAATCGTGTT TGCAATAAAG	4440
ATTG	4444

## (2) INFORMATION FOR SEQ ID NO: 137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GGACGCAAAC GCGGTTCCn TTCAAAGGCG CGCTCGATAC GCCGCGTTCA ACCCCATAGC	60
GTTGCCGGTT GCCGCTTCCn AGACTTcCCC CttACCGTAC AGTgCACGCG CGCGCGAACY	120
TTCCGCAAaG CAGACAGCGA TACTGTCCCA GACGCAGGCT TCCACCCGTT GGGgTATyTA	180
CACAACCGGG CAAAAGATCA ACAACCGGGT GAGGGGTGTC TACCGCAAAT TCTCGAGAGT	240
GTGCACTTGC CAGCAACAGT ACATTGCGCG CAAATTCAAT GACTGCAATC TGCATCCCCA	300
AGCAAATGCC AAGATAGGGC AGGTTCTGCA CACGCGCGTG CGAAACTGCA CAGATCATCC	360
CTTCAATCCC CCGCACGCCA AAGCCACCTG GAATTACCAG CGCATCTGCG TCCGCAAGAG	420

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CGTGCCAGC	GTCCTGCAG	CTGCAGATTT	CCTCTGCGTC	TATCCAGCGC	ATGTCCA	480
GCGCACGATG	GCAAATACCC	GCCGCCGTcA	ACGCTTCGCT	CACGCTCAA	TACGCGTCCG	540
CAAGCGACAC	ATACTTACCC	ACCAGCGCCA	CCGTAAGCTC	CCGCCGCGGA	TAGTACAGTG	600
CACGGACCAT	TGCGCGCCAC	GCCGTAAGAT	CTGGCTCTGC	CCCCTGCCCT	GCTGCAGGAT	660
GCAGACCACC	GTCTGTACGG	ACCGTCCCCC	CCGCTCCCAA	CACAGCCGAC	TGCGCGCCTC	720
CTGCACCGAG	ATTACGCGCC	AcCTGCCCCC	CGCAGCAGGT	ATCAAAAAGA	CGCAAACGCT	780
CACACAAGAG	CGCTCCCAGC	CCTTCTGCTT	CCAAAAGGAG	CGGCACCTCA	TAGATAGAAC	840
GAGCCGTCAC	GTTCTCGACA	ATAGCACGCC	GCTCAACATT	GCAAAAAAGG	CTCAGCTTTT	900
CGCGCACCGC	ATCCGTGATG	TGACGCTCGC	TGCGGCACAG	GATGACATCC	GGCTGCACAC	960
CAAGTCCTAG	CAGCTCCTTT	ACGCTGTGCT	GTAGCGGCTT	GGTTTTCATT	TCACCACAAC	1020
TGGGTAAGTA	GGGAACATA	CCCAAATGAA	TAAAAAGACA	GCGCTCCTTC	CCCAGAACAC	1080
GCCTGATTTG	ACGAATCGCC	TCGATGAACG	GAAGCGACTC	TATGTCACCG	ACGGTACCAC	1140
CGATTTCCGGT	GATAACCACC	CGAGCCCCCG	TGGTAGCAGC	AGCGGcCGGA	ATTCGCGCcT	1200
GgATTTTCATC	CGTAACGTGA	GGAATAACCT	GTACGGTAGC	ACCTCCGTAT	CCTCCCGCGC	1260
GTTCACGGTC	CAAAATAGCC	CGGTACACGC	TCCCCGCAGT	CGTGCTATTG	AATCTACTTG	1320
AAGGCACGTC	CGTGAAGCGC	TCGTAATGGC	CCAGATCCAG	GTCCGTTTCG	CCGCCATCTT	1380
GCGTGACAAA	CACCTCCCCG	TGCTGATAGG	GATTCATGGT	ACCGGGATCC	CCATTCAGGT	1440
AGGGATCAAA	CTTTTGATTG	ACCACGGATA	TACCCCGCcT	CTTAAGCAAA	AGTCCGATGG	1500
CAcTGCGGCA	ATACCCTTGC	CCAGCGAGGA	AACTACACCG	CCTGTAATAA	AGATAAAAGC	1560
CGGATCCATA	CGGCACGAGT	GTAGCGTGTC	CATCGCTTTT	TTAAAAGGGA	GCACCCTGCC	1620
TCTCCCCTGC	GCCTGTAGGG	TGGACTGTCC	CATCGGCTTG	CATCGAACAT	TGCTTTCGAA	1680
TACCATGGGC	CCCATGAACG	CGCGCGCTGC	CCTCGCTCTT	GCCATGGTCT	TCACTTTCCA	1740
GAGGTTGTGC	GCAGAAGAAC	GTTTCGTTAT	CTCCACTGAA	TACTTCGACA	TCATCTACAC	1800
CGAGGCCTCG	ACTGAGTCTG	CGCGTATACT	GGCGAAGCAC	GCTGACCGGT	ACGAAGAACA	1860
AATCAGCCTC	ATGCTCAATC	GGGTTCTCTGA	CAAGAAAAAG	CGCACCACCG	TCGTCCTGTA	1920
TGCCACACA	CAGGATGCAG	GCGGGTCTTT	CTCTTCCAAA	CCGTCAAGGA	AAATAATCAT	1980
CAACGATACG	CGCGTTCCCA	ATCTGGGTTT	AGGCAGTTTT	AAGGATTTCG	TGCTGAGCAT	2040
TTTTTACCAC	GAGcTTACGC	ATAAGATTTC	TCTCGATTTC	TTCATGCCGC	TACTCCCTCC	2100
CCTCTTTACC	GAAGGGGTTG	CCGTCGCCCTT	TGAAAGCAAC	GACGGCACGC	AAGGGCGACT	2160

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GCACGACCCG CTGACAATGC ATTACTTAAT TCAGAACAAA CTGGAAAACG TCTCCCCCTC	2220
CTGGAGGGAG GTTGCCGAGC TCAGATACAA CTACCCCCAC GGTATGCCCT ACGTGTATGG	2280
GGGAAAATTC ACCGAATACC TGCAGAAAAT ATACGGCAAG GAGCGGTGCG CCCGGCTGTG	2340
GCAGAACTCC TGGCGTCTCT TTATTCGACA CCGTTTTTGG GACGTTTTTC AAAAGAATCT	2400
GGGAACTGCG TGGAATGAGT TCATCGACAG CATTCCAATC CCGGAGAAGG TGGCACAGCC	2460
GCAACTCCTT TCTGAACGGG AAGCGCAGGG TCACTACGGT GCACGCAGCG nTGCGCCGAn	2520
CGGctTCGCC TATTATGACC GTGACCGTCA CGCGGTGCGT TTCCGTGACA AAGCAGGTGG	2580
GGTGCGCAGC CTGTTCTCTC ATGACAACAC GCTGCATCAT CTGAACTTCT CCGAGGACGG	2640
ACGTATTTTG GCAGTATCAG ACACCATTTGA CACGTGGAGC GAGCGCACGC ACCGAGTACG	2700
CGTTTTTGAC ACACACTCAG GCTCGTTCTC GCCGGAGGTG TACACTGGCG CGTCCGAAGC	2760
TTGCTTTGTG GGGAACGGGC AGAAAATAGT ATTCGTCCGG GTGCAGGGGC AATACTCGCG	2820
CCTCACGCTC AAGGACCGCA CAGACCTTAC cTTCGAGAAG GTGTTATACG AAGCAGGTCC	2880
TGGTTTGCCA TTCGGTGCGC TGTACGCGCC GGcGTACGCG sTGaTGGCAC CGTCGCCATT	2940
ATTGGCGCAC GCGGTATGGA GCGTAACTTG CTTTTTCATCC CGGTGGACGA CAGGCCAATG	3000
ATGCAGGTTC CGCGCGAGCA GATGCCACAC GCAATGCGGG AACTGCAGTC GCAAAAGATC	3060
aAAGGCTCGT GGACGCTCAC CTTTAGCTGG GCAAATATGA ACATGCTCTC TCGCCTAGGT	3120
TTTTACGACG TGTCCCGCCA TACCTTCAGA CTAATGGACC AGGACGTGTC AGGGGGGGTG	3180
TTTGCACCGG TGGTGACGA GGCACGCTT GCTGCGGTGC ACGAAGAGTC TGCAGCAGAG	3240
GCGACCATAC GCGGTGAAGA GCCGGTTGTG CGTGTGGCCT ACACCGGCAG ACACCGCATG	3300
CACATGAGCC AATACCAGCG GGATGACCsC GCCCTGCGCG AGCGGCGGGT GTCGCTGGTT	3360
CCCTTGCAAC CGGCAGAGGC GGAGGAGCAG TCGCGCCCCG CCACGCTCAT GGTAAACGGA	3420
GAGTTCATAG CAGACGTGCA CGAAGCCGAC CGCGGCAGAC GGTACCGCGC AgCTCAGTGG	3480
ATGTGGCCTC CCACGTTCTC ACCCCGCTTT GTGCCGCCAA ACAGCTTCAG CAGCCTCAAA	3540
GACCTTGGAC ACACCGGACT GGGGGTGAAC ATGAAGTTTG CCGATCCGTT TGGGCTCGTG	3600
GAGGTGAATC TCCAGTCGGT TTCTCATTTT TATCCGTTTT TTACCTCGCT GGGGCTGAAA	3660
AGCTCTTTTT ATGTGGGCAA AACCACGTAg CCCTACGTGC GTATCACGAG ATAGACACCG	3720
GAGGGTTCCG GTACACTAAG CTCGGCGGGG CCTTTGAAAC GCTGACAAAC TTTCTATGC	3780
AGGATGACCG AAACGCGTTT TTTGTGCGAA CTGCCGTGGG GGTAAGTACC TACTCCTGCC	3840
TGTGCGCCAA CGGCGGGGGT AACGGGAATT GCTGCGGCAA CAACGGGGGG CAGCAGTGcT	3900

GCGCCTGCAA	TGGACAGGGC	GCAAACGGAC	CACATTATTA	CAAGAGCCTT	GAAAGCCCCT	3960
TCATTCAAGC	ACAGGTGGAA	ATGGGGTATA	GCTTTTCTCA	GCGTGCAGAG	CGCACGGGAA	4020
CAAAC TGTT	CGTGGCGGAC	GTCACGGGGG	TGAGCCTGAA	GTTACACGTT	GCAAATAGTT	4080
TTGACACCGG	TAAAACAAAA	GACGCGGTGC	TCGTGCAAAC	GAAAGGGTCA	TTCCGCCTGC	4140
CGGTGGTGCC	CCTACGGGTG	GGCGTCagcG	CGTACGTTGG	GTATAACGCC	GGGTGGCGCG	4200
GGGGCAAAGG	AAACATTCTG	GCGGAGCACC	CAGTGTACGG	CTTTCCCGGT	CCTACGTATT	4260
TACCCAAGCT	CGCAGGGGTT	GGTGGTATGG	AGGGCTCGTG	TAAAAAAGC	AAGAGTGCAG	4320
GGTTCGGCGC	TGAAGCAGTG	CTCACCATCT	TGGACTACGA	CATCAGCATA	TATGATCCCT	4380
ATCTGCCCCG	CTTCTACCGA	AATATTGTTT	GGAACGTAAG	CTGCGAGTAC	GTGCTCAATG	4440
CGCCAGACTT	TTCCTCACCC	AAACACCTGT	GCGTTGCAAG	CACATCACTG	GTTTTGGAGT	4500
TTGACCTGGC	GGATGTAAAA	GTACGGGCCG	GGGTTTCAAG	CGGCTTCCAA	CTTGCAGAGA	4560
CGCAGAGCGC	CACAACCCCC	GGTTTCAGCC	CGATTTTTTTC	CATGGCCGTG	TAGGAAGGTT	4620
CCCCCGTGGC	GTGTGCAAAG	CGCGCTACGG	GGGCAGCGCT	TCGGCAAAAC	GCGGGAGCTG	4680
GCTGTCTACG	CTCTGGCAAG	GGTTTTTCTA	TGCATGAAAC	GTCTTACAAA	CCTATCCACC	4740
GGCTGTCCCC	TGACACCGCT	AAAAAAATCG	CCGCAGgAGA	AGTCATCGAG	CGGCCCGCCT	4800
CCGTCTGTGC	CGAATTGCTC	GAGAACGCAC	TCGATGCAGG	CGCCACCAAA	ATCCATCTGG	4860
AAATTAACGC	AGGCGGcTGC	GCGCTCATCC	GCGTGAGcgA	TaACGGCCAC	GGCATGTCCC	4920
CCCAGGATTT	GTTGCTATGC	GCTGAAGCAC	ACACCACGAG	CAAAATATCG	TCTGCAGACG	4980
ACTTATTGCA	GcTGCGCACG	TTAGGCTTCC	GGGGAGAAGC	ACTCGCCTCC	ATCGCCGCAG	5040
TCAGCCGCCT	GCACCTTACG	AGCACCCGAT	CAGGGCCCCCT	CGCGTGGCAC	TACCAGCCAA	5100
AGGCTGCAGG	CACTGCACGg	CACGTACCGC	CGGTGCCGCA	GGgCACCGAA	GCAGGCGTGC	5160
TAGAGCCTGC	AAGTCTTGAG	CGAGGCACCG	TCGTACGCGT	CGAGCAGCTT	TTTGAAAAC	5220
TTCTTGCGCG	CAAACGCTTT	CTCGGACGCC	AAAGCGCAGA	GACCACCCTG	TGCCGCAGCG	5280
CACTCATCGA	CGTCTCCCTC	GCACATCACC	CCGTGGAGTT	TCGCTTCACC	GTCGACGGAA	5340
CGCACAAGCT	CACCCTGCTC	AGTCAGCAAA	CCCGGAAGGA	TCGGTGTCTT	GAAACGCAAA	5400
TGCTCAAAGG	AGATCCTGCG	CTCTCCACA	CCATAGAAGG	AGGTGACTGC	TCGTTTCACT	5460
TTACCTTGT	ACTTTCAGAA	CCCGCCATCT	GCCGCAGAGA	ACGCCGCGGT	ATTTTTACCT	5520
TCGTCAACGG	ACGACGCATT	TTTGATTACG	GTCTTGTCCA	GGCACTTGTG	TTAGGAAGCG	5580
AGGGATACTT	CCCCAATGGC	ACCTTTCGGG	TCGCCTGCCT	TTTCTCACC	GTTAACAGCG	5640

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AACGTATTGn ATTTTAATAT CCACCCTGGC CAAAAAGGTA GGTTCACTh ACAGG

5695

## (2) INFORMATION FOR SEQ ID NO: 138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

AACACTACTCTn AGTAGGATCC CCCTACACTn TATCGCACAC GGCGCACAGA CGGAACGGAG	60
CGCCTGTGTT TCACACATTG AATTTAAAAA AGATAACGTC CCCGTCTTGC ACCTCGTATT	120
CCTTCCCCTC CTGCCGAACG CGGTTTGCCT CCCTCACCTT TGCCCACTC CCACAGGACG	180
CAAGATCATC GAAAGAATAC GTTCTGCAC GAATAAAACC ACGCTCAAGG TCGCTGTGGA	240
TCACTCCTGC CGCGTGC GGT GCAnAGnCCC TGCCCGAATG GTCCACGCGC GACACTCCTC	300
AGGCCCCGCG GTAAAAAGG TACGCAACCC CATCAGGGAA TACTGTGCGC GCGCAAnGCG	360
CACGTCCTGA TTCGCGCAAC CTAATTCTT GCAAAAAGGC GTTTTGCTCT GCCACATCAG	420
AAAGCTGCGC AAGTCTGCTT CAAATTTTCC ACACATAACA ATTGCCTGCG TGTATGCAC	480
ACGTGCGTGC TCTTGACCG CGCGCACGAA ATCATTTCCG TAnTGCATGC CGCTTTCGTC	540
TGTATTGCAC ACGTAnAGGT GCGGCTTCAT TGTAACAAG CGCATATCGC GCACCGGTTG	600
CGCTCCTCAT CCGACAGCGG CGCCATAnAT GnCGCTTTCC CATTTCTAAA TATTCGCGC	659

## (2) INFORMATION FOR SEQ ID NO: 139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AGnTTCCTCC GCCTCCTTGC gCCGGGCTtC CTCCGCCTCC TTGCGCCGGG CTCCTCCgC	60
CTCCTTGCGC CGGGCTTCCT CCGCTCCTT GCGCCGGGCT TCCTCCGCCT CCTTGCGCCG	120
GGCTTCCTCC GCCTCCTTGC GCCGGGCTTC CTCCGCCTCC TTGCGCCGGG CTCCTCCGC	180
CTCCTTGCGC CGGGCTTCCT CCGCTCCTT GCGCCGGGCT TCCTCCGCCT CCTTGCGCCG	240
GGCTTCCTCC GCCyCCTTGC GCTGCAGCCA CTGCTCAAGC GCCGCTATCA TACGCTGCAT	300

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TCGTAGTGTT GTGAAGCAGT CGGGTTTTGG GACACGTACT TTTTATAGTC AGCCAGTGCG	360
TGTGCATAGG CTTGTCGCTT CATGGCAGTG TTTGCGGAT TGAGCAAGGC AGGAGGGTAA	420
TCGTGCTTGA GGGCGAGGGC CTGCTCATAC GCATGTTGGG CTTCCCTCGTA GCGATGTTGC	480
ACGAAGTATA CGTTCCCAG ATTGTAGGCG TATAGGTGCG CATATTCCCTG ACTGTGTACT	540
GGTGGGTTTT GCAGCCACTG GATTGCCcTGC GTGTAGCGTC CTGTCGTAG GTACGCCATT	600
CCCAAGTAGA GTGCTGCTTT CGGGTGGGCG GGTTTTTTGCT GTGCTGCTTT GTGAAGTGGA	660
CCGATGGCCT GCTGTGCCTG CTGTAAGGAA AGGAGGCGCT CTCCTTCACG AAAGTGGtCA	720
AAGGCATCCT CTGCCCAG GAAGGACGCA AATGCGAGCG CAAGAAAGGA GAATAAGCGA	780
ACGGATGGAA GGGAGCGTAC GcKtGCGTAG GTGCACGGTG AGGATTTTTG GCACATTTGA	840
CATTCCTTCT AGGGTGCCT ACCATGGGCG GCATGTCCGC GTACATGGCA CTGCTGGCAG	900
CGGCGTTCTC GTCAAGTATC GTCTTTTTGC TCGTTTTTTT GATGAGAGGT TTTTCCATCC	960
CGCGCAGACA ACTTTTGGTG GAAAAAGTT TTCGAGACGG CAAGTACGCG CTGCTATCA	1020
AGCATGCCCA TGCGGTTTTG GCTAAGGATC CCCATAACTG GGCAGTGCGT GTATTGCTCG	1080
GTCGTGCGCA TCTtGCGGAA GGgAAGcGCG ACGTCGCGCT TATGGAGCTG CGCGcTGCCA	1140
GCAGCAGAGC TkCGTTTCGG AAAgTGGtAr ATGAaGtTgA gTTTcGCAAG ACTATTGCAC	1200
AGCTTATCTC CAGTTTGACC AATCGAnGA	1229

## (2) INFORMATION FOR SEQ ID NO: 140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTGGGACTAG CGCGTACTCT TACCGTCGGG GTTGTtTCTG CTCTCGCGCG TCCCATTCAA	60
AATAAGGGCA GTATCATCAG AAATATGATT CAGACGGACG CGGCGATCAA TCCTGGGAAT	120
TCTGGTGGTC CGCTTCTGGA TACCCAGGGG CGCATGATAG GCATTAATAC CGTTATTTAC	180
TCTACATCTG GAAGTTCTTC TGGTGTGGC TTTGCGGTGC CAGTAGATAC CgCAAAGCGC	240
ATAGTGTC CG AGCTAATTCTG CTACGGCCGT GTGCGTCGCG GCAAAATCGA TGCCGAACTC	300
GTGCAAGTCA ACGCATCTAT TGCTCACTAC GCGCAsTTaC AGTAGGCAAG GGATTGCTGG	360
TATCACAGGT CAAGCGGGGA AGCCCCGCTG CACAGGCAGG ACTGCGCGGT GGCACGACGG	420

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CCGTACGCTA TGGACTGGGA CGGAGAGCAG CGGTTATCTA CTTGGGGGGA GACGTCATTA	480
CCGCCATCGA CAACCAGCCT GTAGCGAATC TGAGCGATTA TTACTCGGTG TTGGAGGATA	540
AGAAGCCTGA CGACGAATTC GCGTTACAGT ACTCCGCGGC AGACGGCAGC ATGTGGTAGC	600
CGTGCGGCTC ACAGAACGCT CAGATGAGTA GCGAGGTGCG GCGCCCCGTG CAGGCTGCCT	660
TTTTCACTGG TTACTTCATG ATGCTGCGTG GTCCTCTTTC CTCCTTTTTC CCCTTCTTTT	720
CCTTTCCCTT GTAGGCGGCG TTTTATCTG TCTCTGGTGT CTTCTTTGGA TCCTGTTGCG	780
TGTCAAACGT TTCAAACGAT TGCGCCATTT CCTCTAGCAG CGCGTCAAGA TTTCCTGAT	840
CGAGATACTG CATAACCTGT GAACATTGAG CAGGAGATAG TGCAATGCGC ACCGCAGGgC	900
AGTTGTAACC ATTTGCACCC GGAATCGTGC GGTTTGCAAT GATAAAATAA GGGCGATCAT	960
CAGTGATAAA CTGATACTCA AAGCGCATAG TGGGGGTGGC ATTGTGCGCA GAGCCAAGAA	1020
TACCCAGGT CATCAGCGGA GTAGTTGTCC CAAAGTACGC CCGCTACTA CTCTTTTCCC	1080
GCGTGAGyky TTGTGCTTCA TATTCGCCTA AGTACTTCTC AATAGcTTCG CGCAGTGCTG	1140
TACGGTCCTT ACGCTCAAGG TAGAGCGTAA TGCCGTCCAG TAGGAATTTG AACTGCATAA	1200
GCACAGTGTC GATCGGCGGG TCAAACACAA AGGTAAAGTC GCGTGGAGAA ATCGCAGTAC	1260
GCAAGCGGtC GACCGTGTAG GCATTCAGGA CTCCTAATTC CTTAGGAGGG TAGTCGTTG	1320
AAACAGTCAT GTTCGTGCTT GAAGCACAGC AAACCAAGAC CCCCCTACCC AGCAGTGCAC	1380
CCAGAGCGCG ATAnCCTGCG CGACATAACC TGATTCCCCA CTTCCGTAAA GGnAGAGTGG	1440
AGGGAGAAAG CATACAAAT CCTnAGCGTT TCCATGGGGA CGTCAGCGTA CACACAAGCG	1500
nTGTCa	1506

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCAGCCTATG GTCTACGGGA ATTATGGGGG AGGCAGCTAC TCGGGTCGGT TTTTCAGTAG	60
GAATATTATA ACTGGAGAGA AGAACTTCA GGGTCAGTAT TTTGAGGAGC GGTTCGACGA	120
ATGCGATGCC GAAGGcAGTG aTGTAATGC GATAAAGCCG GCTTATCTTA AGCAGTTGCA	180
GGATATTGCG TGGAAGTGG AGGATCACAG CCGAGAGATT CGGGAGGTTT GCTTTACTAT	240



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CGAGGCGGGC AGTTTATGGC TTATTGAGCA AAAACCTGTC GAAGCGAAGA GCACAATCTC	300
TTTGGTACGG TTGCTGCTCG ACCTGTACGA GCGCGAGGTG GTGGATGCTG AATACGTGGT	360
CAAGTCGGTA AAACCGGGTC AGCTGAACGA GATTTTGCAC CCGGTCATTG ATATGACGAG	420
TGTGACAGGT TTGAAATCCT CGCAGGGGGG GATTATTGGT GTTCCTGGTG CGGCGGTTGG	480
GCGAGTGATC TTTACCCTG ATTCCTCAT CGAGGCGTGG CGTGTGGCGA AGATGGGCGG	540
ACAAGATACA CGGTGTATCT TGTGTATGCC TGCAACGTAC GCGGGGGACG TTAAGGCAAT	600
TGAGGTGGCA ACTGGTGTTT TTTCTAACGA GGGGGGGTAC TCCGCCACG CTTCCGTTGT	660
TGCCCGTCAG TATGGGAAGA TCTCTTGGT CCGTCCAGAT ATGAAGATTT ATTCGGACAA	720
AGCGGTCGTT GACGGTATGA CTATCAACGA GGGCGATTTT GTAACGCTTA ATGTTCTTCA	780
CTACGGGGAA TCCACCCTGT ATATGGGAGC TCGCGAGcTC ATTGAGCCTG ATCCAGAGAC	840
GTCTGGCCTA GTGAGCTTCA TCGAGCTTGC GAAGGGTTTT GTGCGTTTCG TTCACGTGCG	900
GGCGAACGCG GACAGTCCAC ACGATGCAGA gCTCGCGCTC GCCTTTGGTG CGCAGGGTAT	960
CGGACTGTGT CGTACAGAGC ATATGTTCTT CAAAGAAGAT CGGATAAATG TGTTCGCCCG	1020
TATGATCTTC TCGGAGAATG CTGAGGAGCG GACGGGCAGT CTCAAGCAGT TGCAAAAGAT	1080
GCAGGGAGAG GATTTCTACG GCATCTTCAA GGTAATGCAG GGACATGAAG TGAATATTCG	1140
CCTTCTGGAT GCTCCTTTGC ACGAGTTTTT GCCGCACGGG GAGAGTGAAG TTAGCAAGTT	1200
TTTGAGTAT CTCGAGAAGG TTTGTGGTAA AGGTCTGTCC CGGGAGGAGT TGCAGGAGCG	1260
GATCTCCATG CTATCTGAGG TGAATCCCAT GCTGGGTAC CGTGGGTGCC GTATTGCGAT	1320
TTCATACCCG GAAATCTACG CCATGCAGGT GCGCGCCGTG TTCGAGGCAG TGTACCGGTT	1380
GCAGAAAGAG AAGATCTCGG TGTACCCAGA GATAATGATC CCCATTGTCA TGAATTGCCG	1440
TGAGTTAAAG CAGATTGTGT ATGGTAAAAA GATTGAGGGG CACGCATACC AGGGTATCGG	1500
CTCGATAGAG GAAGAGGTAC GTCTTGCGCT CAAGGCAAAG GAGGTTGACT ATAAGGTGGG	1560
TGCTATGATT GAGCTGCCTG CAGCTGCGTT GAGTGCAGAC GAGATTGyGC gcTACGngcA	1620
GTTTTTCTCG TTTGGGACTA ATGACTTGAC GCAGACAACG CTTGGACTCT CCAGAGACGA	1680
TTTCAATACG TTTATGCCCG ACTACACGAT GTATGATTTG GTTGACGGAA ACCCCTTTGC	1740
GATACTCGaT GCGCgCGTGC scgAGTTAAT TGAGGTTGCT ATGCaGCGTG GACGCTGGC	1800
ACGGCCGGAT ATTCAGCTAG GTTTGTGTGG GGAGCACGGT TCACGGTCAG AAAATATTCG	1860
TTTTTGTATG GAAGTAGGAC TAGATTACGT TTCGTGTTG TCTTACTCGG TGCTATCGC	1920
TTTACTTGCA ATTGCACAGG CGGAGATTGA AAACGCAGAA AAGGAAGGCA GGAAGCCTGC	1980

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ATGGCGGGGA AGGTCTTCCG CGAAGTCAGG CGGTAGGCGC GCTAGGTAAG GTGTCGTTCG	2040
TGCTTGGTGA GCGTCTCTGT GCGTTCCACT AACGGTGCGA GGGATGGCTG CGTCTGCGTG	2100
GTTAGAGGTG TAGCTGGGTG TTTTTTGGAG GTTTTGTGTA CGCGCTGATT GAATACAAGG	2160
GCAAGCAGTA TAAGGTGGAA CGGGGTAGTA GTATCGTTGT AGATAATATC TCCGAAGTTG	2220
CGCCGGGCGG GTGCATCGAT GTGCGTGAGG TGTGTATGAT TGGTGGCGAG GGTTTGACGC	2280
GGATTGGTTC TCCTTATCTT GAAGGAGTGG GTGTGCGCGC GGTGGTGGGG GAATGTTTTTC	2340
GCAGTCGGAA GATTACCGTG TACAAGTATA AGAGCAAGAA GGATTACCAC CGAACTATCG	2400
GTCATCGGCA GTGGTACACT CGCTTGACCG TTAGTGACAT CTTGGGGGTG TAGGCTCTGG	2460
TCCGAGTGTT GCTTGAAGTC GGTGACCGAG GGCAGTTTTT ATCTGCAGTT GCCTCTGGTC	2520
ATGCTGCGCG TGGAACACGA GGCGGTGATG TTGTGTGTGC GGCAGTTAGT GTGCTTTTGC	2580
GCACTGCGGT GCTTGGGCTT GAGCGTTTGG GTCCTCAGAT AGAGGCGGCG GATCGGGGTT	2640
TTCTCTCCTT TCGCGTGGGG GGGTGTCCGG ATTCCGCGTT GGCTCTCTTG TGTTCCTG	2700
CGGAGTTTCT AGAACGTGGT TTACGTACGT TGATGCAGGA GTATCCCAGT TCGGTGCATC	2760
TTTGCCTGCG GAGGGGAGTG GTGTGTGCGT AgcGTCGCGG TTAAGACAAA ACGGGGGGTA	2820
GTATGGCTCG AAAGAGAGGT GGCagTGGAT CTAAGAACGG GCGCGATTCT AATCCGAAGT	2880
ATTTGGGAGT AAAGTTGTTC GGTGGTCAGC ACGCTCGTGC TGGTTCGATT TTGGTGCGCC	2940
AgCGGGGTAC CCGAATTAC CCGGGAGAAA ATGTGGGAAG GGGGAAGGAC GATACGTTGT	3000
TTGCTCTTGC TCCTGGGGTT GTGACCTATC TTCAAAGGAA GGGGAGGCGC CTCGTTTCTG	3060
TGTGCGTGGA AAACCGGCCT TCTTGAGCTT TTATAGAGGG AACCAGGTGC CTCCTGTGCT	3120
TTGTGTCTGT GGTGTAAGAA GGGTCAGGGG GTATTTGCGT GTCTGTGGGA TCGTAGGGGG	3180
CGTGACACAGG TTTTGTAGAG AGCATGGCCA GTTTTGTGTA TGAGGTGCTG ATTCGTGTTT	3240
CCTCTGGTCG GGGTGGAAAT GGCTGTGTGG CGTTTCGGCG GGAAAAGTAT GTCCCgCGCG	3300
GCGGCCCGCG GGGGGGCGAT GGAGGGCGCG GCGGGGACGT TGTGTTCCAG GTACGGCGCA	3360
ACATGCGCAC GCTTGTGCAC CTGAGGTATG GACGCGTGT TCGTGCAAAG AATGGGCAGG	3420
ATGGAGAGGG GGCACGCCGC TTTGGTGCAA AGGGGCACGA TTGTGTTATA CCGCTGCCTC	3480
CGGGTTGTCT TTTAAGGGAT GCGCAGACTC ATGAGGTTTT GCACGATTTT GGTGATGCCC	3540
ATGAAGGTTG CGTGACGCTC CTTTCGGGTG GAAGGGGTGG TTGGGGGAAT TATCATTTCC	3600
GTGGCCAGT GCAGCAGGCT CCGCAACGCG CGCATTCTGG GCAGCCGGGG CAGGAACGTG	3660
TGGTGACGCT TGAAGTGCCT ATTGTGGCAG ACGTTGGCTT TGTGGGGCTC CCCAACGCGG	3720

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GCAAATCTTC	TTTGCTGAAT	TTTTTTACCC	ACGcGCGGTC	GnTtwGcCCC	TTATCCTTTC	3780
ACTACCCGGA	TTCCTTACTT	GGGGGTGCTG	CGTACGGGGG	ATGGGCGCGA	CGTGATCCTG	3840
GCAGATGTCC	CTGGGATTCT	CGAACGCGCC	TCGCAGGGTG	TCGGCTTGGG	GTTGCGCTTT	3900
CTCAAGCACT	TGACCCGCTG	TGCGGGGCTT	GCATTTCTCA	TTGATCTTGC	AGATGAGCGT	3960
GCGCTGCATA	CATACGATTT	GCTTTGCAAG	GAATGTACG	CTTCTCCCC	TGTCTTTGAG	4020
ACAAAGGCGC	GCGTGCTCGT	AGGTACCAAG	CTTGATTTGC	CGAATGCGCG	TGAGTGTTTG	4080
CAGCAGCTTc	tGCACAGCAC	CCATCCACTG	AGGTTTGTGG	AGTCTCGGTG	CACAATCGCT	4140
GGGGTTTAGA	TGAATTGCAG	GAGGCTTTTG	TGCGTCTCTC	TGACGCAGGT	GCGGGCgcGT	4200
TGCGTTCCCC	TGTGTGGCGG	AACCAAGCTC	CCAGTTTAT	GTACGCTCAG	CTTGAGGATC	4260
CGGTGTGTCA	GGTGCGTGAT	GATTTTGGGG	CAACGGTGAG	CTTGAGCAGA	AAACGAAAAG	4320
TGCGCGGATG	AAGTTAGCCC	TGTTTGGCGG	TTCGTACGAT	CCTGTTTCATC	TGGGCCACTT	4380
GCTCTTGGCT	GATGCAGTAC	ACCGGCACGC	CGGGTATGAC	CGCGTGCTGT	TTGTGCCTAC	4440
CTTCGTTTCC	CCCTTCAAAG	AAAAGGAAGG	AAGTGCAAGT	GCGCACGATC	GGGTGCGGAT	4500
GCTCCATTTA	GCAATTGGGA	CAACGCCGTA	TTTTTCTGTT	GAAGAGTGTG	AGATTAGGCG	4560
TGGGGGTATT	TCGTATACTG	CCGAGACGGT	GCAGCATGTG	CGGGAAAAGT	ATGGCGCACA	4620
GCTTGAGGGC	AAGCTCGCGC	TGGTATTGGG	GGAAGATGCA	GCGCGCAGTG	TACCGCACTG	4680
GCACGCGTTC	GATTCGTGGA	GTACACACGT	TGATTTtGTC	GTGGGTGCGC	GCCCTGTGAC	4740
GTCAGGCGAT	GGGGGGAACG	TAGAACGCGC	CACACGCACT	CTACAATCGT	TTCCCTTCCC	4800
ATGGGTTTCG	GCGGAGAAAtG	TGGcGCTTCC	TATTTCGTCA	ACGTACATAC	GCACCGCAAt	4860
TCAACGGGGG	CgTAGTTGGG	GTTaTCTTgT	ACCTtCCCCA	GTTCGTGAGT	ATATTATCGC	4920
GCGTGGACTC	TACCGkTCGT	GAGCCTCTGC	CTTCTTTCTC	CGGAGTGGAC	GATTCTTCCT	4980
GTTCTTCTCG	TTTTCTTTCT	TTCTTGGAC	AGGCGCAGAT	GCCAGCGTTC	TCTTTTGTGT	5040
CTGCAGATAT	GACGGCGCTG	ATTGCGCGTG	TGGmAcCGTA	CGCGCGCGCA	GTGC'TTTCGC	5100
CACCTAGGTA	TGAGCATTTC	CGTCGTGTAG	CGGAGTTTGG	GTGCATGCTG	GTACGGCGGT	5160
ATGCGTTGGA	AGCGCAGCTT	GAGCCGCACG	TTTATTGCGC	GGGTATTGCG	CACGATATGT	5220
GCCGGGAGCA	TTCGGAAGTG	TTCTTGTTC	GTGCTGCcTG	CGTGCGATGG	TTTTCCCATT	5280
GATGTAACTG	AGCGTGGTAC	GCCATTGCTC	TTGCACGGGC	GCGCAGCCGC	GTGTGTGTTA	5340
GCACAGGAAT	TTGGCGTGCA	GGATGAGGTG	TTGTGTCTCG			5380

(2) INFORMATION FOR SEQ ID NO: 142:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CACGCTCAAC CGGGAACGAT TCGTGGTGAT TTTGCTTACG CACCACTACT AATATTGTCC	60
ATGCTTCTGA TTCTCCCGAg AGCsCTGCAC GAGAACTAGC GCTCTACTTT TCTGCGCAAG	120
ATTTTGTGTA ATGGCGTGAC GGGAATTACG ATTTTTTCTA AAAAGTTTAG GGTCTGCGGT	180
GCGTGTCTCT TTTGATACG GTGATCATGT TTCCTCTTGC TGAAGAAAGG TGAGGATCAG	240
GGGAGGGGTT AGGAATCATG GCTTCGATTG CAaTACTCGG TGGAGGGGCA TGGGGCACGG	300
CGCTTGCTGC GTCTCTCACC GTAAACGGTC ACACCGTAAT GCTGTGGGCC CGTCGTAGGC	360
AGACGTGCGA TGCTATCAAT GCACGAAACG AAAATGTTCA GTATCTGCCG GGCATTACGT	420
TGCCCCGAGC CTTGTGTGCC TCTCCCGATA TGGCATATGT CTGTGCCGGC GCGGATCTTA	480
TTGTATTAGC GGTTCCTTCG TGCTATTGGG CTGAAGTAGC TGCGCTTATG AATACCACTC	540
CTCGTTTTCA GAGGTTGCGT ACTGCTGCCG TAGgACAGGA ATATCCCCCT ATTGGTATTT	600
TGACAAAAGG ATTTATTCCG GATCAGGAAG GGATGCCTCA TCTAATTACC GATGCGCTGG	660
GTGCGTTGTT GCCGTCTGGG GCGCACGGGC AGCTCGTGTA TATTTCCGGT CCAAGCCATG	720
CACAGGAGGT AGCGCAGGGA AAGGTGACCG GACTTATTGC AGCGAGCCAA AATCCTATGG	780
CGGCCATTTC GGTGCGGGAA TTGCTGCGCT CGAAGAGGgT GCAGGTGTAT TCCAGTCTTG	840
ATGTTGTGTT GGTGCAAGTG TGTGCAGCGG TAAAAACGT GATTGCCATT GCATTTGGTC	900
TTTTGGATGC GATGGCTGAG CATTCTGAAG CTTTTGGGGA CAATACAGAG TCGATGCTGC	960
TCGCAGCGGG CTTGAATGAA ATTCAAACCA TTGGAAAACA GTTGGGTTCT ACACATCCTG	1020
AAACATTAC ATCGCTTGCA GGAATAGGAG ATTTGGATGT GACGTGTCGC AGCGCTATG	1080
GACGCAACCG ACGTTTCGGA CGCGACATAG TGCATAAGGG GATCCTTGAT TCCTTTTCTG	1140
GAATACAGGA TCTCGTGAGT CGTTTGCCCC AAGTAGGGTA TCTGGCGGAA GGGGTAGTTG	1200
CCTGTATGCA TGTGCAGCGC CTGGCTGAGC GGGATCGGTT GAAGGTTCCA ATTTGCGCGG	1260
GACTGTACGC TATTTTAAAT CGGGAAAAGG GTGCTGACAC CTTTATGCAA GAGATTCTTG	1320
GTTGGTAGCA CGGGGGTGTT TTCTTCCGCG CGTCTCTGTG GGGGAAGCGT AAAGAACGAG	1380
TCTAGGAGTG GAAGTGAGAA CTCTTACCCA AATGTTATTT TTGGCCCATATA ATCCGCGTTC	1440

GGACGGAGAG ATATATGCAT ATCATCAAGC GAAATGGCGA ACCGCAACCT TACATGCGCG	1500
AGAAAATAAT TGTGCTATC AGTGCTGCTT TTAGAAGTGT CCAGAATCCT CTGCTCCTG	1560
AAGTTCCTGC TATCATCACA GATCTTGCCG CGGAGGTTGA GCGACAGCTT TTTGAGATGA	1620
ACCGTGCGGG CGTTCCTGTT CACGTGGAAA AGATTGAGGA CTTTGTCGAA AAGACTCTTA	1680
CCAAATACAA TCACAGCGAT GAAGTGAAGA GTTTTATCCT GTACCGTGAC GATCGCACAA	1740
AAAAGCGTAT TGCAAGAGAA CAGATTGCGT GCTGTTTTAC TGACTCTTCA GTGCTCGGTG	1800
TACTGAAAGA AATCCAACAA GACTTTCCGT TTCCTGAGTA CAGTCTCGAT GCACTCGCCA	1860
GTAAGTTCCT GCTCTTTAAA AAAGAAGTTA CGGACGAGCG TCGGAGTATG CAACTGCTTA	1920
TTAAGGCAGC GGTGGAAGT ACTGCCCAAG AGGCTCCCCA GTGGGAGCTT AtTGcTGCGC	1980
GCTTGCTTAT GCTCGACTTT TCACTCGCGC TAGGAACATC TTTGGAAAAG TTAAATATTC	2040
ACTCCTTCTA CGAGAAAATA ACTTATCTTG AAGAGGCCGG TCTATATGGG GTGTACATCC	2100
GCACGCACTA TAGTCGGGCA GAAATTGAGG AAGCTGCCAC GTATCTTGAG TGTAGTCGCG	2160
ATAAATTGTT TACGTACAGC AGTCTGGATA TGATTCTGCG TCGCTATGTG ATCAGAACGC	2220
GTGCGCATGT ACCTCTTGAA ACTCCTCAGG AGATGTTTCT CGGTATTGCA CTGCATCTAG	2280
CGATGAATGA AACCCAAGAT CGTATGCAAT GGGTAAAACG CTTTATACA GTCCTCAGCA	2340
AGTTGCAGGT TACGGTCGCA ACACCTACGC TTTCAAACGC GCGCAAACCT TTTTCATCAAC	2400
TTTCCTCGTG TTTTCGTTGAT ACGGTGCCAG ATTGCTCGA CGGTATCTAC CGCAGCATCG	2460
ACAATTTTTT CCAGGTATCT AAGTTTGGGG GAGGGATGGG GCTGTACTTT GGAAAAGTGC	2520
GTGCGGTAGG CGTCCCATTT CGGGGGTTCC AGGGTGCTGC AGGTGGTATT CTCCGTGGA	2580
TTAAGCTCGC CAATGATACT GCAGTTGCAG TAGATCAACT AGGAGTACGC CAAGGCTCGG	2640
TGGCAGTGTA TTTGGATGTA TGGCACAAGG ATATTCCGGA ATTTTGTCAA TTACGGACTA	2700
ATAATGGGGA TGACCGCATG AAAGCACATG ACGTATTTCC TGCGGTCTGT TATCCAGATT	2760
TGTTCTGGAA GACAGTACGC GATAATTTGG GGGCGTCGTG GTATTTAATG TGTCCGCATG	2820
AGATTCTTAC GGTGAAAGGC TATGCTTTGG AGGATTTTTA TGCGGAGGAA TGGGAGAAGC	2880
GCTACTGGGA TTGTGTAAAG GATGCGCGTA TCTCTAAGAG GACCATTCCG ATTAAGGAGT	2940
TGGTGCGCTT GGTGCTAAAA TCTGTGGTGG AAACCGGTAC TCCCTTTGCG TTTTACCGAG	3000
ATCATGCAAA CCGTGCAAAT CCCAATGGGC ATCGGGGAAT TATTTACTGT TCTAATTTGT	3060
GTAATGAAAT TGCGCAGAAC ATGAGCGCTA TTAATTTAGT AAGCGTAAAA ATCACCAGG	3120
TTGATGGACA AAAGGTAGTG GTGCAGACAA CGCGCCGGG GATTTTGTT GTATGTAACC	3180

TCGCGTCGTT	GGTGCTGAGC	AATATTGACC	TTTCAGATGA	TAAGGAGTTG	CGCGAGGTAG	3240
TGCGTGTGGC	GGTACGTGCA	TTAGACAACG	TGATCGATT	GACATATTAT	CCGGTTCCT	3300
ATGCACAGGT	AACCAATGCG	TATTATCGTG	CTATTGGTTT	AGGTGTTTCA	GGCTACCATC	3360
ACGTGCTTGC	CCAGCAAGGA	ATCGATTGGG	AAAGTGATGA	ACATCTTGCA	TTTGCGGACA	3420
GAATATTTGA	GCGCATTAAC	CGTGCCGCAA	TTGAAGCGAG	TATGACAATC	GCGCGCGAGA	3480
AGGGTGCGTA	TGGGTGTTTC	ACTGGGAGCG	ATTGGTGTAC	CGGTGCGTAT	TTTCGCAAAC	3540
GCGGCTATGT	CTCTGAAGAC	TGGCAACGTT	TGCAGCGTGA	GGTAGCAACA	CATGGGATGC	3600
GCAACGGTTA	CTTACTTGCA	GTCGCGCCAA	CTAGTTCTAC	GTCTATCATT	GCAGGGACCA	3660
CTGCGGGTGT	AGATCCTATT	ATGAAGCAGT	ATTTCTCTGA	GGAAAAGAAA	GGCATGCTAA	3720
TGCCACGCGT	AgCTCCTTCT	CTTTCGCAGA	AGACCTGTCC	ACTGTATAAA	AGTGCACACG	3780
CAGTGGAGCA	GCGTTGGAGT	ATCCGTGCTG	CGGGTCTGCG	GCAACGACAT	ATTGACCAGG	3840
CACAGTCAGT	GAATCTGTAC	ATTACAACGG	ACTTTACACT	GAAGCAGGTT	CTAGATTTGT	3900
ACGTGTATGC	GTGGGAAGTA	GGAATGAAGT	CACTATATAC	GTACGAAGCC	AGTCGCTCGA	3960
AATAGATTTG	TGTGGGTATT	GTGCCTCGTA	GGAGCGTGCT	TGCATAACAC	TGTCCACTGT	4020
GTAGGCTTTC	TTTGTGACGT	TGCGTACGCT	TCAAGCCGGT	GTGGCGGTCA	GTATCGCTCT	4080
GGATCGTGTG	TGCTTTTCT	GTTATAACGG	GGCGGTGGCA	CACTGTgTAG	TAGAAGCTGC	4140
CGAAGATATT	TTGGACCGGC	GTTTTTCTGT	ATTGGATAAG	GGTTTCGTGC	GTTTGATAGA	4200
TTACCTGGGA	GGGGATGCAC	GCATTGTGCA	GGCAGCGCGT	GTTTCTTACG	GTGCGGGGAC	4260
TAGGACTGCG	CGTGACGATG	CGGCGCTTAT	CGATTTTCTT	TTACGCAATA	AGCATACGTC	4320
TCCTTTTGAG	CAGGTGGTCC	TTACCTTCCA	TGTACGTGCA	CCGATTTTTG	TCGCGCGTCA	4380
GTGGATGCGG	CATCGCACTG	CTCGCATCAG	TGAGGTGTCT	AGTCGTTATT	CGCTTCTTAG	4440
TCATGACTGT	TATGTTCCGC	AGGAACTTC	AGTTGCAGTT	CAGTCCACGC	GTAACAAGCA	4500
GGGCCGCGCG	TCCGAAGGTA	TCTCTCCTGA	ACAGCAGCAG	GAAGTGCGGG	CAGCGTTTGA	4560
AGCTCAGCAG	AAAGCGGCGT	GTGCCGCTTA	CGACGCATTG	ATTCAAAAGA	ACATCGCGCG	4620
GGAnCTAGCG	CGTATTAACG	TGCCgCTTTC	GCTTTACACC	GAGTGGTATT	GGCAGATTGA	4680
TTTACACAAT	CTTTTTCATT	TTTTGCGTTT	ACGTGCGAGC	GCTCATGCGC	AAGCAGAGAT	4740
TCGTGCGTAT	GCAGAGGTAA	TCATTGAAAT	TACCCGTGCA	GTTGCGCCGT	GCGCTACCGC	4800
CTCTTTTGAA	AATCATGAAA	AAGATGGGGT	GCAGTTTTCA	GGGCGGGAGT	TTGctGCGCT	4860
TAAGGCCTTA	CTGGCTGGAG	AGGGTCTCTC	CCTTGAGGGG	AAGGAACGTG	CGCGCTTTGA	4920

AGAAAAATTA CGCTCTGGCC TGCAGCAGTA GAAGTCTATA GTGCGCTCGT CTGTGTGAGC	4980
AGCAAGAGTA TTGCCTTTCT GTGTCTTAAA AAGGTGAATG TGGTCATAGG TATGCTGAKG	5040
AAAAGGAGAG CGGTCAGTTA TGGGGATTGA GTACTCAGCG AGTAGCATTa CTGTATTGGA	5100
AGGTCTTGAA GCGGTACCAA GCGTCCGGGG ATGTATATCG GCTCTACCGG TCCTAATGGA	5160
TTGCACCATC TGGTGTACGA GGTGGTGGAT AACTGTATCG ATGAAGCCAT GGCTGGGTAC	5220
TGTGATCGTA TCACCGTGGT GCTCGAACAA GGAAACGTCG TGGGTGTTGA AGACAACGGG	5280
CGAGGTATTc CTGTTGACGT GCACCCTCAT GAGGGGGTTA GTGCGCTTGA GGTGTACTT	5340
ACTAAGTTAC ATGCGGGGGG GAAGTTTGAC AAGAAATCGT ATAAGGTGTC GGGTGGACTC	5400
CACGGAGTTG GAGTTTctGT GGTCAACGCG CTGTGCTTGT GGGTAGAAGT GACAGTGTAT	5460
CGTGATGGTG CTGAGTATTA TCAGAAGTTT AATGTGGGGA TGCCGCTTGC TCCAGTAGAG	5520
AAGCGGGGAG TGTCGGAAAA ACGTGGcACT ATTATCCGCT GGCAGGCGGA CCCATCCATT	5580
TTCAAAGAAA CGGTGGCCTA TGATTTTGAC GTACTCCTGA CGCGTTTGCg TGAAC TTGCT	5640
TTTTTGAATA GCACGGTAGT TATTCAGTTG CGTGATGAGC GGTGCGGAC CGCTAAACAG	5700
GTTGAATTTG CGTTCGAAGG AGGTATTCGT CATTTTGTCA GTTATTTAAA CCGCGGTAAA	5760
TCAGTTGTGC CCgAACGTCC TCTGTACATT GAGGGATCGA AGTCGGATGT TTTAGTGGA	5820
GTTCGCTTGC AATATCACGA TGGTTATACG GAAAACGTGC AGTCATTTGT CAATGATATT	5880
AATACCCGTG AGGGGGGCAC GCATCTTGAA GGATTTAAGT CGGCAC TTAC GCGTGTGGCG	5940
AACGATTTTT TGAAAAAAG TCCAAAGCTT GCAAAGAAGA TAGAAAGGGA AGAAAAGCTC	6000
GTTGGGGAAG ATGTGCGTGC TGGATTGACA GTGGTGCTTT CTGTGAAAAT TCCTGAACCC	6060
CAGTTTGAAG GGCAGACAAA GACGAAGTTG GGAAACAGTG AGGTGCGGGG TATTGTTGAT	6120
TCTTTGGTGG GGGAGCGTCT GACGCTCTAT TTTGAGCAAA ATCCAGGTGT GCTTACAAAG	6180
ATTCTTGAAA AGAGCATTGC AGAGGCGCAG GCGCGTCTTG CAGCACGTCG TgCAAAGGAA	6240
rcTGCGCGCA GAAAAAGTGG AATGGATAGT TTTGGGTTGC CGGGAAAGTT GGCCGACTGT	6300
TCGCTCAAGG ATCCGGCGAA GTGCGAAgTA TATATTGTGG AAGGGGATTC TGCAGGAGGT	6360
TCGGCGAAAA AAGGACGGGA CAGCAAGACA CAGGCCATTT TGCCTTTGTG GGGGAAGATG	6420
CTGAACGTGG AAAAGACACG TTTGGATAAG GTCTTGCATA ACGAAAAATT ACAGCCAATT	6480
ATCGCAACGC TCGGTACAGG TGTGGCAAG GATTTTGATT TAACAAGGAT TCGCTATCAT	6540
AAAGTGATCA TCATGGCGGA TGCGACGTG GATGGCTCTC ACATCCGTAC GCTTCTTTTA	6600
ACGTTCTTCT TTCGATACCT GCCGCAAATA ATTGAAGCTG GTTACGTATA TCTTGCGATG	6660

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CGTGACGAAG CGCTAGAAAG TATCGGTAAA AAAAGTGGTG TCGCTGTGCA GCGTTATAAA 6780  
GGTCTGGGGG AAATGGATGG CACTCAGCTT TGGGAGACAA CTATGAATCC AGTGCCTCGC 6840  
AAGATGATGC aGGTGGTGCT CTCAGATGCG GTGGAAGCAG ACCGGGTGTT TAGTACTCTC 6900  
ATGGGTGAAG ATGTCGAACC GCGCCGTAAG TTTATTGAAG AGAATGCAAT ATATGCGCGT 6960  
TTGGACGTAT GAATGTTTTG TGCATTTGTA TTCCATGTG AGTGGTGCCG TCTGACAGGG 7020  
GGAAGGATCA GTGGCGTATC AAGTGACGGC AACACGGTAT CGGCCGCAAC GTTTTCAGCA 7080  
CGTGTTGGGT CAGAAGTTTG TAGTGGCAAC ACTGCAAAA TCTCTTGAGG AGAACAAAGT 7140  
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CCTTGCAAAG GCATTGAATT GTGTGCAAAG AGAAGCGTCT GAACCGTGTG GAGAGTGTCC 7260  
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ATCCCACCGT GGAAGGGGAT ACCACCGCCT TGTATGTGCA AAAAATCCTT GCAAACTTTC 9300  
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TCTTCACCAG TACTATCTAT GATAGATCCG GATTCTGAGA TCGGcTGTGC CAGCAGTATA 9840  
GCTCCCTGTG TGCTCTGTGA GGGACGATAT GCGTGTATAG TGTGTATCGT AGTGTATCGG 9900  
CTAATAAGAA ACGCCACCGT GCACAGCACA AAGACAACGG CCCCTTCCTG TCGTGTGAGT 9960  
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ATGGAGAACG CGACGACTTT GTTTCGTCCA GCGATGGTCA CCGGGCCATT GTAGGCGGTG	10500
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AGAACGGACA ACAGAGCTGG GTGTGTCGTT CTATTTGACG GTTGAAATGA CAAGACCGAA	11160
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CCCGTGAGCG CCTTTCGTTT TTCGCAGTGC GCTTTTACAA AAAGCCGCAC GTGGGGCAGC	11820
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GAATTACTAT CACAAATGTA GGTGGCAAGG GGAATCGCTG CGACTATCAT TTTCTGCAG	12060
CCCAGGTGCG GGTAGGAGAG CGTGTGGTAT TACATTGGCG TAACAGGATC CTGCTTCGTG	12120
TGATGAACTG TCTGCTGAAA CGGTATCGGC AGGTTTCGCG GCCTGTGCGC GTGCACGCGA	12180
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GGAGCAAGGG GCGTGGCTGA GCACGCACGA GCACTTCCCT CTAAGAGAGA GTCACTTTTT	12420
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TAGCCTATCT TCAATTTACG TTGCACATAC GATGTGGACG CTTTACCCGC GTATTGCACT	13680
ACCTGCACTG CCTGCTCGTA TAAAGGATCG CTTTCATCCA CAAAATTTCC AGATATACTC	13740
GCGTCGTCAT CGTCAAAGAA AATTTCTTCA TCAAGATACT CAGGCGTTCC CCACGCGCGT	13800
ACATGGGCGA TCACGCGCGC TAATTCTCGC TCGGAAACAT ACGCACCTTG AATCCGCGTA	13860
GGAAAAGACT GACTCGGGTT CATGTACAGC ATATCCCCTC GTCCCAGCAA TTTTCTGCG	13920
CCCATCTCAT CAAAATAAT ACGGCTATCC ATTT	13954

## (2) INFORMATION FOR SEQ ID NO: 143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AGGGTGCCGT ACACCGGCAA CCACTCTAAC AACTCCACGC CAGAAAACCC ATACGACTTC	60
ACCCGTTCAA TGAGACTGAA AATAAGATCA GACTCAAGTA AATTGAGCTC GAGCTTTGAA	120
GCACCCTTGA ACAAGGCCTC GCGAAAATAC AACTTCGACC AGCGCTCATC TCCCGCAAGA	180
GCGTATGCAT CAGCAAGTTC AGCAAGAATT GCAGAAGAGT CTGGCTCCAA AGAGACTGCA	240
AACTCAAGGC ATTCACGCGC AgcATCGTAA TTGCCCAATG CTTTATAGCA CAGCCCAGTC	300
TTACGATAGA CTTCCGCGGG ATGCTCGCGC GCATCACCGG TGATAAGACT CCCATAAAAC	360
CGCAATGCGT AAGTGAACAC ACAACAGCGC AATGCATACA TAACAGGTTC GACAACGCCA	420
CCACGTTTTT GCATATATGC AACGAACGCA CCCCATTGTC CAACAAGATA CTCACCCTGa	480
CTAAGACCGC CAGAGATAGT ATGTACACGC TGCATCCGAT CCTCCCAAAA GCGAATACCG	540
GTAAGCGCGT ACAAACATC CCGATTGTCT AGCTCTTTTT GAAGCAAATC CTGCAAATCC	600
TGGTGTGCCT GCGCAGATC CCCCTGCTTC AGTAAATCCA GTGCTGACTC AAGCTCTACA	660
CGAATCGATC GTGCAACCAT AGCGGGATAT TGTATCGGTA TCAAAGCGCC ACGTCAACGA	720
AAGTACTTTT TCAAAAACAA AACCAACGCT ATGTAAATAA ACACGAGCTA CTCGCAGTGT	780
CCTTTCCTG TGACATAAAA ATCCCGCAAA CGCGCACGCA CACACTGGTA GAGCTGAGCA	840
CTTCCCTGCT CTTTCAAATC GTCCGGCACC ATCAATTCCA GCGCATCATC AATTGTGCAT	900
ACCGCCCA CA GTGAAAGTA CCAGCACGCA CCGCATCTG CACACGTTCA GGCAAAAACA	960
ATTGTGCACA ACTACTCTTT GGGATCAAAA CTCCCTGCAT TCCCGTCAGT CCGTTCAGAG	1020

790

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CCAACTGGTT CACACTTCCT GTTATTGCGC GGTCTTGCCG AAGAGGAAAC CGGCCAATCG	1140
CAGAAAGCAA TACTAAAAAT TCTGCAGCAG ACGCCGAATC CCCATCAATC CCGTGATACG	1200
ACTGTTCAAA ACAAAGCGCT GCAGAAAGAC ACAGTGGAAG ACTATCCTGC CCCTTTCCAA	1260
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TGCCAAAGCT ATGGCCGCAA TGTTCTTCGA TTGCCAGCGC GTTAATTCTC CCTATTGAT	1500
ATCCCTGTAC CTCTACCAAT AACTCTCCAC AGGCTATCAT GCGCTGAAAA CGCTCCCGCG	1560
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ACAATCGCGC GTACGCTGAG GAATCAAGTG AGAAGGTGCC ATAACGCGCC ACAACTCTAT	1800
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AGCATGGCTC GCCAACCAAA ACAAGCTTGC ATGTGAGCGG AACTCCTTCA GGCCGCAACA	1980
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CCTGCACATC GgTTTGTATC CGCTCTATGT ACGATATGAT GCGCGCACGC ATTTCTTCAA	2400
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CCGCACACGA AACAGGTGGA GGGGAAAAA CCGGTGCATA ACACGCCACG CGTTTTTTAA	2520
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GCCTAcGCGC GGCCCGyCGC gCAGTGCAGC ACGTATGGAG CAGCGAAGAA ACCTCATCAC	2640
AGGAAAGACG ATATCGCGCA TGGAGTTCGT GTACTACACA TCTAGAAAGC TTCGCGCGGG	2700
AAGCTAAATC GTGCAGCGCT TCAAAGCTAC TGTCTTTTCC CTTTAATAGG GGAACATAAT	2760

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GACGAGGTAC AAAATCTTTT AATAGATATT GGAGCGTAGT GCGCTTCCCG GTGCCTGACG	3120
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ATGCAAGATA	CATCCTCGGT	GACCGTCACC	TACCGCACCG	TACATGGCGC	ATGCTCTTTT	6360
TGCCGCAACT	ACATCATGGC	TAGAGTGACT	ACCCGGACCG	GTCATAACCC	CGATGTGATA	6420
ATCCTCCACC	GCTTTTCGTG	CCCCGGTATT	TTGTGGAGCA	CGCGCGCCCC	CACAGCGACA	6480
CAACAGTGCA	CCGACACATA	CCACCCATAC	CTTCAATAGA	AACTGACTTT	TCATAGTCTC	6540
CCCTTAACGA	TCTGCACACA	CCATCTCTCC	AAAACGCTTA	GGCGTATGGT	CCACCCCCCC	6600
CCCACGGGAA	AATCAATTGT	GTATTTATGA	TACAGCATCA	AAAAATCATC	GTGTGCAAAC	6660
CAAAAAGGTA	TCCCTTCCCT	CCCCCTTATT	GAAGGCTCCC	TCACCACAGA	ACCTTACACG	6720
AACACACGAG	cTyGtCCGCT	TATCCGGCCA	AGAACCATGC	TCCAAACTTA	TGTAGGGACG	6780
ACGCGCAAGC	ATTCCCTGCG	ACCACTCAAT	GAGCAACTCA	CATCTTTCAA	ACGGACTCAC	6840
CGCCACCCCT	ACCTGATAAT	ACAGATTTTT	ACCTGCGCGG	AACGTGCGGT	TCCTCTTTAn	6900
CGTTCCGGCA	GCACCACCTG	GTCCGTAAGA	AAAACCCtGC	GCACCATATG	TAGCGCCATA	6960
CAGCGAAACC	ATCGGTCTTA	TCCATGCGTG	AGcAGnCAAG	AGTAATCCGG	TAGTTAAGCC	7020
ACAGTTTCCC	CACAACAGGC	AACGCGCTGT	GTGCACCCGG	ATGGACAACA	CCGGGTGGAG	7080
GAAGCACAAA	CGCCTGAGGC	TTCTTTCCCC	GTGTGGAATT	CGGCGTACAG	GAGCCAGGTT	7140
CCAGGTACAA	GCCATGAGTG	AAAGGAATAT	ATAAAcGCGC	CTcGAcACyT	CCGCTCAGAC	7200
CGGACACAag	CTTAGAAAGA	GAATCGTACC	ACTTACTTTC	CACCCCG		7247

## (2) INFORMATION FOR SEQ ID NO: 144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AACCGnTTCC	CGTTGTGCTT	CTGCAATTTT	TCTGCTGTGC	TCGCTGCTCC	TGAACTGGCC	60
TTACGCGCGG	AGGCTCTCGG	CCTGTTGCGT	TGCCTTCTGC	GCAGTGTGAG	CCGCCTGCTG	120
AAGCTTCCCT	GTGCGCACGC	TCGGCGAACG	CGCTCCTTCT	CTTTTGCTTC	CTGCGTACGC	180
GnCCGGGTCC	GGTGAAGTTC	TGCGCCGCGT	GCTGAGCTTG	CTGAGCTTCT	CGGCGTGTCT	240
TGTCCGCGTG	TGCCTGGGCG	CGCTGAGCCT	GAGTGGAAcA	cTCCGCCGCG	CGCTCCTGCG	300
CCTGCTGTGA	CTGCTGTGCT	AGTTGTTGGG	CCCGGCGCGT	TCCTTCTGCT	GCCTCCCGCT	360



CTTTAAGGTC AATCATGTcC CTGCGCAGAT CAACGTTCCTT GTCCGGATCT TCACGCAGCC	420
GCTCCACCAC CCGCTTGTCa GAAATGGCGC CGGTGTCCAC TGCCTGAGT GCGTCAGAGT	480
CCCCGGAAAG GGAATGACG AGCTGCGTTT TTCCCGGCCA CTGATCGAAA CGGCGCGCAA	540
TACCGACGTG CTCGGGGGAG AGATGCGCCG TTACCACCCC CTTGTAGCGC GCCTTGAATG	600
TGGGAAGGTC TGCACGATAC ACCGCGTTGT ACACCGTTGT GAAGGTTGCT ATCGTGCCTG	660
CGTCCTGCAG GCGATAGCaT AGGCGGCAGA AAGATAGGCG GCGACGATCT CGCGTATGTT	720
GTCGATATGG TCCACCCGTG CCTGTGCGCC AATGATGAGG ATGTCTGCAT CAAAGCCATT	780
GGTCGTGTGG GGACCTAcTG CGTGAATAAG cGCGTAACGC gcACGATCCC CCGCAACACC	840
GCCGCGCAGT GCAGAGGCCA AGCCCTCCCC GATGCGCCTG ATAGCGGCGG CGCTATCTAC	900
GTCCGTGTGG GTTCCTGCAA AATTTTCAAA CTCTACCGTG GCGTTTGAC GCTCAAGCTC	960
ACGCGCATCC ACCTCGAGTG CAAAAAGACA GCCTGCGCCC AACACGGCAC ACATGGGCAG	1020
CACGTTCTTC ATGACCCTCT CCCCTTCTA CACCTTTGTT TTTGAATACC GCACGCCTAG	1080
ACACCTGAGA TCCCAACCTT CCTGCGTCAT CAAAGCCCCA TCAGCGTACA TnACTCTGAA	1140
CGAGAGTTCT TGCATAGGCC CGTATGGTGT ACGGGAAGC CCCCCTGGAG ATGCGGGAGA	1200
GTTCTGAGAC TGCCTTTTCA GAAAGGGTGC GCGGTGCACT GCGCGCGCAT GCAGCGAGTG	1260
CATCGCACGC TGCACGCATC AGCGACTCGG CGCGTGCGTC CTTAGCACGC GTGACTCGGT	1320
ACAGCGCAAG TAGTGCCCGC TCATCGAGGC CGAACGTGCA GCGGGTGAGC CCTTTGAGGA	1380
TACCTTCGAG CACGGTGTAG TCCTGcTCTT TGAGAAGCTC AAGGAGCGCG TCTCGGTATT	1440
CGTGTCGCC TAAGGCTCCT AACAGCGTTG CTGCCTGCGC TCTCCTGGCA GAGGTCACTG	1500
CAGGCGCCCG TGCGCGGGgT GATGCGGTGA AGTAAGAAGC GCGTGCAACG AGCGGGGCAT	1560
AGGCCGGTTC TCGAGGTcMT ACATTcCTTC CTTCAGGGAT GTTTGCACTG CCTGAAGGAG	1620
AAGCTCAGGG GTGGCGTACG GTCCGGGCGG CGACGTTGTG TCGTCTCTT GCGCGTTGTC	1680
TGTCTTTCCG CTGTTTTTTG CAGGAgCGGG GGAAGAGAAG AACGGGTCGG AaGAgATTGA	1740
GTCATAAGGC GACCGCTTAG CAGGGGCAGC AGGGCGAGAA GGGGAGCCT CTTGCACGTG	1800
TGCACGGCGT GAAGAACCGA GCACGTGAAA ATACTATCGC GGTGTATAT GGGCGTGTGG	1860
TCAATGAGTC TTGTTTCTGC ACGGTATGCG TTGAGTACCC AACCGCCTGC AGATACTACG	1920
AGCCCGTCCG TGGTGATAAG CGGAGTAAAC GGTGTTTCGT ACAGCGAAAT GTTCCACTTC	1980
AGCGCGCCTC CTGCGCTGAG GGTAATCGCC CGCGCTGTAT CGCTGAGCaT ATTTCTGCCC	2040
CCTGTACGCG GCACTGGGCA GCCGAGGAAA AGGTACACGG AAGTGTGAGC GAGAAAAGCT	2100

795

CATTTTCCCC ATCTGCGTCG TAGGCACGCA CCGCACCGTC TGCAAAAAGG GCGATGAGCA 2160  
 TGTTTTCAGT AGCAAAAAGA GCGACACAAG AGCGCTGTGT GCTGATGCGC ACCGGCACCG 2220  
 GCGCCTGGTG nCTGTTTCGCG GTCTTTCCCG CCTGAGTCTT ATCAGGCGTA CTGTTTAGCG 2280  
 TGTCAGTGCG CACGCGCCAC AGGCCCTGAT CCGTGGCAAC GACGTACCCG CGTGGGGTGC 2340  
 TCCTCAGCGC ACGTACGGAC CCTGATGCGc GCAGGGCGCC TTTTTTTTCT CCAAATATGG 2400  
 ACCAGTACTC CACGGTTCCT GCGGGCCCGT GATGAAAAT TCGCGCGTTT TTGCATCTGT 2460  
 CGGAGGAAGG AGGGGCTTTG CGCCAAGCTT CTGACTCCAC AGGCGCTGGC CGGTACTGCT 2520  
 GAAGCACAGC AGGGCGTGTG CgGTGGTGTA CAGCAGCCGT CCGTCTCTTA AAATTACAGG 2580  
 CGCGGTGCAC AGCCCCCGT TCGCCGCGTT CACCGCACGC TTTGCACCGC GCGTGGCAGC 2640  
 AGGCAGGACA GCAAATTCTC GGACGGGTAT GCCCTGGCTG GAGAAAACCC ATACGCGTCC 2700  
 GCTAACCTCG CTTACGTACA CGAGTCCATC GTCAGAAACG CTGAGAAAGG GAGTGCCGAC 2760  
 TACGGGGCAG TTTCTGCGCC ACACGAAGGA TCCTTTGGAG TTTACGCAGT TGAGGGCGCG 2820  
 ATCTGCGCTA AATGTATAGA TGAGCGAATC GTAACGCACC GGCTGTGTTA CGTTCTGCCC 2880  
 TGCAAGGACC ACACTCCA 2898

## (2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CACGATGTAC TGCATTCCGn GGCATGCCCA GGA CTCCGnG GATGCGCGCG TCAGAGGTGA 60  
 TAGCGGATAT CTACCCCGGC GGTGACAAAC TGCGCATGGC GCGTGTTAGT CTGcTctCTC 120  
 TctTCTTCAA CCACTTTTTT GCACGACCGG GGTACGCCGC TATATGCAGC ACTGGCACCC 180  
 AAGGACCAGC GCTCTGTCAG CTGAAGgTAA CAGCCGGCCC CTGCTTTGAG CAAAAGACCG 240  
 TAGTACGTAG ACGTGTAAGTA GTGCTGGTAG CTGAAGCCGG CCCCCACCGT CAGCGGCAGA 300  
 CGGATGCGCC AGAAGGCGAG CGTGTAAC TT GCATTTCAGCG TTACAGGAAC GGCAAGgTAG 360  
 GAACACAGCC GCTCCTTCTC GTAATAGAAC GGATAACTGC AGGAGTGCTG CGCGCTCGCA 420  
 TCAATCCCGA GCGACAAGCC GCGATACACA AAATACTCGT ATCCAAAAGA CACCCCAAAC 480  
 GCGGGGTAAA CTTCcTTATT CCCGTTGGCT GCAACGCCCC CAGATCCCCG CGGGCGGTAT 540

TGCACCAGTC CACCTGGAAA AGGGGCACCG CGCCAATAAA CGAAACGCGC GCGATCCCCC	600
GCCCCGCGnC GGTTaCATCC CACGATGCGG CAGGCGCCAC CTCCTGCGCA TACGCTGCAC	660
CCGCGGcAAC ACCCACCCCG CAGcGcAGAC CTGCAGAAAG CGTATCCCGT GTGCCGCGCA	720
CTGTTTTAGC TGTTTCATAC GTTTTTTCGC TCCACACCTT TCAAAAAGCT GCGGGCAACC	780
CACACAGCCT TCCAAAATTC TACCCCCCCC CGGCCAACAT TTGTCGAGTT CTTTTTTTGC	840
AGGAGGGTCG CGCCCCGCGC ACCACCGCTG cATACCCAGT GCGCGCCTGT AACATTCTGA	900
CCGGGGAGGT GTTTTCTCAC ACCGGGGAGG TTTTATGTGC AAACCGCGCG TGTGGCGCAT	960
CGCCCACACC ATCGTCCATG TAGGCGCGTT GCTGCTCGGC ACCAGCCAGC TGACAACCTG	1020
TGATTTCTCC GGCATTTTGT CCACCATTCA GCAGGAAGTT GCCATTAAGT CGCCGTCTAT	1080
TCCGGGGGCG ATTTATGGCC TGGTCAAGGC CGGGGATAAG CTCTATGCCA CCAACGGTCG	1140
GCTTTGGGAA AAGGAGCTGA ACGGCATTAA GTGGAAGCCG GTGCCTTTTC TTGACGGCCA	1200
AGATAAGCGA ATTGATAGCC TTGCAGCCAG CAACACGTGC GTATTTGCCT GTGTTTCAGG	1260
AGACGGTGTG TACAAATACA CCGCCGGCAC CACCTCTTCG CAGAAGGAGA GTAATACGGA	1320
TAAAGCGCAG GCGGTGGTAC AGATGTCGGA CGGAAAAGTG GTCCTGCAGT GTGCCTTGGG	1380
GGATGAAAAG ACGACCCCGA GCGACGCAGA CGAAAGGTTG CTGGGGGGCG GCCAGGGCTA	1440
CCTCGTCACA TCCAAGGGAT TTTACACCCT CCCAGGGTCA GCCTCCTGCG AGGTTATCTC	1500
CGAAACAAAG GACGTCACCT GTAAGGCAGA GGCGCCGATC CTCGCCAGCG CCTGCGATGG	1560
CAGCAATACC TATATCCTTA CCAAGGACAA GGTGTACTGC CGGTATACGA ACGGCTCAGG	1620
GAGCACCCCC aCTACGTGGT GCGACGTGGA ACACAAGGTA TCAGAGCCgc TTGCGCTTGC	1680
AGTGTTCAAA AATAAGGGTG AGACGTTCTT GCTCGTTGGG GGACAGCAGG GATACGGGGA	1740
AATAAAAATA GCCACGGCAA GCGGCAGcTC CTCTTCTTCC TCATGCGTTC cCCTCACGGC	1800
GGAAAACGTG CACGCCACCA CCGGGTGGGG CGCCAACCTGC TCCACCCCGG AAGGCAGCGC	1860
CGAGCAGTAT CGTAGTACGA TCGGCCGCTG GGCAGTGAGC GGTATTTACG TAATCAAAAA	1920
AGACACTAGC GGTGGGCGGA AAAAGCGGag CACCTCAACA GACTGCGAAA GACCAGACCT	1980
CTACGTGGCG GTGGGGGATG CGAGCGACAC CTACACCGGG CTCTGGAAGT TCGACACCGC	2040
TACGAATACC TGAATCGCG AGTGATGGCG CGCagCAGAT GcGTGCACCG CGTGGTGAC	2100
CAGGCAGCGT GCATCGGGGT GATAGGCCTG AGCACCAGCG CGCTGACCAC GTGCGATTTC	2160
ACTGGCATCT TTGTGGCCAT CCAGTCGGAA GTGCCCATTA AAACGCCGTC TATTCCGGGG	2220
GCGATTTATG GCCTGGTCAA GGCCGGGAGC AAGCTCTATG CCACCAACGG CCAGCTTTGG	2280

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AAAAAGAACG TAGCAGAAGA AGGTAAAGAC TGGGAGCGGG AGTCCTGTTT CCACTCGGTG 2340  
ATAGGCGACA GCCGCATCAC GAgcTTGCGG CAGACAACGG CGAGAATGGC GTGCTCGTTG 2400  
CCTGCATTCT TGGCAAGGGG GCGTACAAGT GGTCCGAGGG TAGCGCCGAC CAGACAAGCG 2460  
GAAATCCGTC TGCCCTGAGT GGCACAGAAA AAGCACTCAG CGTGGTAGGG ACCGGGACAT 2520  
CATGCGTGTA CCTTAACCAC ACGGATGATA AGGTGCGGGA AACCAGTAGT TCGGAAAGTG 2580  
GTGGAaTGcT GCGTCAGGAG AAACGAATGA GTTCTGCCTG CACGCCGGTA ACGGtTTTTA 2640  
GTTACCACCA AAAAGGTGTG TGTCGGTAGT GATGGTTCTC CCGTGGCAAA GAGTGATGGC 2700  
GAAGAACCAG TTCCGCCGAT TCTTGCGGCA ACTGAÇGACG GGAGCGGGCA CGTTTATATC 2760  
CTCAGGAAAG ACAAGGTGTA CTGCAAAAAA GTTAATCAAA GCGAAGGGAA AATTCAGGAT 2820  
TGCCACAGT CTGCCGAGC AGCGCCGGAG CCAACCGGGG CACACAGTGT TGCCATAAG 2880  
GTAGCAGACG CGCACTCCAT AGCGTTCTTC AAAAACGGCA GCGACGAGTT CTGCTCATC 2940  
GGGGGCCGGC AGGcTACGGA GAGATAAAGC TGGAAGAGG TTCAGGAAGC AACGGGAACG 3000  
GAGCACAGTG CGTCCACCTG AAGGAAGAGA ATGTACACGA TCAAACCGGC TGGCATGAGA 3060  
AgGGCTCCAC CCCGAAAGGC AGCGCCGAGC AGTATCGTAG TACGATCGGC CGCTGGGCAG 3120  
TGAGCGGTAT TTACGTAATC AAAAAAGCA CTAGCGGTGG GCGGGGAAAG CGGAGCACCT 3180  
CAACAGACTG CGAAAGACCA GACCTCTACG TGGCGGTGGG AGACACGAAC GATACGTACA 3240  
CCGGCTGTG GAGGTTTGAC TCCGCCGCGC AAAAGTGGA CCGCGAATGA GTGGCTCTAA 3300  
CCtACGCTTC CCCTACTCCC GCGCGTACGG CGGGGCAGGC GTAGGGCGTA ATTTTGAAAA 3360  
ATCGAGCAGA TTCTCAGTAC AAAAAGAGGG TATAGGTGCG CCGGTTCTcG cGChGTACCG 3420  
CTTTGCAGTT CAAATGTTTT TTGCTTTCCC GCCTCTTTTT TATTTTTACG TCACATATTC 3480  
CCtAGACGGG TGGGGGGGGG TGAGGTAGAA GTGAGAGGAG GGGGAGTGAG TGGGCAGGCA 3540  
GGTGATGCAA GCGGGGkyAC TTGCGGGCAT GGTATGTGCT GCTTCTGGTT ATGCAGGCGT 3600  
ACTCACTCCG CAGgTCAGTG GCACAGCCCA GCTCCAGTGG GGCATTGCGT TCCAGAAGAA 3660  
TCCACGCACT GGCCCGGGCA AGCACACCCA TGGGTTCGCG ACTACCAATA GTCTGACTAT 3720  
TTCCCTGCCG TTGGTGTCAA AGCACACCCA CACCCGCCGA GGGGAGGCAC GCTCAGGGGT 3780  
GTGGGCACAG CTGCAGCTGA AGGACCTGGC AGTAGAGCTT GCGTCTTcTA AAAGCTCAAC 3840  
GGnCCTGTCC TTTACCAAAa CTACCGCTTC CTTCCAGGCA ACCCTGCACT GTTATGGGGC 3900  
CTACCTGACA GTGGGTaAG TCCTTCCTGT GTGGTTAACT TTGCCAGCT GTGGAA 3956

(2) INFORMATION FOR SEQ ID NO: 146:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

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GGAAAGCACT GCGTACTAGT GAAGCTAACG CGGAGACTCC CGCGAAAGTC AAGAAAAAGC      60
GCGCCTTTGC TCGCTGGGAT ACCAGAGAGG ATAGCTTGGC GGGCGAAACC TTTTTTTTCC      120
GCTTCTGGAT TGGGGTAAAG TCCTTTTTTC GGTCTTCGTC GGTGGAAGCG TTGTACGAGG      180
AAACACTTCT CCAGCGTCTG GGCAATGATC TTAAGGCGCA TTACGCGCAG TACATTGACG      240
TAAAGGAAAA AACCTTCACA AAGGTTTTTT ACGACAAGAT GGGCGAGTTG CGCAAAACAC      300
AGGTATTTTT TGATTCAATTG CTCGCCTGCT ACAATAGCGA TAAGGGGGAC TTCTACCTCC      360
TGTTGAGCTC TTTTATCACT CCCGTTGTGT ATGAGCAGCT GATGGCGTGC AGCGATCCGT      420
TTGCTGCGCA GGGAGATGGT ACTCCTTCTG GTTTGCGTGC GTCCCTCCTT AAAAGAATGG      480
ACGTCGCCCT TGCCACCCTG AGTGGTCCTC ATAAACTGA GTTGATCAG GCGGCGCGCG      540
CTATCGAGTG GATGAAGGTT TTTGTGAAG TGCCTGTCGA TCGTATTCTG CTGCGTTTTA      600
CCGTCATCTC CCCGGCGAGT GCCGTGTGTC CCATTACTAT TTTGCAATCT GAATTGAAAA      660
AGCTTGCGTG TGTATCCAT GACAGCAAGC ATATTCCCGA CGCGGTATTG CAGGGGCTTT      720
TTGTGCTGAA GAGTAAACA TCGCTGCATG ACGCGCAGGT GGATAACGCT GCGCACGCTG      780
CTGCCTTTCT TAAGGAGGCG AGTGCAGCGC TCGTTGTTAT CAAGGATTTA TCGCACAGCA      840
TTCCTATTGA GGATTTTGTC CGTTTTCAG GTAGGAACAT TCGTTGGCAA CCTCGGGCAA      900
TTGCCGGTGG TGAGGATTGG TTTGTCCTTT TTAAGAAAGC GTGGAAAAAA CGTTTCAATG      960
AAAAATGGGC GCTGTGGTCT ACCGCACAGA AGCGTTTAGT GCTTAAGGAG CAAATGCTTT      1020
CTCTTCTCGG AAGGGAGCAG TTCTCAGAGT TGAATCATCG GCCATGGGAA GGGTTTTTGGT      1080
ATCAGCTTGT GTTTAGGCGA GAGATGTCTT TTGTCTTTTT AAAAAATTTG TTCGAAGgTG      1140
CGTATGCGCG CGTCGTTTCA CCGCCGCTGA ACGTTATTCT TGCTGAGGGC AGTTTCTATC      1200
GTCGAGATGA GTTGATAGAG TACACTGACG CGGTAAATGT ACTGGAGCAG ATGGGAGCAA      1260
AGATTAGGAA TTTCGAGGTA AGACTTTCGC CGGTGGGGGA ATGGGGAGTC GCCT      1314

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## (2) INFORMATION FOR SEQ ID NO: 147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs

799

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GTCGAGTATT TCGTTTGAGT AGGTAATTCC TCCTTGTGTG TTGTCCTGTC TTGTCGGGGT	60
GCGAAACATC AGATTACAGA ACTGTGTTTC AAGCGGCGAT ATGCGCAGTA TTTTCTGTTC	120
GAAGTGTTTA GAAAGATATG TCCCTCGTGC ATATGGCTTT CCGTTGGTGT AGGAAAAGTC	180
TGTTCCAACA GAAGTGATAC GGGTAAACCC TAGAAAGGAA GCCACCGAAT AGGCGGCGCC	240
AGCAACCGTT nCCCCGAAC TA GTTTCTAAAA AAGGTAGGGA AGAAAAACGA CTGCGTATA	300
CACTAAAAGG GTGACCTCCT CCGGTGAAAA TAAGTGAATT ACCATTCAAA TAAAAACTGC	360
GTACTGCGCA TGGACACGCG CATATGTCGA ATATTGCAGT TACCTGTGAA GGAATGAACA	420
CATAGTGTGT GGCATACGAG ATGTATTGCG GATCAATGCT GATAAAAAAA TCTGGCATAA	480
GACCGCCTGT GCAaCACACG GGAAAAGCAG TATCGCATGC AAAAATAGTG TACACATCCC	540
TATGTGAACG TATTTTTTCA ATACCTTTTT CAAGACTTGG CCCTGCACCT AATATGATCG	600
CCTCAGTTTG TGTATTGATG TTCGGTAGCT TTGGTGTGAA TATCTGTGCA TATCTTAGAT	660
TGAGTAATGC GTTTCTCATC CAAAGCTTTC CAAAGTGCAC TTGGACTGAA AAGTCGGCAC	720
GAATGATTTT CATTGCTTGG CTGGTAAGCT CAGCGATCTT TTGTTGCTT GTGGGAAAAA	780
ATGCCTTCCA GGGTTGTAGA TAGTGAACAA AAAAATTGCC GTGGATGATG GGCATATAAC	840
ACTGTGCAAT TTCTTGTGAT GCACTACCGT GGGTGAGCGG ATGAAGAAAG TGGACGCGTT	900
CTTGGACGAT AATATGCGTG AGGTCCACCT GGCTCCAGGA GTGCACGGAA ACTCGCGTAA	960
TCAAATTCAC ATACCGCGCA cATGCGTGGA CGAAATTTTT CTAAGAAAAC ACTGATGTGG	1020
GATACCTGCC CCGATGCCAC AAAAAAGAAT GGAAGCAT	1058

## (2) INFORMATION FOR SEQ ID NO: 148:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

TGACCGGCCA GCAAAAGGCT CATGCTCAGG CCGGCnCCGT TGCAGGACCG GGCTCGTACC	60
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800

CCGnTGGGTG CCGGTTTATC CCCCACCAG GGTTTTTTGG ATGAAGTCTG CCGCTGGCCA 120  
 TTGCGTGTG ATGGACAgTT TctGGCGATT GGCGAGCctT TTTTACGCAA GArTgCgGTG 180  
 CaCGATGTGA CAGCGTTCaT TGATGCrCAC AATGCgCGCA AAAGGGCGCC gCGTGCCCCg 240  
 CTGTTGGTTC CgGAcTTTtTA GCTGTCaTGG GGAAAgCGAA TTTATATGCg CGTATTCGTG 300  
 TCTTGGCATA AGCaAAAGGA TAAGGGGGaG CGCGAAcGCg CAGGTGCGCT GCaGGGAGCG 360  
 TGCATAGGTA CGCCTGAGCA CCGCCAGtTT TTGCGCTGGT AGGAAGAAGT GGCAGCGGAA 420  
 AGAGTTTTCG TGCGCAGATA GTGATGCGGC GTTTTGATAT AGCGTTCGTT ATAGACGATG 480  
 GATTGCTTAT TCGTGAGGAT AAGATTATTG CAGtCGCTCG GCAAAGCAGG AAAGGACGCT 540  
 GCTtGCGGCC ATACGGGTG CGCTCTTCGA GAACACGATG CACCGTCGCG TAtTGCCCGT 600  
 GTGTTGACGT ATTTTCTGTG TGGGTCACAG AACAAAAAGG TGCTCATTCT GGGGACTTCA 660  
 GAGAGGATGG TGCGCAGAAT AGCCCTTCGT GTGGGGCTTC CTGAACCTGG GCATATCATC 720  
 CGCATTGAGG ATATTGCCTC GAGCGAAGAA ATTGCCTcCG CgCgCaCACG GCACGTGaGG 780  
 GCACGCACGT CATTCCAGTT CCCTCTGGGG AGGTACGCAA GAGCTATCCT AAGATCTTTT 840  
 ATGAAAGGAT AAAACTCTTG cTGCgTAGAG AGGCAGGTGC GGAACGAATa GGACGGTGGG 900  
 CGCACGCCAT ATGGCATGAG GGGCTCAAGC GTGcGTGCAG CGGCGCGCAC cGCATGtATT 960  
 TGAAAAATCA ATAGTGCgTC CACCTTTCTC ATGCAATCTG CGCGTGGTGG CGGCGACAGA 1020  
 GGGCACACAG GATGCGTCGC CTGTTGTGGT GCCGCTCAC GAGGAGCTCG CTCTCCAGCA 1080  
 GTAGGAGAGC GATGACAGGA GAGGCAGTAG TTTGTCCCGT AGCGTGTGGA GCCGGAnGGT 1140  
 CGAAG 1145

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TAGGAGTTTG TTTTCTAGAA nTTGTTTTTC AATAAAGGGC CGGTTCTAAG TCACGCTCTC 60  
 CCTTCTGCCG ATAGAGGGnG CGGAGGTGGG GATGCTATGG TGATGGCCGC GGCGCCTTTA 120  
 CAGAATTTGT GTTACGACGG ACTTTTACAG GTAACCTCAG GGGGCAATAT CTCGCTCCCT 180  
 GtACCCTCGA ATCAGGTGAT ATACGCTCAT TTCGAACATG TTGATGCGAC TCCTGCGGAg 240

801

cGGAGrCAGG CAGGGGTGTC GGTGTCTGAG CTGCAGATTT TGGACGCGTT GGTCGAGCGG 300  
CTGATAGTGC AGCGTCGGGT AGCGGCAGAA GCGGCAGACA TGGCGGTGCA GAAGCGGCAG 360  
GAGACACTGC TCCGCGCCGC AGAGCTTTTT TCTCAGAAGC AACTGGACGA GACCAAACGG 420  
CGGGGAGAGT CTCTTCCTTA CACCTCAGTA GAAGTACAGG GGCCTGAGCT TTTTGACTTG 480  
CGCGCGTAGG GCACGTGCAG GCAGAAGTAC TTGACTTTTT TGAGGATAGG GGGGAGACCC 540  
CGCCTGGCCG GAGTTCTGAG GCTGGGTATG GACTCTTTTG GAGAGTGGGG GTTGTGTGGG 600  
TATGAGAAGA TTGCTGGCAT GTTCGGCGGG GGTGCTGTGT TTTTCCCAGC TTGGCGCGCT 660  
TGAGTTGTTT CTTTCTCCTA AGATTGGGAT CACGAGTGTG TATCAGTTTG GGAGTAACGG 720  
TGTTTCGGAC GGTACgTCGT CGGGTAAGGG TGTGTCTTTT GATAGACTGA TTGGAAGGGT 780  
TGACCTGGGG CTAATTTTGG TGAACGGCCT AACGATTTCA GCTTCGGCGG AAAGTTCGTT 840  
GACCAATGTC TTTGTGCGTG 860

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TAAAAAAGGT ATGGATGACT TGTGACTAGG AGTGAAAGGC TAAACAAACC TGGAGATAGC 60  
TGGTTCTCCC CGAAATGCCT TTAGGGACAG CCTTATACAA AACTGTCGGA GGTAAGCAC 120  
TGGATGGGCT AGGGGGTTTC ATCGCCTACC AAACCCAATC AACTCTGAA TGCCGGCAGT 180  
CAACGTGTGG GAGTGAGACT GCGTGCGACA AGTTTCGTAG TCGAGAGGGA AACAGCCCAG 240  
ACCGTCAGCT AAGGTCCCGA AATACCGCTT GAGTGTGAAA TGAAGTGTGG GTACCTGGAC 300  
AGCCAGGAGG TTGGCTTAGA AGCAGCCATT CCTTGAAAGA GTGCGTAATA GCTCACTGGT 360  
CGAGTACGCA TGCGCAGATA ATGTATCGGG GCTAAGCGGT ATACCGAAGC TACGGGTCTT 420  
GCATTTTTTG TGCAAGGCGG TAGGGGAGCA TTCCATGTAC TGATGAAGGA ATATCCGGGA 480  
GGAGTTCTGG AGGGGATGGA AGAGAGAATG CAGGTATAAG TACACGAAAA GGAGGGTGAG 540  
ATTCTTCCC GCCGAAAACC TAAGGTTTCC TGGGTGAAGG TCATCTGCTC AGGGTAAGTC 600  
GGCCCTAAG GCGAGGACGA GGGTCGTAGT CGATGGGAAT CCGGTTTATA TTCCGGAACC 660  
TCTTGCAATT TCGATGGCAG GACGCGTGAG GTGAAGCCCG GCCAAAGATT GGTAGTTTTG 720



GTCTAAGTAT CCGAGCCGTT TTAAGAGCGA TAGGCAAATC CGTCGTTCTGA GGTAAGGTGC	780
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GTCTAAGGTT AGGTTGCAAG AGACCGTACC GCAAACCGAC ACAGGTAGGT AGGATGAGTA	900
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GGAGAAGTGT GACCCTTGCC TTTGGTGAGG GTGGCAGAAA GCAGGTCCAG GCGACTGTTT	1020
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CGACCCGCAC GAATGGTGTA ACGACTCTGG ACGTGTCTC GACGCGAGAC TCGGTGAAAT	1260
TTATGTACCG GTAAAGAAGC CGGTTACCCA TAGTTAGACG GAAAGACCCC GTGAACCTTC	1320
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CTTGGCCGTC AGTTAGGCG GAGTCAACAG TGAAATACCA CCCTTGGTAC GTCAGGTTTC	1440
TAACCTTTGG CCGTGGATCC GGCAAAGGGA CCGTGGTAGG TGGGCGGTTT GACTGGGGCG	1500
GTGCGCTCCT AAAAGGTAAC GGAGGTGCGC GAAGGTCTCC TCACACCGGT TGGAAATCGG	1560
TGCGCGAGTG TAAAGGCACA AGGAGGCTTA ACTGCGAGAC CGACAGGTCG AGCAGATACG	1620
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GGTACTCCGG GGATAACAGG CTGATTTTCC CCAAGAGTTC ACATCGACGG GAAAGTTTGG	1740
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CGCCAAATTA AGCGGTACGT GAGCTGGGTT CAGAACGTCG CGAGACAGTT CGGTCCCTAT	1860
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CGAACCTCTG GTGTACCAGT TATCCTGCCA AGGgTACGTG CTGGGTAGCT ATGTTCGGAA	1980
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## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TTTCATACG CTCGCTCCAC ACCTTTGCTT TCTTTTTTAC CTCCTCTGCA TCTTGTCGCT 60  
 CGTTGAGCAA CAGGTGGACC CTGCGCAGCG CGTGCAAGTA GCAGACAGCC AATTTAAAAT 120  
 CTTCAAAACT GGAGGACGTC ATCTCATACT TTTCCCGGTA ACGCTCAGCT GCCTGCAGGA 180  
 GTAATTTCTT TACCAAACGC AGGTGATAGA CCACTGTCTC GTACTCGTCA GCCTGTGGAT 240  
 TCAATCCAAT CTCAGAAGAA TTCGCTAAAT CCAGAATATT CTTGCGCCACC GTTGCCTAgc 300  
 GCGCCTGGAG CTCTACAAAA GACCAATACC ATTTAGTATT CGTCCCATAG GCGCTAATAA 360  
 TGGAATCAAT GCGGAGTCCC ATCTTACGGA TAAGATAATA ACGCTGCTGC TGACTTACGT 420



810

TCGCTATCTG CGCCACCTGT TCCTGGTAAT CGGAAAACGG CGTGTC AATT AAATTGGTAA	480
CAATTTCTTC AAGATAGATG AGCGCCTTAT AAAGCGTTTT CCGCGCCTCA TTCAGCAGAT	540
CCTCCTGCTT ACCACCTACT ACTACAACCT GTGTCTGATA TTTAGCAGCG TACAGCGTAC	600
TGAGGTAAAT CATGTCATCT ACCAACCGGA GCTTCTTGTA CGCCGCGCCC GTCCCATCCC	660
GCCTGATCAG TTCTAAAATG TTTTTCAC GCGTAAAGAT TTGATCAATA GTCCCTTGGT	720
ATACGTTCAA CTTTTCTGG TACAGAGCAT TCTGCTCTTC CTCAGTCACC GCACTCCCCC	780
CTTCTCTGCC GCGCACCTGC GGCAACAACCT CCTGCGCATG CGCTAGGGAG GTTGCACTGT	840
GCGTGTCGCC TGCTAGCATG CGCGCAACTT CTTGAACCCG TCGTTCCCCC ACTACATGCG	900
CCGCGCTCGT ATTCGTGTGT TCTCCACTCG ACTCTTTTTT CACACACAG TGC GCATCCG	960
CGTGCGCCGC TATCATAGCC AAATGCGTAA TGCACACAAC CTGCTTGTGC TCAGACAACG	1020
CTTGCAAATG CTCTGCAACC GCACGCGcCG TTTCACCTCC AATTCCCACA TCAATCTCAT	1080
CAAAAATCAA CGTGCCCACT TCATCGACCG ATGAAAGCAC AGTCTTTAAA GCAAGCATCA	1140
CGCGGGAGAG TTCCCCCCT GAAGCAATCT TTGCTAGCGG ACGCGCAGGC TCTCCTGCGT	1200
TGGCGCTAAT TAAAAACTCA ACGTCATCAA AGC	1233

## (2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GTAAAGCAAA ATCACTCAGG ACAAGACTCA CTTCTTACTT TCGCTGCAGG CACGACCCAA	60
AGACACGCGT GCTGATGTCG CGCGCCGCTG CACTTGAATA TCTACAAACA CAACACGAAT	120
ACGAGGCGCT GCTCCTTGAG AACACACTCA TAAAAAAACA TACTCCGCGC TACAATATCT	180
GCCTCAAAGA CGGGAAAACC TATCCTTTGC TCAAGCTAAC CTGCGAGCCA TTTCCGCGTA	240
TTTTTCGCAC ACGCCAATTC TGTCAAGACG GTGCACGGTA CTTTGGTCCC TTCCcTGACG	300
TGCAAATCCT CGATTCTTTT CTTAAACTCA TTTTACGCAC CTATAAAATC CGTACGTGCA	360
CCACcTTGCG GAAGAGAAAA AATCCTTGCC TCTACTATCA CCTGAAGCGC TGCGATGCCC	420
CGTGTGTGTT ATGGGTCTCT CCACGCACAT ATCAAAAGGA CATACATGAG ATTACCCTGC	480
TGCTCGAGGG GAATATTGAC GCGACTGTAG CGCGTCTAGA AAAGCGCATG AAACGAGCAG	540

TCCGCCAAGA AGCATTCGAA GCTGCCGCGC GCATACGCGA TGATATCCAG GCAATCCGCT	600
GTATTACACA CAAAAGTCTT GTTCAAGACA TGGACGAACG TGCACGCGAT TACATCGCCT	660
GGTCGAGCAC GGGAGCAATC GTCACCTTCG CCGTTCTACG CATGCGGGGA GGAAAATTAA	720
ACGGTAGAGA ACTTTTTCGC ACACGTTTCAT TAAAAAATGA AGAGGAAATC CTTTCAGAAT	780
TTCTCATCAC TTACTACTCT GACCATACCA TACCCCCACA TCTATTTGTA CACTCGTCTG	840
CAGGGTTAGC AGAACACTGG CTCAGCCATA AAGCAGGTAC ACAATGTACC GTCACGCTCA	900
TCCCTTTGCA TACCTTTCTT ACGCCGCGA CCCCTTCTTC CACTGTCACC ACAAACGCTC	960
CTACCTTTCG AGCTTCGCAA AATAGCAATG CAGTACAAGA TTCAGGGTTA CGTTCTTGCA	1020
GCGAAACGTC CACCATGCAT ACGCTTCAAA AAGCACACGA CGCCTGCACT GCAAGCGAAG	1080
GCACACGAGA AAACACACCG CACGAGAGCG CGCACACTCC TCATCACCGC GCCATTTTAG	1140
CCATGGCGCA GTTAAACGCT CATGAAGATA TTACTCGGTA TCTGAAAAAT CGCGGCGCTG	1200
ACGATGCACT CAAGGAATTG CAAAAGCAAC TGCATCTTGC ACGCATTCCT ACGCTCATTG	1260
AAGGATTTGA CATTTCCCAT TTGGGTGGAA AGTACACTGT CGCAAGTCTC ATTTGCTTCA	1320
AAAATGGGGC CCCCAGACACA AAGAACTACC GATTGTTTAA TTTACGTGCG CACGACACCC	1380
GTaTTGACGA TTTTGCATCG ATGCGCGAAn AATTgCCCCG CGTTATACCC ACACACCAGA	1440
GGGCTACACT CTGCCCCGATC TTATCCTTGT CGATGGGGGG AATCGGTCAC GTTCTGCTG	1500
CACAGCACGT CCTCGACGCT CTTGGTCTTA GTATCCCGCT TGTAGGTCTT GCAAAACGCG	1560
CAGAAGAGCT ATTTATCCCC AATTCTCCTA CACCACTAGT TCTGGATCGT CGCAACCyTG	1620
CACTGCATAT GCTgCAACGC ATCCGAGATG AAGCACACCG cTTTGCAATC ACACGGAATC	1680
GGCATCTACG CACAAAGAAA GAGCTAGTCT TAAGCTTTGA GCGTCTCCCC CATGTGGGCA	1740
AAGTGCGCGC ACACAGACTG CTTGCTCACT TCGGTTCGTT CCGCAGCCTG CAGAGCGCAA	1800
CTCCCCAGGA CATAGCGACA GCCATTCTATA TACCGCTCAC CCAAGCACAC ACCATCCTGC	1860
ACGCGGCAAC CCGCTCAACA ACCGCCCCTG TACGAGAAGA ATATAAAGAA CACGAGCACG	1920
ACCCCCAGGG AGAATCACCT GGACCAGGTC GGAAAACAGA CTAACGCGCA CCCGGCCTAC	1980
GACGACGCAT CCAGGAGTCG CTCAAGCTCA TTCTTTCCCA GAAGCTCGAG CGGACGATTT	2040
TCTGCAAACG AAAGCGCAGC GcgTGAAAAC GAAGAAGACG TCACCACCAC CCCACGCGCT	2100
ATACCACGCT CCTTCATGCG CTCCAAAATA GCGCGCAGGA AGCTGTCATC GAGCACCCGC	2160
GCTTCCCGGT AAAAAACAAC GACTTTTGCG TCGGTACGCA CGTTGCTCCA ACCCTTCTCG	2220
TCCCTTTCTG TGGCCACTAT TTCACAACAC CCGCGCACGT CCTGCACCGA GTCTATGGAT	2280

812

AAGCGAAGCG CcTTACTCAC AATTCGCTGA CACAGATCGA AAAAGGAATC GCCATCGAGG	2340
GTCAAATACT CCTTCATCCG GTCGTTCAAA CGTATATCCT GATATTGCGC GAGcTTATGG	2400
TCACATCCTT AAAACCCGCA GACCGTGCGT TGATAGCCTC CCACTGCTCA ATTGCCTTTT	2460
CCACATCCCG CTTTTTTTCG TAACAGGAGG CTAAGAGATA ACGTATCTGC AAATCCTCAT	2520
TTTCACCCGA CTGCGACTTG CAGCGCAGCg cAcGGTCAAA CTCAACAATG GCCCGATCCA	2580
CATCCTTCGC ATCCATGTAG CAACAGCCAC GCTCGGTAAA ACACTTCTGC CGCAGCACAG	2640
GA CTCTCGA CGCTTGCTCA AAGGAGCGAA GTGCCGCCGC ATACTCCCTT TCTTTCCGCA	2700
AGAGCTGCCC CTGGCAAAAAG AGAGCCTCCG CATTTCAGG TTCCAAGGCT AGCACAGTAT	2760
CGAGCTCTGC CCTTGCTTCT GCAAGATGAC CAGACCGAAG AAGCAACGAA CCGAaGCGmr	2820
CATGCGCTGC AGGATGCGCA GygTCCATAC CGaTGCACTG GcGATAGTAT GCCGCAGCCC	2880
GATCGGTAC ATTCTTGCGT TCAAACAGCT GCCCAATACG GTAGTGATAA TCTGCACACG	2940
TAGGGT	2946

## (2) INFORMATION FOR SEQ ID NO: 153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

TACTGAAAAA CCGACCCGAG TAGCTGCCTC CCCATAATT CCcGTAGACC aTAGGCTGAa	60
TAAGGATGGC AACTCCaTCT TCCCCaTCCT CCTCAAACGA CaGCAGTTTA CTAACAaGCC	120
TTACCGCTTC TTCAAGCTGA ACGTAGGCAT CATCGAAAAA GCCGTC TGGA aGCAAGGCTC	180
GATACCGATT CATCGCCTCG CGCCCAGAGG GAGAAGATTT TCCTCCCTGC AAAAAAACCT	240
CTATTTCCCTT CAGGGTTTCG ACAAACCTCCG AAGCACCCCTT GGTGTTCTCC TCACTTTCTG	300
CGATACCAAG CAATACCCCA AATACACCCT TCAAAAGGAA GAACACCTCG TCGTTGCAA	360
AATGCTCCCC GACACGCTCG GCAAACCCCG CGAAAGTATC CCGTGTCAAA CCAAAGTTAT	420
GTAATACCGG ATAATTGCAA ATGGCCAAAT TGGGGGATAA AACCACCTTG AGGAGCATAG	480
GATTCTTTGC ATCCGCATAC TCTTTTCTGT TTAAAAGCGT AAACCTTCCTT AAATACGGAC	540
TTAGCGCGGA CCGAAGCTTC TCCCCATACA GACTACGAGA GACTGTCGCA TCAATAACCA	600
CGCTCGGAAG CACGGGCAAC CCCAGACTTG ACAACTCATC CGCCTGACGA CCCCGAATCC	660

813

CCAAAAGCCC TCGGTCAAGC CTCTTATCGA GAGCCTCTTT ATTGCTCAGA AAATGAATGG 720  
ATTTGGCAAT GTTCATGTGT CACTCCTAAA ACAAATTCAA CACCGTGTCT GGGGAACCGT 780  
GCAAAAACAC CTCAAAACGA GAACTCGCCC CCTCCTTGAA ATACTTAGAG AGCTTGGACA 840  
AATCCTTAAT TTCCTCACCT GAACTGCAA ACTGAATCAC ACTCCCGTGC TTCACCTTTC 900  
CCCATTGAA GAGAGTGTTA ATATCCACAA TACGCTCACC ATCGTAGAAC ACAATGACCT 960  
CTGAAGAAGG GTACCGCGCG TTGTAAGTCC TGATAATACG CTTCCACGCT TCCACATTCC 1020  
CGTTATGAAA CAACTCGTTA GAAACAGGCA CCGATATTAA CTGAGACATC CGAATCGGAC 1080  
CTGcAGAGGC TTGAGCAGGA GGACGCGCGG TAGGAGACAC AGACTCAGAC GAAGCCCGAT 1140  
CACAGGTAGC CCCTTCAGAC GCCCTGGCAG CGTCCGCACC CGACTTCTTT GCCGATCGAA 1200  
CCCTCTTGCC AGAACCTCA GACTTTTTCG TAGACACAAA TGCAAAAACC CCCGAAAGGA 1260  
TTTCTTTGGG AACCACGAAC TTACGATTCT CTATCAGAGC AATCAAACCC TTGGCGrctT 1320  
CGTCTGCAAT CCGTTCATCA AGCGGTCCCC TATCCTGCTT TCCCACGTAC ACCAACAAGA 1380  
GCTCATTTTT CCGAAAACCC TCGACAAGGG AGGCGTTTGA AGGATTCTTC GGGTTTATTG 1440  
CCAAAAATCC AAGATCGGGG TGATGATAAC CAAGTACAAT ATCCACTCCC TTCCACCGCG 1500  
CAGTTTCCTG AGCAAACCCG AGACCCTCGA CGGAAACCTT CCTTAGATTG TAAGAAAACA 1560  
GCCGATACCC CCACGTGTCG ATGAGTAGCA CCGACAGGAG CGCTGCAACC TGCTCGCTTT 1620  
GCATCTCctT CGCACAGAGC AGCAGGTTGA CCTGGTCTGC GACGTTATTG TTCGGATCAC 1680  
ACTCATCCAA CACGCTCAAA ACGCCCTTCA CATGACGCAC TAGAGCATTA AAGTTCTTCT 1740  
TCACCGCTGC AGGCACGTAA AAAGTAGATG CACTCACCAC GTAACACTCC TTTGATGATT 1800  
AAAAAGCTCC CCGAAACAGA AAAGTTCCAG GGAGCTTCGG ATCAGACAA AGTCTATCTA 1860  
CAATCTCGCT AGAGTTCGCG AATGGCAGAC CGTCTACCAC GTCGA 1905

## (2) INFORMATION FOR SEQ ID NO: 154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGGATCTTTT CCTCAGTCAA CTCCAAACGA TCTCCATCTA CATCCAGATA CAGCGTCGTC 60  
CCCTCGAGTA TCTCCTGAAT TTCTGCAGAA GACAACCGCT CAATGCTGAG CGCTGCACGC 120

814

TTTGTCTTCG ATCCAAGCTC TTTTCCGAGC ACTCTAAAAT TCGCTTTTGC ACGGTACTCT	180
ACTATCTCGT CTTCTTTCTC ATGAAACACG AGCTCTTTTA CATTAAGCTC ATCAAGCACA	240
TCTTCTTCCA TTTCAAGAAG TGCTGAGCGC TCCATCGGGT TACGCGTAAT AACCTGCATA	300
GCTTTAAGTG GCTGGCGTAC TTTGAGGTTA CACTGCGCTC GGATCGCACG CGCCATAGAA	360
ACAACTCGCT GCACTGTTTC CATTTTAAAC TCGAGTGCAT CGTCTCGCAC CATTGGTGTA	420
CAAACAGGAT AGTCTGCAAG ATGCACAGAc TGCACATCAT CCGCGGCGCG ATTATTCTGC	480
CATATACTCT CGGTGATGAA TGGCACCACG GGAGCAATAG CGAGCACACA TCTTTTCAGC	540
ACGCAATACA ACGTGTGTGA CGCACATCGT TTATCTTCAT CGTTGATGCT TTTCCAAAAT	600
CTCCTTCGAG ATCGGCGGAT GTACCAGTTG TTCAGCTGAT CTACATACGA AACGATAGGA	660
TCCGCAACTT TCGATACATC GTAAGCATCA AGTGCACAGG CAATGTCTTG CACCAATTTT	720
TCGTGCAGCG ACAAGATCCA ACGATCTAAC GGGTTATTCA AATGCGTCGC TAAACGCGTG	780
ACCGCCTGaC CCATTcCGTc AACTTTTGCA CATAcAGGcA GGATCGATAC CATCGATGTT	840
CGCATACGTA ACGTAAAAAC TGTAACtATT CCACAATGGG ATAATCACAG TCTTCAAAAT	900
ATCTTTcACC CCTTCGTCAG AATATTTTAA ATCATCCGCA CGGACAACCG CAGAACGAAC	960
AAGAAAGAGG CGGACGCGTC ACACCGTAGC GATCCATGAC TTCATTGGA TCCGCATAAT	1020
TGCGCAGGcC TTGGACATCT TCTTTCCATC AGACGCAAGT ACCAACCCCG TAACGATACA	1080
GTTTTCAAAC GCAGGACGCT CAAAGAGTGC CACAGCCAAG ATGGTAAGGG TGTAaaACCA	1140
CCCTCGCGTT TGATCTAACC CTTcAGAGAT AAAATGAGCA GGGAAATACC GcTCAAAGTC	1200
AGTTGcATGT TCAAACGGAT AGTGcTGcTG CGcATAAGGc ATTGcACCAG ATTCAAACCA	1260
ACAATcTAGC ACCTCAGGkA acGCGTCGCA TcACACTCCC AcAGGsGcAA GGaATTGTTA	1320
CCATATCTAC AACGTGcTTA TGCAAACTCTT CAAGCAACAT GCCGGrAgTT	1370

## (2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATGAGCGATC TCTTTTTTAG AAAGAACCTG TCAAAAGGAC AAACGGAGCA TAATGCACAT	60
CGTAAGAGGA AAATAAAATT TCTGTAGAA TCGGATTGAC AACTCTCTAT GAGGCTTTGA	120

815

CGCATATTTT AACGTATGAA GCGTCTCTTT TATTTTCTGG ATGGACATmC CTTTGTAA	180
AAAACTCTGA TGATCAAATA ATTCAAGCGG TTCTCTCAAC TCGAAAGAAT CAAGATATTC	240
AGAAACCATA AGTTTCATTT CATGAGTGAT AGTATATACA ACCGGTTTTA TArGAACCCA	300
CCTGTCTTTC TGCCAATGTG CAGTGTGTGC TTCGATAaGC TTCTGAATAG TACCGTTACT	360
ATTTTTCATA ATAACATAA TATCAACGAG CACCTTTTGT CCTCTGTGAT ACGCACCCGC	420
AATGGAGATT ATCTTACCAT CAAAAGAAGA AGCAACAACG TCATTTTCAC TATCCCCCTG	480
AGCATAGCTC ACAGTACGTG CAATGATTTT ATCCTTTTTT GACTGAGAAA CAACTACCAC	540
ACTATTGTCA AATGCAAATA TTCCAATTGC TAAGAAACAC ATAAAACCAA ACCACGGGCC	600
TACGATACTA AAAAAAGATA ACCCACCGAA ATGGATGGCA AGAAATTCAT TTTGGACATA	660
CAAGATTGCG ACAGTATACG TTGCAGCAAA AAGCACAGAC AAAGGACAGC ACAGCAGTAC	720
ATAATGTGGG ATAGATACAT ACCATATCTT CACCAAAGAA GAAAAACGAT ACCCATTCGA	780
AATAnAmTGC GTAAGATTAA CCAGAATATC AATAGCATCG AGAATCATAC TCGCACACAC	840
GAGCActAGA AAAAAAATTG GTAAGAACAT GTCCAACATA TACACCTGCA GTATTTTCAT	900
ACTGCAGATT TTCTCATTGA CAAATCAAT GCAGTAAAAA ACAATGCGGC GTTTGGAATC	960
CACAGTGCAA GGAAGGAAC AATACTAAGC CTCAACGCAA GTTCTTGTC TCCGATAGAG	1020
ATAATCCAAT ACCCTAGTAC AACAAATAAGC CCTCTACAA ATCCTTTCCC CTG	1073

## (2) INFORMATION FOR SEQ ID NO: 156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

TTTAAAnTC AGGGAGCCCG AGAATTGTCA AAAATATCCT CAAAAATATn GAGCGTTTGA	60
TCAAGAAAAA TTCCAGGCAT TTCTGCAACA AATCCTCAGA aACGTaAAAA CGCAGGAAGA	120
CCCCCGcGTG CTCGACGCCT ATCGGCGCCT TTTTCGCAAG AGCGTCCCCT TCTCCATGCG	180
CTCATACGTG GCCGCACACC TGGCGCACAC GCACTGCCGC GCCGGCGCCA CCGCCGcAGC	240
ACGCGGCGCA CCGAGCGCG GGAAGGTATA CGTACCGGCA GCGCGCACGC GCTTTCCTGC	300
GCCACGCGCC TGCCAGCGCC GCCCGCGCGC GCGACTTTGA GCGCAAAGcG cGCgGACTAC	360
CCCCGCCTCT GCCCGGGGA CACCACGAGC ATCTTCATCA GTATTGGAAA AAATCGGCAC	420

816

ATCTATCCGC GCGACATCAT CGCCCTGCTC ATGCAGCGCG CCGATGTTGC ACGCGAGCAC	480
ATCGGCACCA TCCGCATCCT CGACCACTAT TCCTTTATCC AAGTCCTTTC GGGTGAGGCA	540
GAAGCGGTTA TCGCCCGTTT AAATGGCCTC TTTTACCGGG GGCGCACCCCT GAcGGTGAGT	600
CACTCACGCA GGGCGGACGA GCATCCCGCT CCTTCTACAG AGCCGCACGC CGCTGCCGTT	660
GCACCAGAGC CTGgACTTTA TGGgCAGAGC CcATCCCCGg CCCTGGgAAG AATAAGGgAA	720
CATGgCCGTt CAGTgCAGGG gCGCCGgCCc GGGGCGCGGT GGGCAnTTCG GTGCGGTGCG	780
GCAGTTTTTCG GTTGACAGGG CTGCGCGTGG GAATCCTACC TgNAGCGGCG CTCAATGGAG	840
GCGCACGThc AGGGCCGTTT GCCATTATGG GCAGCCCGCT TTCT	884

## (2) INFORMATION FOR SEQ ID NO: 157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GGGGAGGTTT ACATGCGTAA TACCGGATCC GCCACCTACG CCCGCATCGG CGGTGTGTTC	60
CTCTCTTTCT TTGTGCTGTT ACCCGTCTTC TGCCATGGCA GCAAAGAGAA GGGAAAGGAA	120
GAAGAACCGG TTCGCCTCTC AGTCCTCATA CGAGAGAAGC ATTACTCTTC GGGCCTGCAG	180
AATGTGTTTA CGAAGTTGGA ATTGGAAGAA GGAATCGCCG TCACCGTCGA AACCATCCAG	240
GACGATCAGT ATCCTACGGT GCTTCACGCG CGCCTTGCGAG ACGGGACCGC TCCGGATGTT	300
GTAGAGGTGT CTCTTCCCTC GCTCCATGCC CTTGACCCAT ACCTTTACTT TGTAGATCTG	360
AGCAAAGAAG CCTGGATACC GGATCTACTG ATTCTCCCA CAGATCCGTA CGGCAAGACA	420
TTTGCGCTTC CCTTAAACTG CGCCGTGTCT ATCAATGCAC TTTTCTACAA CAAGGACCTT	480
TTTGATCGCT ACGGGATATC CGAGCCCAA AGCTGGAATG AACTCCTAGA AAGCTGCGCT	540
CTCATTGTAA AAAGTGGCAT TTCTATCGTA CCCCTCGCGC TCAGCACAAAC GGAAAGCTTT	600
CCACATACGT TGCTTGCTGA CGCGATTACG AAAGTGCTCG GTGAGCAGGG CGCTCGAGAT	660
TTAGTCAAAC GTGCCACAGA CGACTCCATC GATTGGACGC ACGAGCGTGg CtCTATCCTG	720
TACTCGGAGC CTATCTGGAA CTGTTCAAGC GGGGATACGT AAACAAACAC CACCGGACTG	780
CGCGCGTGCG GAAaTCATTc ATGATTTTAC ACGCGATCGC ATCGCTATGT ACTTTGGCAG	840
TCACCTGGTT GCAGATGCAA TCATAAAAGA ACGTCCTGGA ATCAACTTGG GCGCGTGCGT	900

CCTCCCTATA ACCGAAAATG CACAAGACGT ACTGACTGGA AGTTTGGAAG TGCAAGGACT	960
CGCAGTGCAC AAAAAAAGCG CGCGTGTGGC AACC CGTGT CGTGCACTCT CTGTGCTTGC	1020
GTCTGCCGCG TACCAAAACA GTTCTTTGA AGAACACAAA GGGCTTCCTG CGTTTCGAAA	1080
CACCACCAGC GCAGTTATTC CTGCGTGCCT CAGTGcCCTG TTTAAAAGCC ATATAGAGAA	1140
AGGAAAAGTA ATACAGGCAA TCGACGCGTA CGrCAGGCGC AAAACACACC CCACAGAGCC	1200
TCTGTTTTTC CAGATTTCGC CGCGTATGTA ACCGACCCGG CACCAACTGC GCACACCATG	1260
CTGCACCGCG CCCAACTGA AGCGCGGAGG AGAAGAGAGC CGGTACAAA AAAAGAATGA	1320
GAGCTCCTGC GCGGGCAATA CGTGCCACGA GCGCGGAGC TTAACCTACC GCGCGACAAG	1380
ACAATCTTGC CACAGCCGGT CGAGGTCATA AAaGGCGCG ksCgCGyTcA TAAGATGAAC	1440
CAGGATAGAC CCAAAGTCCA GCACCCGCCA TTGCTCTTCG CAAAGGCCTC GTTTTTTTTCG	1500
ATGTACTTCT CTTAGGCCAA AGCGAGCCGC CTGCTCGCAC ACCAGACGAT GAGTGCCGTG	1560
CAAGAGGCCA GGCACAGTGG CAACTACCGC AAAGTCCGCC CAGCCGCAGC GCGCGCTTAC	1620
ATCAAACACA CATACTCCT CCGCGCGCGC ATCACACAGA GCCTCTGCTA CCGCGGAAGC	1680
AGCTCCGTTA GCACTCACGT TCCCTCCTTT ACCAGATATC CATTAAAATC CTTCCCCAGG	1740
ATAAGCGTAA AATCGATGCC CGTTTCCACC CCATACTCAT CAAGCGAGGC GCTAGTTGTC	1800
TCAATATTCT GACAACGAAT CACcTgCGCC ACCACTTTAG CCACTGCAGG ATTCCCAATG	1860
CGATCGACGA GCACCGTCTT TTGCACACTT TGCTCCAATG CATTATCAAC GCGAACTACG	1920
TCGTAACCAA ATCCTTGGTA AATATTGCGC GTCGTGCGCG CAAGACCGTG CGATTCAGTT	1980
CCGTTAAGAA TTTCCAACGC ATACACACGC TCAAAGGCCG TACCATTCTC TGACGCAAGC	2040
ACCGCAAGCG TCTGGCGCAC GATTTCTTAA ATTTGCTGTC CATCaCGAGA TGGAAAAAGG	2100
AGTACCTTGC CGTCTACCAC TCGTTTAGTC CCTGAAAAAC GCTGCGGCAC TAGGCGTTCT	2160
GAATCCAACCT TAGATAATTC ACCTATAAGC TTTTAAAGT CAGCACGCCG AACGTTAGAA	2220
CGTATTAGCC TGTTCAAGGA AAAAGCACGA GTTGAATGAA CAAAAAATC ACTGTGATCA	2280
TTAACACTAC GCAACAAAGC TAAAATAGCT TTCTGTTTCC TCGATGCTGA CTCCCCTTCT	2340
CCCTCATCCT CGTCTTCGTA TAAAAGATAA TCACGCATCT TATCCCCATC CAAAGACACT	2400
GATCctGACG GTAACAGGAC ATGCCCTGCA CGTTCTGTGT GCACGTCGAT GGGCGTAGGG	2460
ATAAACACCG ACAGACCAGA GAGTAAATCT GTCAATTTAG AAAAGTTATC CAGCGAGCAC	2520
ACTACAGAAA AAGGAACGTT AATTCCCGTT AACTTTTCTA CCTCCCTTTT ATACTCCTCA	2580
ATACCACGCT CGCTGTAAAG cGAACCGATG CCATCCGTAC GGCCAAGACT CTGCAGAATA	2640



818

AGTCCCATAT TATGGGGAAT ATCAACATT GCCGCGCGCC TCGTTGCAGG ATAATACGCA	2700
ACAACATTGC TGGAGATTGG AACGTTCTCG TGTTCATGA CAAACAACAC CTTGAGAATA	2760
TTGTGCTAG AAAGTGAGGA TTCAAGCGGA TCGCGCTTCA TACCAAAGAA GACTGCAAAG	2820
ACGGTGATAA CCAGCATAAA AAAAATGAGG AGTAAAAAA GCCCATGTCT TCCCATATCC	2880
AACACTTTCA TTGCACACTC CCTGGCCTCT CGTCGAACTG CGGCAGATAC ACACACTGCC	2940
CTACTTTTGC CCGACTGCCA CCCGTTACGC GGGTTGACTT ACATCCTTTC CCAGTGCACG	3000
CAACATCGCA CACGTACGCG GATGGGGCGT GGTACGTTTT CGTCTGCGC ACACAATACT	3060
CGCACTCACT ACTTTTGCAG CAAGCGCATC TAACGTTAAC GTTGACACTG CACCGCGCAA	3120
gGACGCCGCC CAAGCACGAG CTGGcTCAAt TTTGTCTGAT ATAAAAAGAA TCTTTCCTAA	3180
CACACCAAAG TCTTCACACC CAAAGGnATG CCAGCGCACC GCAGACAACA ACACCTCATC	3240
CTGnACG	3247

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

CGAGTGCTAA AAGCTCATGA CACAGATCCG AGCGATCCTT TTTTaTGGCA AGCACCAATG	60
CCGAaATCCC ATCCGATCCC GTTTGTCGAT TGGATATCCC TTTGCCAGTA AAAGCCGAAA	120
TGTCTGCACG GGCACATTTT CCATAACCGC AAGATGCAGT GCGTCTGCC CGTCAGAATT	180
TGCCAGGAGC GGATCCTTCC CCACGACTGC ACCGACAAAC GTATCTCctT CAACAGGGCA	240
AGTGACAGCG GCGTAGTCCC GTACGAATCG CGCGCAAAGG GGTGCTTCC TGCAGCGCGC	300
AACGCCGCAA TAACTGAcTG CGAATTGCAC AGTACCGCCT CGTGCAAGGG AGTGCGTCCA	360
TACATATCCT GCTGCACAGG ATTTGCACCC GCAGAAAGGA GCATGTGCAC CGACTCTTCC	420
TGATCTGCCA AAACCGCATC CGTGAGCGCA GACTTACCCG TCTCATCCCC CATGTGCAGC	480
GCCACCCGAT GACTCAACAG CAACCGGATA AAGTCGACAT TCCCCGCACG AGCTGCAAGA	540
TGCAACGGGG GTTTCCCAGA AAGATTCCGA GCATTTAAAA GAGATACATG CCGCGtCATC	600
tTCGCGGATA AGCACGTCAG CCGAACGGAG CGCAGACCAA CGCACACACG CATGCAACAC	660
CGTATTTCCA AtGCGTCCCG TCGTCCACA AGCGCAGGAT TACCTGCCTG AGGATGCAGC	720

819

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AAAATTGAAA TAACCTCCGC TGCATCTGAC TTTACCGCAC TGAAAAGAGG CGTTTCTTGA      780
TTCAAATTGC GTGCCTCTAT CTCTGCCCCC TTGCGCAAAA TACCATTAAT CGCCTGCGTA      840
AGTTTCCACT CGCACGCCAG ATGCAGCGGC GTGTTTCCTC CTGTATCCTG AGCGTGCACG      900
TTTGCCGCAG TCAGAATCCA ATCCTCGCGA CCGCCACTAG TTGTCAACGC TGTTTTCAGC      960
GGTGACACGC CATGCACGTT TGTACTGAAG ATATCAGCTC CTTCCCTCAT CAAAAACTCA     1020
CCGACAGCAC GGTCATCGTT TGCAACCGCA TAGTGCAGCA GCGTGTTTCC CATCGTGTCA     1080
CGTGCAATCA TCTGTTTTGG TTCGCGAAAT AAGAATTTAA CTATGTCAAG GTGCGCACGC     1140
CTTGATACTG CAACGTGCAA AGGATCGCGC CCCACCACAT CTTGTTTATA CAAGTTGCTA     1200
TCGGTGACGA CAATTTTTTAC TGTCTCCAAA CCGCGCGCAA GTGCCTTGGT AAGCGGCGTT     1260
TCTCCGCGCA TATCTTCTGC ATGGATATCT GCCCCAAGAC TGACAAAGTA CGCATCAAAT     1320
CCCGATGATC ACGGTCAATC GTGAGGACAA GCGGCGTTTC GCCCTTTTTG TTCCGTTTCA     1380
AAATATCTGC GCCTGCGCCT AcTAGACGCT CTACAAACGC CCTGTCCATA CCTAAACGGG     1440
CCGCGACGTG CAAAGGAGTC TCGCCATAGT CATCCTTTAT GCGGACAGAA GCGCCTGCAT     1500
CAAGCAGTGC GCCAACCAAA CGGACACGGA AGGGAGCAGG AGCGACAAGG TGTAACAGG     1560
TGTTCCTCGA CGCGTCACGC ACGTTTGGAT CGGCCCCACT GCGCAcNCAA AGACCGCaGC     1620
ATCCACCTGC CCTGCACGCA CTGCTTCGTG cAAAGGGGTG GcGCTGGaTA GTTTTTTGA     1680
TTGAGATTGA C                                                                1691

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## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

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TGCGCATCGy GTGaGAGGaT TGACATTTTT ACTTGCTGAC GAGGCAGGCG TATTCAAGAC      60
GGTGTATTCT GATTTTGAAG AGATGGCAAC GCATGAGATG GAACATCAGT CGTTACAGTA     120
TTTTTTCAAT CAAGATGTTC TTATGATCAG AAAATCGGAT CCAGTTATTG ACCATGCACG     180
TCAGGCAATT CGGACAGATA TCCTGCATTT TTTTGATATA ACGCACGCCC AGATGATTGT     240
CTTGATTCCG GAAGCTCAAA AACTTATTGG ATGTCTATGT TTTGGTATGA AAAACAACGG     300
CGTAGAATAT AGCAATCATG ATCAGCAtGT TTTAGAAAAG TTGTATtCAC ACTTtGTATT     360

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820

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GGTTTCCTAT TACTTACAGA aTATtGCAAA GCAAGACGTG GTTATCACGg TGGACAAAGA      420
ACTTAAATG TCCCATCAGA TTATTGAGTC AATACAACGG aAAAGGGATT TTATTcAGGA      480
TGCCCTCCGTT GAGGTGGATT CAATTGCGTA TTCTGCGCAC CAACTTGGGG GCGATTTTGT      540
TGATTTcATT AAACtGTCCG AGAAAaGATA CCTGCTAGTT ATCGGGGATG TATCGGGGAA      600
AGGTCTGGCA GCGAGTATGT CAATGGTGAT TTTGAAGTCT GTACTGAGTA CCTTtCTGCG      660
GGGACTGTGC CTGGAAGAAA CGGCAGTATT TACAACCTTT ATTGAGAAGA TAAACCGGTT      720
TATCAAAGAC AATTTGCCGT GTGGGACTTT TTTTGCGGGT GTATTCTGTA TTCTtGACct      780
GGCAACCCAT ACgCTCTACT ATGCGAACTG TGGCATAACG CTCATGTcGA TGTACGTcGC      840
TTCATACAAG AACGTGGTGG AGATACAAGG CGAGGGGCGC GTGCTGGGTT TTGTtAAAGA      900
TGTtATGCCC TTTTTGCGGG TGAGGAAAGT TCAACTCGGT CAGGGGGACG TGGTGGTATT      960
TTCCACTGAT GGAATGGTAG AAGTACAAAA TTTCAGCGG GAGCGCTTTG GTAACGAGCG      1020
TGTGGATAGG ATTCTACAGG AAAGTCATGG TCTTCCGGTT TCTCAAATTA CCCGTACTAT      1080
TTATGCTCGG CTGTGTGAGT TTATGGCGCG AGATATGCAG GATGATGTAA CTGTtCTGGC      1140
AATAAAGTGC CTTGGGCCTC GGTAGGAAAT GAGGAAAAGT TCGGGAGCGC CGTATGGATA      1200
ATATAAATAT CGCCAAAGAC GTTCGGCCTG GGTGCGTTTT ATTAACGGTG ACTGGAGCGG      1260
TCAGCTCCTA TACTTACGGG GAGTTTGAGT CGCGTGTGCA TGGGGCGCTC AAAGAGAATC      1320
ACGTTGTTTT GGATCTCTCC GGCCTGACGG CTATGTCTTC TTCGGGATTG GGGGTGCTTA      1380
TCTCTGCATA CGATGAGGGA CTGAAGTACC AGCGTCGTCT GTGCATtCTT AATCCTTCTG      1440
AGAGCGTAnC AGAGCGATAG AG                                          1462

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## (2) INFORMATION FOR SEQ ID NO: 160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

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TGGAACGCGC GGTtATTACG CGTcCTGCAT ACGCGGTGGA TTATGCGGTG CTATTCCCTG      60
TACAACTTGG TATTGATTTG CAAACAAAAA GGGTGAGCGG GCTCTTTTCT GCAGGTCAGA      120
TTAACGGAAC ATCCGGCTAT GAAGAAGCTG GAGGTcAGGG TATTATCGCC GGGATTAAcG      180
CTGCGCTGTA CGCGCGCAGT ACTAAAAcCA AAGAGGAGTA TCATCCATTT GTTCTGAAAC      240

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821

GCGACGAAGC ATATATTGGC GTCATGATAG ATGATCTTGT AACACAAGGA ATAGACGAAC	300
CCTATCGGAT GTTTACCGCG CGTGCGaGTA TCGTTTGAAA CTCCGTCACG ATACTGCGGA	360
TGAACGTCTT ACAGAAAAAG CTTACGCCAT TGGGCTGCAG AAGAAATCTG CTGTAGAAAC	420
GTTGCAAAAA AAGATGCGTA CGAAGCACGA GATCTTGCAT CTGCTTCAGA CCAACAAAGT	480
TAGTCTTACC CATGCAAACG CATATGTTCA GCTGAAGCCG CATATAGGTA AATCGTTTGC	540
AGcTACGCTA CGTGATCCGG TAATACCTCT TGGGCTTawC kCTTCGCTGA ACGAGCAGAT	600
AGCGCAGTTC CCTTTGGAAG TGTTCCAGTC GGTGGGGTG GAGATACGCT ACGAACACTA	660
CATCGCTGCA CAGGATCAAA GAATTGCACA AGTGGAGAAA ATGGAAGGAA TAAAGATACC	720
AGCGCATTTT GATTACGCGC GTATATCAGG TCTCTCTGTA GAATCCCGTA CACGATTGGA	780
ACACGTTCGC CCGGACACTA TCGGGCAGGT TGGGAGAATG CGCGGAATCA GACCCCTCTGA	840
CGTAATGCTG TTGCTCGCCC ACTTAAAGCG GTAGCAGCTA CCGCAGAGAT AGAAGAACCG	900
CCTTATCAGG CAGGTGTTTG TACGTACTTT TAACGCACAG CAAGGAGCGC TTCGGCGTGA	960
AGTTCGGTGA TAAGGCCACA GGAGACCATA TCAAACAAnT GTnCGCTATT TGT	1013

(2) INFORMATION FOR SEQ ID NO: 161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GTAGTCACGG CGTGTGCCCC GCGTCAACCA ATGCGGTAAT ATCTGCCAGC CGAATTTTTT	60
CATGTGCAAG GCAGTCCCCT ACGCGGTTTT GCGAATCGAC GAGTACTGAC AGATATACAT	120
CTTTCAGTTG TGCAGGCGCT TTATAACGCA AGAACTGAGA AGCTGCTGTC CGATCAGCAG	180
GCAGGCGCAT ACGTGCACGT GCAAGATCTA GCGTAAgcTG TGCGTTAATG GTACCGTTTT	240
TCCAATCCTG CACCGCATCG GTGTGTACGG CATCCTGGGT CTGCGCACCA GACGGCGCGT	300
GAGAAAACAG AACAAAAAGG AGGAGGAGAA TGAAACGCCT CGCACTGCTG CGTACCACAT	360
GGGGCGCACT TCGTGCCTC CACACCAGGG AGAGAGCGCC GAACGGAAAA CGGCACTGAT	420
TTGAAAAAGA GGCAGCACGC GTCAGGCAGG ACACTCCCAT ACCCTACCGT CTCGGCGTTT	480
TGAGAATCAT TCCAAGGAG AGCGTGCCGT CTACTGCTAG ATTGTTTTCC TCTGCCAGGT	540
TTTCTACTGA AACGCCGTAG CGCTTTGCTA AGGACCAGAG GGTATC <sub>s</sub> CCC TGCTGCACTA	600

822

CATGCTTGCC GACAAAGGGT GCTGCAGGGG TTGCCCGCGC CGCTGTGCTT TCCGGCGGTG	660
GTGGCACGCT CGGGGGTGCC GCGCGCTCTG CTCCCGCGCG CGTGTCGCGg CCCCCGGGCG	720
TCGGCGGCGT CATTGAGGAC GAGGGAAnTG CGGACAtTCC GGCAtGCATG CTCTTtCTGA	780
TCCATTACTC CAGGTGCACG CGTGCCTGCC CCCCAGGc GCGCGCCGGG TCTGCCCArT	840
CCGGATGGTG GGAATGATGA GCTTTTGTCC AATCTTCAGG TGAGTGGCGC TGTGTGCGCG	900
GTTATGGGst TTTAGCGTAT CGACGCCCAA CCCATAGCGG CGGGCGAGTG CGTAAAGCGT	960
GTCTCCTGAA CGGATGGTGT GCAGGGTGTG ATGGACGAGC ACGGCGCCTG GGCGGTTGAG	1020
TACTGCCTGG ACCGCTGCG CATGTGTGCT TGGCACCCGG AGGGTGTACG CTGCATTCCG	1080
GGGAGTAATT GAATAGCGGA GTGCAGGGTT GAGCGTGTGC AACAATTGC	1129

## (2) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GTGAGCTGCG TGCAGTAGAG ATTGGAAAGC TGAAACAGGC GATTATTCC CTCGAAAACG	60
ATTTAAGGAA TGAGAAAGTT TCGGCTGAAA GCGGCTCCG CGTCCTCGTC TCATCAATCA	120
TTTTTTCTGG CTCGTTGATC ACTATGTGAA TGTGCAAGAA GACAAGAGGA ACATCGACGA	180
AGTGTTACTC AAAATTAAAT TGCTTGATGA AGCGGTTTAT CATCGCTATG TGAGGATAGC	240
GTGAAAGTGA GGGTGAAGTA ATGTCAGAAC ACATAGAACA CGACGTTCCG GAAATGCTCA	300
ATGAAGAAAA ATGGACACGC GCGACCTTAC CGCGTATTCT GCGGAAAAGT TTAAGGAACT	360
TGACAGAATC ATTGCGGAGG CGAAAAGACa ATCTATCCTT GATGTACTGA AAGGTATCTG	420
TGACGAACAT CTGGCGCACT CGAAGAACAG TATAATCGCG TTATACATTT CTGGGATTAT	480
TTGCTTTTCT AaGCAGTTGT TAGATGATTC GTGTTTAGTG ACGCTGCTGA CTATCTTTGG	540
TGATAATCAC AAGAATCAAA TAGTTGAGCA CCTCTGTACC CGTGTGCTTG AGTACGGTGA	600
ATCAAAGCTT GCGTTGCGTG CGTTAGGAGA ATGTTACAAA ACCTCTGGAA ACGAACAGCT	660
CTATGATGTT TGGGAACGGT TAGTTAGGAT CGATTACGAA GAGGCGGAAA TCACTCGTGT	720
GCTGGCGGAT AAaTACGAGC mGGAAGGGaA TAAaGAGAm SCTACGGAGT TTTACAAAAA	780
AGCGCTGTAT CGTTTTATCG CGCGGAGGCA GAACGCGGCC ATAAAGGAGG TTTGGACTAA	840

823

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GCTTGTGCA CTGATTCCAG ACGATGTCGA GTTTTTTAT CGTGAGCAGA AGAAAATTC 900
AGAGAAACTG GGAGAAGGGC GCGGGAGCGT GCTCATGCAA GATGTATATG TCTATTACAA 960
AGAAAATGAG GATTGGACAA CGTGCATCAA TATACTCAAG CATATTCTTG AACATGATGA 1020
GAAGGATGTT TGGGCGCGTA AGGAAATCAT AGAGAATTTT CGGTGTAAGT ATCGCGGACA 1080
TAGCCAGCTT GAGGAGTACC TAAAGATATC GAACATTAGC CAATCTTGGC GCAATGTCTT 1140
TGAAGCCATT AATGATTTTG AAAAGCATAT TTCCTTTGAC GAGGGTAGTT TTGTTTTTCA 1200
TCGAACGTGG GGGGTAGGTC GGATTGCGAA GGTGTGTAAC GATGAGTTAC TGATCGATTT 1260
TGCGAAAAGG CGTGCGCATA CCATGCTTTT GAAGATGGCT ATTAGCGCGT TGCAAACCTT 1320
TGGCAAAGAG CATATCTGGG TGCTTAAGTC GGTACTGAAG CGGCAGGATC TTGCTGCGAA 1380
AATAAGGcAG GATCCTGAAT GGGCACTGAA GGTGATCATC ACAAGTTTCG ACAATAACTG 1440
TAACCTCAAA AAGGTTAAGC AGGAATTAGT TCCTTCTTTG CTTtCTGTGG GGGAGTGGAC 1500
GAGTTGGAGT ACGAAAGCAC GGAAGATTTT GAAAGAAAGT ACTGGATTTG CTGCGAATCC 1560
CAGCAATATC GATTTTATA CGGTGCGGAG CTGTCCTGTT TCCCTAGAAG AAAAActtGC 1620
TGTGGAATTT AAGGCACAAA AAAATTTCTT CGCGCGCATC GACATCCTCA TACCTTTATG 1680
GACAAGGGCA GATACAGATT TCTGGAACGG GCC 1713

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## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

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CCGTTATGGT ACAGGAGCGG AAGACTTCGA GTAATAAAAC CAAGCGACTT GAGTGCTTCG 60
TTCAAAAACC CCTGGTTCCC CAGGATAGTG ATCCAGGCGT TTATCCTGAT GAGAGAATTG 120
GTCCAAAAGG GGACGATAAT TAGGAACAGG AAGAACGTTT GCCTCCGGCT GCGAGAGAGC 180
GCGTACCTGC AGGAAGTGCC AGGAGCACGC ACAAACAGGT GACGCCTGTA CTGATAAGCA 240
GGGTGCGAGC CAGCAGTGCG CCATAGCCGG AGGTAAGGAC TTGCGCATAC GCCCGGATGG 300
AAAActtCCA CACAACGCCT CCGTACAGGC CCTTTTGCAA AAAGCTGTAC ACAGCGACCA 360
CCGTAAGGGG GCACAGAAAG AAGACTGTAA GCCACGCAGA CAAGGGGAGC GTGCACCAAA 420
AACCTAAACT GCCTACGGTA CGcGTCGCGC CACGCGCAGC CGGsTGCTcA CGaCTCGATG 480

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824

TCCTCAACCA CGTAGCCGTC GTGTGCAGAC CAGGACACGT AAACAGTGTC CTTCCACGCA	540
ATCTCAGGGC CAGTGTGCGAG ATACTTCTGG TGTGCTGAA ACACTTGGAT AATAGCGCCA	600
CTTTCTAACT GGACGAAAAA CTTAGATTGG AACCTGCAT ATACAGGCTC CTCTACAAAA	660
CCGCGAAAAA CATTGAGCGG CGCACTGGTG GTACCCGGT CTTCAAGGGA AATGTGG	717

(2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCTATTGTCT GTCCAACTC AGTACGTGTC TTTGCAAATG CTTTCCCCAG GGCGTACCTC	60
AACTGTTTTT TCGTATCGTT GAGAACAACA TCAAGCATTA CCTTCTCGAT ATGCTGATAC	120
AAAGCACTGA TGGTATATTG CATCCCTGCT GCAGCAACGC GTGCACGCAG TGTGTCGCTT	180
TTTTTCTCAT CCAGGAGGAC ATCACGTAGC CAATCATTTT CTTCCCCAAG ATTATATTTA	240
GCAACAAGAT CAACAGCCTT ATGTAACACC GCATCAACGG GATCAGACTG TGCCCGGTAC	300
AAAACATACG GGAAATACGA CGCACACAAC ACCCGTTCTG CAACTGCTAA TGCCCTCTAGT	360
CTTGCTCTGT AaTGTTGATC CCTAAAACCT TCAATGACAA TATTACGCGC TTCATCTGTA	420
TCGAGCAAAC CTGCTCCTTT AATCGAGGCT ATTCTCAGAA TAGGATCTGA CTCTCAGAT	480
AACACGGATA ATATTTCAC CGCATCGGAA CGTCCAATAC CTGCCAGTCC TACAGCAGCA	540
GAAGCTCGAA CGACACTATT TTCCTCCGAG CTCATTACCA CCAGTTTAAA AAAATCAAAA	600
GcATGCTCAG CATGCAACTG CTCAAGAGCT GCCATAACGT TTTGTTTCCT GATCAACGTC	660
TTTTTATCGT CATCGAAATG AATATTCTCA TAATACCTCA CTAAAAATTC GGAATCTTCC	720
GTACTCCCCA TGTTTCCAAG TGCGACAATG CATTCATCAG CATACTGAGA CACTTCACTG	780
CTCAACACTT CCCTTAATAA AGGAGTCAAC TCTCTCGCCT CAAGACCTGA GATGTATCGT	840
ATCGCTGACT TAACTACCAT CGGATTATGT TCCGTTACCT GTTGCAATAC ATCCACCGCA	900
ACAGACTGCG CACAATCATT TTTCTGAAAC AAGAAAAAAT CAAACAACAA CGCCTTTAAT	960
TCAGAACTTT TTGTGCGTCC GCACAACATA CACAACGTTT CGTTTAATGA GGCGTTATTT	1020
TCCTTCTTTA ACTCTTCTAT CAAGGAGATA ATATCAGAAA CTAATCCATA CTTGATGGTA	1080
TTCATCCTTT TCTTTAGAAG AACCGTTTTT TCATCAGTGA TATCTATATG ACGCTCCTGT	1140

825

TCTTGCACGT GCTGCGTTCC CGTTTCCTTA GCAAACATGG GGACACCCCT CCCTAAGAAA 1200  
AGGATTGCnA CATGCACGCT ACAGTAGTGC ACGAAAAGAC TGChCCCTTT CACCCCATTT 1260  
CCCCCTCCGTT CCATTCTATA TCT 1283

## (2) INFORMATION FOR SEQ ID NO: 165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CAAATCCAAC TgNAAATAGA TACCCCGGcT TAACCCCCAG ACAAGTGAGC GCGTGAAACA 60  
GTGTGCACAG CGTCTCTACC GAATCGTTCA CCCCGCGCAA CAGTACCGAC TGCgATTGCA 120  
CAGGGAGGcT GCGCcTACGC AGGCCnCGAG CACCGCGCGC TGCgTAGAAC CGAGCTCTGC 180  
CGGGTGATTA ATATGCGGAA TTATCCACAC CGGCTTCATC TCCTGCAGAA ACGCAATCAG 240  
CTCGGGAGTA AAGGCCTGCG GAGCAAAGGT GACTGCGCGA GTGCACAGAC GAATAATCAA 300  
ATCCGGCGCT AACTTGgCAG TGCsCGGAAA AGCGATGTGA CCTGTGCAA AGAACCAGTG 360  
AGTGGAACAC CACCTGAAAC CAGGATTTCC TTCACCGAAG GGGTAGCACG AAGATACGTA 420  
ATAATCTTCT CGCGCTCTTC GTTGGGGATC CACCCTGCAC GTTGGGCGAT GAAACCGCGG 480  
CGAAAACAAT AGCGACAGTG TGAAAAGCAA CGTCCTGTTG CCAACATCAA CACACGATTC 540  
GCATACTGAT GCACCAAAAA GGGTGTACG CATACCGGTC CTCACCCAAT GGGTCGGCAC 600  
ACTCGCAAGC ATGCACCACA CGTCCTGTG GCGCAAAGCA CACCTGACGT TTCAGCGCCT 660  
GgCGTCCGCG CCCTGCGcTT GTGCAATTAA ATGCGCATAC GCTGGAGAAA TATGCTCCGT 720  
CAGCGCATCT GCCGCGCAAG AGGCAGGACT CAACGTCCGC CAATGCTCAT CAGCACGCCC 780  
TGCACCTCGT CTCTTTCTCT GTTCCCGGGT AACTCAGCC ATAGACACGG ACCACGAGTG 840  
CGCATCCTAC GGTAAAAATG CATGCGTGTA CAAGTCACGC CGTGCACCGC ACCCGTGCTG 900  
CAGGATCGCA TACCGTAGTG TTGACACACG TACCTATTTG CAGAGACCCT GGTCCCCATG 960  
GTCAGACTCG AGCGGCTAAA GAAGACATAC GCAGGTGTTT CTATACTTCG AGATATTTCT 1020  
CTAGAGATCC CAGCGCACGG AATGTATGGA ATCATCGGCA AAAGTGGTGC AGGAAAATCA 1080  
ACGCTACTGC GCATCATGAG TCTTTTGGAG AAACCTGACG AAGGAGCCGT TTTTATCAC 1140  
ACCACGAGGG TAGATTTACT GCGCGGTGCT GCCTTGCGTG CACAGCGCAG GCGCATAGGA 1200



826

TTGATCTTTC AACAAATTTCA TCTGTTTTCT TCCCGCACCG TCTTTGGGAA TGTTCCTAC	1260
CCGCTTGAGA TTGCACGGTA TGCACGTAAG GACGCCTACG CGCGCGTGTT GCATTTGCTA	1320
CACTTGGGTTG GTCTTGCAGA CAAAGCACAG GCGCGTATCA GCACGCTGTC AGGTGGGCAG	1380
AAGCAGCGCG TACCATTGCG CGCGCCTTGG CTGCAGAACC TGCAATACTC TTCTGCGACG	1440
AAGCAACAAG CGCTCTCGAC CCTCAAACAA CACAGTCAAT TCTGACGTTG CTGAAAAATG	1500
TGCAAGTCTC ACTGCGTCTG ACGGTCGTAT TGATTACACA CCAGATGGAG GTGGTACGCG	1560
ACTTGTGCGA TCGGGCCGCC GTATTGCATG AGGGAGAAAT AGTGGAAGAA GGAAGGGTGA	1620
CACAACTTTT TGCTGCGCCA CGGCGGCTGA TCACACAGCA GTTGTGTGCG GGCTGTTCTT	1680
TTGCCTCTTT TGCAAAGTCA GAACCCTTCC ATCGAATGTC TTCGGGTGCG TGTGCCGTGC	1740
ATGCTATTGA CAAGGCACAC TGGTAATGGC GAACCAGACA CTGTGGCTTT TAGTAGCTCG	1800
TGCAACCGGA CAGACAAGTC TGATGGTGTG TGCTTCAGCA AGTATTGCGC TAGCAGCGGG	1860
AACCCCGTTG GGGATATTGC TGTGCGTAAT GTCGCTTGA CACGTGTGGG CGCATCTGCG	1920
TGGCATCGTG GTTTAAGTTC GTCAATGAAC GTCTGCGCGC TTTCCCATTT GTGATTTTGC	1980
TGGTGGTGTT GCTTCGCTC TCGCGTATGC TCACAGGACG CACAGTGGGA ACGGCGGCGG	2040
CTATCCTCCC GCTTGCgAta cTGCCTCCC TTTCGTGGCA CGGGTGATTG AAAGTGCTCT	2100
GCTGGAGGTG GAGCCAGGGA TAATCCAAGC GGCGGTGGCA ATGGGTTCAA GCATGCGGCA	2160
ACTTGACTA AAAATCATGC TGCCTGAGGC TGCTCTGCA TGTGTTTCTG GTGTAGCACT	2220
GATGGTAATT AATCTAATTG GATACTCAGC AATGGCAGGG GCGATTGGGG GAGGAGGTTT	2280
AGGAGACGTA GCGATCCGCT ACGGGTATCA GCGCTTCCAA CCAGAGGTGA TGACAATGGC	2340
AGTGCTTGCA ATCCTGGCGC AGGTTGCGtA ACGCAATGGA TCGGGCGTAT AATCTGTACC	2400
CGAATACGAG CGCGtCAGgT AGTACCCCGC CAGAGTTAGG CAGGACGTCT GTCCTTGCA	2460
GGGTAATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG TGGAACGAA ACTCACGTTA	2520
AGGGATTTT	2529

## (2) INFORMATION FOR SEQ ID NO: 166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TGACGGCTCT TACCCGATTG AGCGAAAAGA AGGGAGCAGT ATATGGCAGA GATATCAGCA 60  
ACAGCTTATG CTGkCCAGGT TGACGACCTG ACGCTTGCGT ATCGGCAGAA GCCGGTGCTT 120  
TGGGACGTGG ATGTGCGTAT TCCAGAGGGG GTTATCGAGG CCATTATCGG TCCTAATGGG 180  
GCGGGCAAGT CGACCCATT GAAGGCGATC ATGGGTCTTC TGCCTCTCGC TTCCGGAGAG 240  
GTGCGTGTCT TTGGGCGTCC TTTTTCAAAA GAGCGGCGAC kTGTGCGTA TGTCCCGCAG 300  
CGCAnTGCAG TGGATTGGGA TTTCCCTACT ACCGTTTTTG ATGTGGTGCT CATGGGTTCG 360  
TACGGTTTCG TCGGTTGGAT TCTTCGTCCG GGAAAAAGAG AAAAGGCGCG TGCCCGGGAA 420  
GCGATCGAGG AAGTAGGAAT GGGCGCCTTT TTAGACCGAC AAATCAGTGA GCTTTCAGGC 480  
GGTCAGCAGC AGCGCGTGTT TCTCGCGCGG GCCTTGGTGC AGGACGCGGA TCTTTACTTC 540  
ATGGATGAGC CATTTCAAGG TGTGGATGCA GCTACTGAAC AAGCAATCGT TACTCTTTTA 600  
AAAACGCTGA AAGGGCGTGG GAAAACGTTG CTTGTTGTGC ATCATGATTT GCAGACGGTG 660  
GCAGAGTATT TTGACCGCGT GCTGCTTTTA AATGTTTCGCG TCATCGCTGA AGGGGCCGTC 720  
GTGTCTGCCT TCACCGAAGA ATACGTTCAA AGAGCCTATG GCGGACGGAT TAGTTCCACC 780  
CTTTTCCGA GAGGAAATAA GGAGGATGTG CACGATGCAC GCGCTCATGC GTCTGTCTC 840  
TGA CTATACG CTGCAAAATG TGGTGTAGG CACGCTTTTT TTGGGTTTGG GTTCTGGGCT 900  
GGTCGGCAGT TTTGCGGTGC TGCGTCGACA AAGCCTTTTC GGTGACGCAG TTTCTCATGC 960  
AACCTTCCGG GGATTGTTAT CGCGTTTCTT TTAACCGCA CGAAGTCTAC TGAGATACTT 1020  
TTGCTGGGTG CTGCCCTCAG TGGTTTAGTA GGAAGTGTGG TGATGCTAAT GGTGATGCGT 1080  
ACTACAAAAA TTGATACCGA TGGTGCAGG GGCATTGTGT TGGGTGTTTT TCTTGGGTTT 1140  
GGGTTTCTAT TACTCACCCA CGTGCAGAAG TCGCCCCAGG CGGCAAAGGC TGGTCTGAAC 1200  
AAATTCATTC TAGGGCAAGC GGCCACGATT TTGCAGCGAG ATGTCCTGCT CATCATTGCG 1260  
ATGGAGGTGG TGATCGGTTT GCTTGTA CTGTTTGGGA AAGAACTGAA GCTTTCTACC 1320  
TTCGATCGAG ACTTCTCTGC GGTGCAAGGT TTTTCTCCAC AGCTTATGGA GTTCATGCTC 1380  
ACGGCACTCA TCGTAGTTGC AGTTGTCGTA GGGGTTTCAGG CAGTGGGGGT TATCTTGATG 1440  
AGCGCACTGC TGA CTGCGCC TGCA GTGGCA GCGCGG CAGT GGACAAACAG TTTAAGGGTT 1500  
TTATGCGCGC TTGCTGCTTT ATTG GGGGT GTCTCAGGTG TTTCAGGTTT GGTGTCTCT 1560  
GCCCAGGTTT CCAGGCTTTC TACTGGCCCC GTGATAGTGT TGGTGCTGAC GGGTATTGCG 1620  
CTTGCTCTTA TTATGCTTGG TCCTCAGCGG GGTGTTTTGT ATCAACTGTG GCGGAGAAGA 1680  
CGGGTTTCGC TTCTTCAAGA GGAGGGGTAG AATATGACCA TGGAGGTTGT GCTTATTGCA 1740

GTGGTTCGTGT	CGGTTGCGTG	CGCGCTGTGT	GGGGTTTTCT	TAGTGTTCGG	TAGAATATCG	1800
CTGATGAGTG	ACGCGATCAG	TCATTCCGTT	ATCCTGGGGA	TAGTACTCGG	TTATTTTCTG	1860
AGTCGTACGC	TTTCTTCTTT	CGTGCCTTTT	GTGGGGGCAG	TGATTGCGGG	GATATGTTTCG	1920
GTAATCTGTG	CAGAACTTTT	GCAGAAGACA	GGGATGGTAA	AGAGCGATGC	AGCaGTCgGG	1980
CTTGTGTTCC	CTGCAATGTT	TGGGTTGGGG	GTGATCCTTG	TGTCGTTGTA	tGCAGGGAAT	2040
GTACATCTTG	ATACAGATGC	GGTACTGCTT	GGGGAAATTG	GACTnGCGCC	CTTGGATAGG	2100
nTTTCGTTTT	CAGCTTGgTC	CTTGcNTAGG	AGTnTGGTAn	AGATGGGGTC	CGTcNTGTGT	2160
GGATTACTGC	TGTTGCTTGC	GCTCTTTTTT	AAGGAACTCA	AGATTTTctAC	GTTTGATCCG	2220
GTGCTTGCCA	CGAGTTTgGG	TTTTTCTCCT	ACGCTTATTA	ATTATGGGCT	TATGCTCGsG	2280
GTGAGTATTA	CCTGTGTGGG	AGCCTTCGAT	TCGGTGGGTG	CAGTGTGGT	CATTGCATTG	2340
ATGATTACAC	CGCCTGCAGC	AGCGCTTTTG	TTGAcAGATa	mCTtgTwGTt	GATGTTGGTC	2400
CTTGCTTCAT	TGCTCGCCTC	TTGTGCGTCC	ATTAGTGGGC	TTTTTCTTGC	GGTGAAGATA	2460
GACGGCAGCA	TTGCAGGAGC	AATGGCTACC	ATGGCGGGCG	TTCTGTTTCGC	GTGGTGTAC	2520
CTTTTCTCTC	CAAACACGG	GGTTGTGCGC	AGGTGTCTGG	TAATGCGTGC	TTTGAAACTT	2580
GATCTAGATG	TGGTGACACT	TGCCGTGCAT	CTTGCAAcac	ActTACACGG	TGGAGCGCAG	2640
CGTGGAGTGC	GCTGAAGTGC	ACCTGACAGA	ACATGTGAGT	TGGTCTGcGC	GCAGGGCGGC	2700
CCGCGTGGTG	CGTACCGCGC	TCAGGCGAGG	GATGGTAGAG	CGTCACGGTG	CCTTGCTGCT	2760
ACTCACTGCG	CAGGGTGTGT	nCGCTCGCGC	AGGCGCGATT	GGATGTATCC	GTGTAGGCTG	2820
AGTCGATGTC	GTTAGTGTCA	GATATTGCAG	CAGAGAATTA	TTTGAAGACA	GTGGTAAAGG	2880
CGTTGGCGCG	GTCTCGTCCG	GAGCGCGTGG	GTACCGGGGA	GTTGTCTCGC	CTTTTACACG	2940
TGACGCCGGG	GAATATCAGC	ACAATGGTGA	AGCGCTTGGA	AAAGGGTGGC	TATGTGCAAC	3000
GCACGcATCG	TCCTGGCTGT	ACGTTAACCA	GAAAGGGGGC	AgTTTTTTGGA	TCTGCaGTGT	3060
TAAGGAAGCA	TCGCTTGTTG	GAGAGTTTTT	TTTCCCAGGT	ATTGTGTTTA	GAAGCAGGGG	3120
TGGTGACAA	AGAAGCGGAA	ATGCTTGAGC	ATGCGTGTTC	TGACGAGCTC	ATCGACGTTA	3180
TTGATCGCTA	TTTGACAGTAT	CCTACGCGGG	ATCCTCACGG	GCAGCCGATC	CCAAGAAAGG	3240
ATACGCTTTT	GGATTGTAT	GTTGAGGACG	ATGTGCCAGG	TGTATGATCT	TTTTGTATGG	3300
GGTGAGGATG	CGCCTTTTGT	CAGATAAAAG	GGGATGTGCA	AAACGTATTG	TTGAGAGGAG	3360
AGGGCCATGA	AGCTTGTGTT	GATCCGTCAT	GGAGAAAGTG	AATGGAACAG	GCTGAACCTG	3420
TTCACTGGTT	GGACAGATGT	TCCGCTTACC	CCACGTGGGG	AGTCGGAAGC	CCAGGAAGGA	3480

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GGCCCGGTAC TGCAAGAAGC GGGGTTTGAT TTTGACCTAT GCTACACTTC TTTCTTGAAA 3540  
CGTGCCATTC GTACGCTCAA TTTTGTACTC CAGGCACTGG ACCGTGAGTG GTTGCCGGTT 3600  
CACAAAAGCT GGAAATTGAA CGAGCGGCAT tATGGGGATC TACAAGgTTT AAATAAGACA 3660  
GAGACGGCGC AGAAGTATGG TGAGCAGCAG GTTAGGGTGT GCGCTCGCTC CTTTGATGTG 3720  
GCTCCTCCTC CGCTTACTGT AGGGGACGCA CGTTGTCCGC ATACTCAAGC CTCCTACCGG 3780  
GGGGTATGCG CGTCTGGTCG GACGCCatAC TTCCGTTTAC GGAAAGTTTG AAAGATACCG 3840  
TTGCGCGTGT GGTGCCGTAT TTTGAAGAGG AAATCAAACC GCAGATGATT TCCGGACAGC 3900  
GTGTGCTTAW TGTGGCGCAT GGTAACTCGT TGC GCGCACT GATGAAGCAC ATAGAGTCTT 3960  
TGGATGAGAC TCAGATAATG GAAGTAAATT TGCCTACCGG TGTACCGCTT GTCTATGAGT 4020  
TCGAGGCGGA TTTTACCCTG TGTGGGAAGC GTTTTTTAAG 4060

## (2) INFORMATION FOR SEQ ID NO: 167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CTTTTACCC AACTCATTGC CAATGCGGTT ATGGAAGCGG GTAACGAGCA TGGTTTGAAA 60  
ATCATTGAGA ACTTGCAGGA TGAGGAGAGT GCGCATGAGC TTGACGAGTC CGTTTCCTTG 120  
CACGAGGAAG GGCGCGAAAT TACTGACTAT GAAAATTATA CTCCTCCTGA GGAGCGTGAG 180  
TATTCTGTGA ACGATGAAGG CGATGTGTTT GATGAGGATG AGTCGCTCTA CGAGGGGCGT 240  
TAGGTGTGCC CTCCGCGGTC TCTTTTGGA TGTGTGTCTG GGTAGGCATG TTTGCATCGA 300  
AGTCTGATCG GAAAATGCTG TCAGGAGGGG TACATGGAGA TTGCTGCTCG CGACGTTAAG 360  
TCTTTGCGTG ATAAAACCGG GGCCGGGATG ATGGATGTAA GCGTGCCTC CAGGAGTGTG 420  
CAGGGGACGC TCTGTGTGCA GAAAAGTATC TTAAGGAGAr GGGGCTTGCT GCCATCGAAA 480  
ACAGGCGTGG GCGTGCCACT GCTGagGGAG TCaTCGTTAt TAAAGCACgG CaTGcAGAgG 540  
GCgCgGCCTG TgGGGCGAGC GCTGTAGCAA TGGTTGAGCT TGTTTGCGAA ACAGATTTTG 600  
TGGCAAAGAA CGCAGAGTTC ATCGCCCTTG CTGAGCGTAT AGCTCAGGCG GTGCTCGAGC 660  
ACGCGTACAC TGAGGTAAAC CAGGTnTGCG CGATATGGTG GTGGACCTCG CAACGCGCGT 720  
ACGGGAAAAT ATGAGCTTn AccGCCTTGC GCTCTTACGT GCCGcAGTGC CGGTGCAGGT 780

830

CAGTACCTTT CCTnTACGTG CACCCTGATA AAAAAACAGG GGTAGTGCTC TCCTTTTCCT 840  
 CCGATGCGCC GGATGTGTTC CTGCGATCCG ATGTGCGGGC cTTCGCGTAT GACTGCTGTT 900  
 TGCACGCGGC GGCATATACC CCTCGyTACG TGC GCGCAGA GGACGTGCCT GCTGAGTATG 960  
 TGC GGGAGCA GCGTGAGGTG TTCCAAGCGC ATGTTGCGTC TCTCCAGAAG CtGCGCATGT 1020  
 CAAGGAAAGT ATCGTGCAGG GTAAACTAGA GAAGCATTTG GCTGAGATCT GTTTTCTGAA 1080  
 GCAGCCCTTT GTTAAGGACG wCAAGCTTTC TGT TGAAAAA AAGATGGCAG AAGTGGGTGC 1140  
 CCGCGCAGGG GGTGCGCTTC GGTTTACTCA GGC ACTGATA TACCAGCTAG GGTACAGTG 1200  
 AGTGGGAAGC ACGGATAGAT CCTGCCaCCC TGCAGGATGG GGAGCAAGCA GGCGTGGGGG 1260  
 AGCTCGTGCT TCTCTCTTGC CGCACTGTGT TGTGAGGGGA AAAGATGGGT ATCGCTGAGT 1320  
 GCTATGAGCA GAAGATGAAG AAGTCCCTCT CAGCGCTGCA GGAGGGTTTT AACACGCTGC 1380  
 GTACTGAACg TGCGACTGCA CATTTGCTTG ATCAGATTAC TGTCGACTAC TATCAGCAAC 1440  
 CAACCGCGCT TAGTCaGGTG GCTACCGTTT CGTACCCGAG GCGCGTTTGA TCATTATCCA 1500  
 GCCTTGGGAT AAAACGCTCC TTGCGGATAT CGAGCGTGCA ATTTTAAAGT CAAAATTGTC 1560  
 GCTCAATCCC TCCAACGACG GCAAGGTTAT TCGTCTAGTG ATTCTCCAC TTACCCAGGA 1620  
 GCGAAGGAAG GAGCTTGTCa GGCAGGCGCG CGCGTTAgCC GAGCAGGCGC GCGTTGCTAT 1680  
 TCGCAATATT CGCCGTGAGG GAATCGAGGA AGCAAAGCGC GGGCATAAGG AGGGACTGCT 1740  
 AAGCGAGGAT GCACTGAAAG CAGCAGAAGA GGCCTTCCAA AAAGCGACTG ACGCTTCTGT 1800  
 CGCAGAgTtG CACGGTACTT GGCCGAGAAG GAAAAGGATA TCCTGGAAGG TTGAGTGCCG 1860  
 TGCAGCACGT GGCCATCATC ATGGATGGAA ACGGGAGATG GGCGGAAAGG AGAGGGTTGC 1920  
 GGCGCAGTGC AGGGCACCGG CGGGGGCTGC AGACAGCGCG AGAGATTGTC GCGGCGCTGT 1980  
 GCCGATTCGG GTGCCTTTTG TTACTCTGTA TGTGTTTTCT ACTGAAAACT GGAAGCGCTC 2040  
 TGCnATGAAG TGCATTTCTT GATGAATTTA ATCA 2074

## (2) INFORMATION FOR SEQ ID NO: 168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CGCCGGGnTA TTCCTTGCGT ATGCATCGAT GATCATTTGC ACGTTTTGCC GACCTAAAAT 60

ATCCGCTGCA TTGGTACGGA TTACCTGAGT CAGGTGCGTG GCGATGATTG CAGATGGAGC	120
AACTACAGTG TAmCCGACAC GCTCAGCACG ATCGCGATTT TCTTCAGAAA TCCACACAGC	180
AGGGAGTCCA AATGTAGGAT CAATTGTTCG CTCCCCTGGA ACCTCCTCTG TAAC'TTGACC	240
AGACTTTATG GCGAGAAACC ATCCCAAGCG CAn'TTTyCCC CGCGCAACTT CTAATCCTTG	300
GATTTTGAAA CAATAACTGC TCGGATCTAA ACGCATATTG TCAATAATTC GAATTTTAGG	360
AGCAACCAAT CCGAGATCCA ACGCGGCATC TTTTCTAATA ACTGTAATTC TACTTAGGAG	420
CTCTGCACCC TTTTCTTTAT CAACAAGAGG AATTAATCCA TACCCAAGTT CTAGCGAAAG	480
TGGATCAAGC GGCACAATAG GACCCATTTC AGAAGTACTA TCTTGAGTCT GTTGCATACC	540
CTTTTATCT GAAC'TTTT GCATCTCATG TTCTTGAACG TGTACCCGTT CCCTTTTCCT	600
TAGCTGCAGT CCCACAAAGG CAAAACACAC GGCCATAAAA AATAAAATAC TGTGGGGAAA	660
ACCCGGCAAT ACCGCCATAA CGATCAATGC ACCTGAGCCA ATAAATATAA CAAGTGCAC'T	720
TTTTGAAAAT TGTTCC'TGTA CGTTTTGACC AAATGACCCT TGATCGCTTG ATCGAGTGAC	780
AATAAACCT GTTGCAACAG ACAACAACAA AGAAGGAAGC TGTGCAAGCA ACCCATCTCC	840
TATCGTTAAA TTTGTATAGG TCTGCAATGC TGCCTGAAAA CCCTCCCTAC GAAATATGAC	900
ACCCACTATC AGGCCTGCAA TCACATTTAC AATGGTAATA AAAATACCAA TTTTGACATT	960
GCCCGATACG AACTTACTCG CTCCATCCAT TGcTCCAAAA AAATCTGcTT CACGCTGaAT	1020
TGCGCTcTtA yrCTcTCGCG cTTcTTCwTC GGTGATAACA CCTGnCATTA TATTcAGCAT	1080
CAATAGACAT Gc'TTTTGGTT GCATTGAAGT CTAAGGTAAA ACGCGcAnAA ACTTCTGcAA	1140
TACGCGTCGC ACCCTTAGTA ATAACAAAAG CTTGCACTGC AATTAAAATG ATGAATACCG	1200
TAAACCAAT TACTAGACCT TCGTCCCGG ATCCTCCAC CACAAAAGAA CTAAACGCAC	1260
GGrTCATATA CCCGCTAAAC CGATCTCCTA ACGTTAAAT CAACCGGGTG GAAGACACGT	1320
TCAGTCCAAG TCCAAAAACG GTTGAGGTCA ACAAGAGCGA GGGrAATACA GrAAAACTG	1380
TTGGTTTTTC AACAAATAAC ACCATAAGTA ATATCAAAAG GTTAAAGATA AGATTAAaGG	1440
CCwTCAACGC aTCGAGAATT TGCGTGGGCA GAGGAACAmC AATAGAAAaG ACAmCCACCA	1500
AACTGAAAT CGCAACAAAA GCGTCAGTAG TGAAAagGCA CTCTTACCGT GCGCCATAGT	1560
ATGGGTACC TCTTACGCTG TGCATGTGTT TTAAATTTAT CCAGCTTGGT AAAAATCAGC	1620
ACTAAgCATT AAAATATTCG TAGGGAAC'TT CTCTCCCGAT AGCAACtGCG TGTACAACGC	1680
ACGTGCAAGC GGTTTGT'TT CTTCTATCAA GATACCTGCC TCTTTTGCCA ACCGTTTGAT	1740
TCGGTATGCA GTCCCATCAG ATCCTTTTCG AACCACAGTC GGCGCAGTCA TGTATGCAGG	1800

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CTCATATTGC ACCGCAcTGC AAAATGAGTC GGATTAGTGA TCACAACATC AGCGTCAGTG	1860
GTATTCCGAG CAGACTCTCT AACAAGAGAT TGCATCTGCT TTCTAACATA ACTTCTCACG	1920
AGCGGGTCCC CTTCCTGCTC TTTTAACTCC TCTTTCACCTT CCTGCCGAGA CATTTTTAAC	1980
GAATCGATGA ATTGCCTTCT TTGGAAGAAA TAATCGGGAA GCGAGAACAC CACTAACAGC	2040
AAACTTACTT CGAGGAGAAC TTACCCGCA AGGGATGTAA TGTAAGAAAT ACTCTGGGTA	2100
AGACTCACAC CCAATAAgAA ACAAACATAA AAAGATCATT ACGTATAGTA AAATACGATA	2160
CAAAAAaTAT CGCTGTaATC TTTATGAGAG ATTTAAGTAA ATTGAAAAGC CCTTCTGTTG	2220
AAAAAATGA GCGTTTGAAA AAACGAATTA CATCTGGAGA TATTTTCTTA AACTGCGGTC	2280
GAATCGACTT TACCGAAAAT AAAACGGTCT TGTTTTGAC AATGTTTGCC GCAACGCCAG	2340
AGACCAGCGC AACAAAGGAT ATCGGAAGTG CAAGTTTCAT AAAATACCGC ACAAATACAA	2400
AAAACCATCC AGTATTCTGG ATGGACGCGG TAGTAGCACG CGTAAAGAAA AACCTGAGTA	2460
CACCGATGCA CTCTCTCAAT ATAAATGGTG CAAGCAAGAA CAAGGAAGTT GATGTGAAGA	2520
GCATCACAAA CGCTCCATTT AGATCCgGCT TTcGGAACAC GTCTTCTTC TCGTGCTTAC	2580
GGAGTTTTgt TcGGTAGaTC CTCTGaCCTC CCTTCaTCCT CAGCGGCAAA CCACTGGCAA	2640
ATCAATAATA AAAAGAGGAA GCGGAAATGT TCCTTCTTGT TCTAT	2685

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

AATCTTGAC GCCCTCGCTC AAGCCTTCGT CACTGGTCCC GCCACCAAAC GTTTCGGCGA	60
GAAGCAGGCC ATTATCGCCG GCATGGGGnC CGACGCGCTG GGCTACGTCT TGCTGGCGTT	120
CGCGACGCGA GGCTGGATGG CCTTCCCCAT TATGATTCCC AATAAAAATT GCGCGTGCCG	180
CACACCGTAA TCAGTTTACT GAAGAAGTGC TCCAATCCCT GCGGATTTCG CACCAATGCG	240
GTCTGTGTTT TGCCGCCTGT ACTGCGCGTA TTCCTCTTGC AAAACTTTTG CACGATGCAC	300
AAGAACGCGC ACTGCATCTT TCCCGTGCTC CAGTCACCAA AATAGAACCC CACTCCACAC	360
AAAGCGTCGG GAAACTATC CGCGAGCACC TGCCAATGCG CACCGCTGGA GTACAAACAC	420
GCACCCTTCC TTTACACCGG CTTAAGTGCT GGACAGAACA ACAGTGTA CT GTTGGCGCTG	480

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CTTGTTGCGC ACGTGTTTCGT CGTTGCAGCC ATGCGCGACA CGGTCGnTnT TTTTCCATCG 540  
 TCAGTACCGA ACTCGGCGCA CTGAGCGCGC GCTCGTTCAA AACTACGCA CACCACATGT 600  
 GCCCCTGAGC GACTCTCTCG TACTGGGCCT GCTC 634

## (2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CTGAACACGT TGCACGGTGC GACGCTCCTT ACAGGAATGr AAAAAAAGA ACgCCGCGCA 60  
 CAkTGCACCG CCCACATATG ACGCACACCG CCTAGTTTTTc ATCACGAAGA CcTTCTGAAG 120  
 AAAAAACACGC GCGGTGACAC GCTTCGAGCT GTCCATTTTC CACGTGTGTG TACACCTGGG 180  
 TAGTTGCAAT ATCTGCATGG CCGAGCAGAC ACTGAACCGA ATGTAAATCG ACACCGCCTG 240  
 CAAGCAAATG CGTCGCATAT GAATGGCGAA ACGTATGAAC GTGCGTCTCC ACCCCTGAGC 300  
 GGATTTCAAT ATCCTGCAGG CGCTTCCATA TACCTTTACG ACTCAGACGA CCCCCCTGCC 360  
 TGTTTAAAAA GACAGCTCCT TTTTTTTCAC TATTCTCCGG ATGCTTCGCG CTCGTAAAAAC 420  
 GAACACGCGC CTCACGTATA TACTGCaTGA GAAAGTAACA CGCCTGTTCT CCAAAGGGAG 480  
 CCATACGCTC TTTGTTCCCC TTACCTGTCA CTTTTAGCAG ACGTTCTGCA AAAAAATGT 540  
 CAGAAAGGGA AAGAGAAACT GCCTCACTGA CCCGCAAACC TGCAGCATAA ATAAGTTCAA 600  
 AGAGCGCGCG ATCACGCACG CCACCTGGTG TGCACAGTGG AATGGATTGC AGAAAAGTGT 660  
 TGACCTGTTT GGGAGACAGC ACGCGCGGCA GTGAATACGC ACGACGCGGT GCATCAACGT 720  
 CTTGCATtGG GTTATCAGGA CGCACCTGCT CCAAAaTGAG AACTGATAG AACGCGTGCA 780  
 GGCCGCCATG TCCTTcGCAA TCGTTTTGCC TGAGACACCC GCAGCACTCC GCTTTTCGAT 840  
 AAAACGTACA CAATCGTGCG CATTGGCGCT TTCAATGTTA CACGGCGGAT CAAGGTTTTT 900  
 CTGAAAAAGC ATCAACGTAG TCACGTACGT CCGTGCGGTC AAAAGCGCGT GCGCCTCTGC 960  
 CGAAATTAAG TACGCGTAAA AGGATTGCAC ACGGATATCG ACGTCTTTCA CAGACCCTTG 1020  
 TTCCTATTTT TCAAAAAGGT CGGTTcATCC AAATCTTCAT TTACCGAGGG GAGCGGAACG 1080  
 CCAAACGTGT GGCCCTtCAC TCCGTTCTTT TCCATACGCG TTTCTTGAAC AGCGCTATTA 1140  
 CGCGTAGCCA GACCAGGTAA GTTTGGCTGT TTAGAGCTTT TAGCTCTGTT CCATTCGTCA 1200



GAAC TAATAT ACACACCGGT ACTCACC GCA CCGTACGATG ATGTTTTTAT CTTT TGAGAA	1260
CTGTGTGTAT CTCCCGCTAT CGAAATACTC GCTTGCGGTA CACCCGTTGC GATAACCGTA	1320
ACCC TCACCC TATCCTGCAT ACTCGCGTCG ATGGACGTGC CATGGATGAT AATCGCATCC	1380
GGATCAATGG TCTTTGCAAC CACAGACATC ACGCCATCGA CTTCTCCCAT GCTCAAGTTC	1440
TCTGAGCCAC GTACCGCAAC CAGCAGTCTG GTAGCACCTT CTATCCGCGT CTCTTCCAAA	1500
AGCGGATTAT TAATTGCAGC GGTGCGCGCA TCTACTGCGC GGTTTTCCTT TCTTCCCTCT	1560
CCCACACCGA TAAGCGCGTA CCCCTGCCCT TCCATGGTGT TTTTACATC CATGAAATCT	1620
AAATTCACTT CTCCAGGAAG GGTAATTAAA TCAGAAATAC TTTGCACCGA CTTGCGCAGc	1680
aGATnCATCT GCAACCAGAT ACGTCTCTTT AATCGGGCAG CGTTTATCTA CCACACTGAG	1740
TAAATTCTGA TTAGGGATCA CAATCACGGT GTCCGAGTGC GTGCGCAATT TTTCGATCCC	1800
TCGCTCAGCG AGCATCATCT TTGCTCTGCC TTCAAAGCGA AACGGCTTCG TGACTACGGC	1860
AACTGTCAAA GCACCAAGTT CCCGTGCAAT CTTTGCAATA ACTGGGGCAG CACCTGTTCC	1920
CGTACCTCCT CCCATCCcTG CGGTGATGAA CACCATGTTC GCGCCCTGCA ACGCACTTGC	1980
AATGGCTTCA GCATCTTCCA TTGCAGCCTT CTCGCCAATC TCAGGATCAC CGCCTGCACC	2040
CAACCCCTT GTCACCTTGG TGCCAATGGC AAGCTTTTTA GGCGCGGTAG AATAGCTCAA	2100
CGCCTGcACA TCTGTATTTG CTGCAATAAA CTCGACGCAC TGCAAACCGC AGCTCATCAT	2160
CCTATTTACC GCGTTTGACC CACCACCACC GGCACCGATG ACCTTTATGA CCGTTGGACT	2220
TAGGGTAAAC TCTTCGCCTG AAGGTGCAAG CTCTATATTC ATCATTCCCC TCCCATCCCC	2280
CTACACCGCG TGCCGCATGC TGTGCGCGGT TTAACAAG TTCCTCCAA TATCCTTCAC	2340
TTTAGTAAAC ACTCCCGCAC GCTCCATCTC AGCACGGCCC TGATAAGCGC GCTGTCCCTG	2400
CTTATGGGTA TATTCTAAAA TCAGTCCTAA CACCACTGCA AACTCAGGAC TGCGATATTC	2460
CCCTGCCAAT CCTCCCAAAG TACCTGGTAT TCCAAGGTGC ACGCGCGGTG TATCAAAAAT	2520
TGcTGACGCA AGCTCTACCG CACCGGTAAG cTGCGCGCCA CCGCCGAGA GAATAATATT	2580
TTCAATGATA CCACGACCGC TTTGcGTCTC CACCGTCGAA AGACGATCGC GCACTATCGT	2640
AAAAACCTCA CACATGCGCG CTTCAATTAT TTCGGCGATT TCTCGTTTAG AAATTTCTAC	2700
AGGAATCCGA TTTCCCTGGC TGGAGATGAG AACACTCCCT TCTCCCTCAA GCAGGGGGAT	2760
CCAGCAACAT CCATCTTTAA TTTTAATGCG CTCTGCAGTT TCAAGCGGGA GGTTTTTTAC	2820
CTTTGCAAGA TCAGAAGTTA CCTGACTGCC CCCAACAGGA ATCGAAGTGA TAAGCACCGG	2880
GGAACCTTG TACATTGCAA TAACATCCGT AGTTCCCCCA CCAATATTAA TGAGCACACA	2940

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CCCTACATTT CGCTCGTCAT CGTTTAAACAC AGAACGAACA GCAGCGAGCC CGTTATGCAT	3000
TAAAAAATCG ATGTGCAAGT TCGCcCGTTC ACGCAATCGA TTACACTGCG CATAACGTT	3060
GCAGAACCGG TGATCATATG CACyCTcTTC CAGGCGAACC CCAATGATAT TCGCGGATC	3120
GGTGATGCCG TGCTGATCAT CCACCGAATA AACTTTGGGA ATAACATGAA GAATTTTACG	3180
ATCGGGAGGA AGAGAAACTG CACAGGCAAC TTCAaGCACC cGATCAATAT CGCTTTGATC	3240
AACTTCGCGA TGCCCCtTCC CcTTATCTGC AACCGCCACA ACACcTTTTA AATTTCTACC	3300
CTCGATGTGG GTACcTCCAa GCCCCACAAG CAGTGCGCAA tTCGATACCG GACATCATCT	3360
CCGCAGCTTC AACCGCGTGG TGGATACCCA CAACTGTATT CTCAATATTG ACTACTACAC	3420
CCCGCCTCAA ACCCTTTGAA TGACCGACGC CTACACCTAC AACCTGTAAC GCACCACCTT	3480
CCAACCGCTC GGCCACTACC GCCCTGATCG ATTCGGTACC GATATCTAAG CCGACAATAA	3540
CCTCACCCAT AACTTTCCCTC TTCTAGCGAT ACACCGCCGT CCCACCTCTC ACGTCAAGCT	3600
CCTTAATGCG CCTCTGCGTT TGCCACTCCC GCAGCGCATC AACGAGCAAT ATGACATACC	3660
GCAACTTTTC TTCGCTAAGG TTTTGTCCA TCGTACTCT GATAGGTGCA CGCACCAGGT	3720
AAAGCGCTAA ATCATATCCC CCGTGTCTTT TTTGTTCAAT GCTTATCTCA GAAATTTAC	3780
CGAGCAAAAG AGGGTTCCGC TTGCTCAAAT TATCTAACTG CACAAAAAGA GGAACAAGCT	3840
GATCGTGAC GCGTAGCCCC ACGCGCGGAT TACGAAATTC AAGACCACTT ACTACCGGCA	3900
ATACTGTATC AAGAGGTGCC GTCCCAACAC TAAAACTGT TCCTGTCTTG TCAATCTGCA	3960
CCGGCATCGC ACGGCCTTGA ACGTGACAA AACCAAGTGC AATAGCAACA CGCTCTACCA	4020
CATGAACATG CATCGTATCT GG	4042

## (2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

TTGCCTTTCA AATAAATAAG TATTTTTTTA AAAGGnGGGA GGGGGTTTAT ACTTCACAAT	60
ACTATTATAG GACATGGTGm TTTATCCCTT GCGTAAAGAA CCTGGAAGTG TTAATGCAAC	120
TTGCAAAAAA AGAGGCATTG GTTACTTGGA GTCACAGGGA GTCAAAGGAA GGTATTAAC	180
CCCTTTTTTT GTTCTGTTTT CGTTTGTTTT CAAACAAGTA ACTGGCCATG ATGATACAAA	240

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CACATACACA ATGACTTGTT AAATTACCTT TTCAAACAAA AAAAGTTATT TCACCCCTGA 300  
 GACCAACCAC CCATGAAACA AGGGAGAAAG ACAGAACCAA GTTAGAGAAG CCCCAAAAGC 360  
 AACATGCTGC ATTGCTCCAA AGACTGCCAG GTTCCCTTGc AAATAAAGTA CTTGCAACAc 420  
 CCCCTTGAG CTATGTGGcT CTGTGTGTGT TTAcTAGCAA AGCCAGTCTT TGraATCTTG 480  
 AAAC 484

## (2) INFORMATION FOR SEQ ID NO: 172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TCCTTTACAC GGTATTGCTC CACCCTGAGG GCATCGAACG CGCTGTCAAA CTTCTCCCGT 60  
 GAGCTCCCCG TTGCCAGAAG GCGATTACTG CATCGGCAGG GTCCTGGTGT TGGTTACCGG 120  
 CGTCGAGGGC GAAGGAGAAG CGCCGCACAT ACCCTTGCAA TCCCTCGCCT GTAAACTGAG 180  
 CGCGCACAGC CCCACGGGGA AAACGCGCAC CCCACCGTA CCCGTTCTCT GGCCACACG 240  
 ACAACCCCTC ACCAAACCAC CTTACCCCA CAGATAAACG TGCCAAAGTA ACGCTCAGAC 300  
 CACATATCTC GGCAcACCCA TGTaAGGAGC GTCAGCAAGC ACCCCCTGTT CCCACTGGGC 360  
 GCTGAGCTCC ACTATCAGTG GCAACTTCGT CAGCGTAGAG ACGAGCGTAC CGTCCTGCAG 420  
 CGTGAGGGCA AGCCCCACCC GTCGAGAAT CGAGGACTCC GCCATCTGTC CCAGCAAAAA 480  
 TTCAAGATAC TTATCCTTTA CACGGTATTG CTCCACCcTG AGGGCATCGA ACGCGCTGTC 540  
 AAActTCTCC CGTGAGCTCC CCGTTGCCAG AAGGCGATTA CtGCATCGGC AGGGTCTTGG 600  
 TGTGTGGTTAC CGGCGTCGAG GGCGAAGGAG AAGCGGAAGC CGGCGCCTGG TTCGAGGGTG 660  
 AGTCGGCCTC CTACTCCCCA CAGGAGTGCT GTTTTGTTTT CGTTCGTGGA GTCTTcGGTA 720  
 CCCTTACGGT AGTGCTGCTC CAGTGTGGCA TTCCCTGCCA GCTCCAACGT AAGCAGCCGC 780  
 TGACGGTCGA CGCCATAGGA AAGCGTTGCA TCGGCCCCGA AGCCATACTT GCTGTGCGTG 840  
 GTGTCAGTAC TATCCCAGGC ACCATTGGA AGGAAGGAGA GGAAACCGAT GTCCACATCT 900  
 ACTCCGCTGT TTCCACATT GTGGGCCTGG TAGCCGAGTT TTGCCCCGGA GCCGGAGAAA 960  
 CCAGGGGCAT AGCGAGTGTC CTTTCTGAA TAGGCACGGG TGACAAAGGG TTTCCACAGC 1020  
 TGGGCAAAGT TAACCACACA GGAAGGACTG GTACCCACTG TCAGGTAGGC CCCATAACAG 1080

TGCAGGGTTG	CCTGGAAGGA	AGCGGTAGGT	TTGGTAAAGG	ACAGGGCCGT	TGAGCTTTTA	1140
GAAGACGCAA	GCTCTACTGC	CAGGTCCTTC	AGCTGCAGCT	GTGCCCACAC	CCCTGAGCGT	1200
GCCTCCCCTC	GGcGGGTGTG	GGTGTGCTTT	GACACCAACG	GcAGGGAAAT	AGTCAGACTA	1260
TTGGTAGTGC	GAAACCCATG	GGTGTGCTTG	CCCGGGCCAG	TGCGTGGATT	CTTCTGGAAC	1320
GCAATGCCCC	ACTGGAGCTG	GGCTGTGCCA	CTGACCTGCG	GAGTGAGTAC	GCCTGCATAA	1380
CCAGAAGCAG	CACATACCAT	GCCCCGAAGT	ACCCCcGCTT	GCATCACCTG	CCTGmCCACT	1440
CACTCCCCCT	CCTCTcACTT	CTAmCTCACC	CCCCCCCCAC	CCGTCTAGAA	GACACGGAGA	1500
GCTCTATCTC	ATGAGCACCT	ACACACTCGC	CTTCTCTTGG	GGGACAGACA	GAACTTCCGA	1560
AGAGAGAACA	ATAGGTTCCG	GCGATGTTTC	GAATAGGGTA	AGGCGTTCTG	ACGCCTcCTC	1620
TAATGACTGC	GCCAGACGCG	CTACCGTGGC	TTTGCTTAAC	GCAACGTtGC	TgCGCCGATT	1680
CGATCATCGC	CTCGTACTCT	TTGATCCCCC	GTCGATATnC	CnCGGGGGGG	GGGGGGGnGn	1740
nnnnGCACAC	ACGCTGGGcN	GACTIONAGCT	TTTGACGGAG	CTTGCGGCAC	TCTACCTGAT	1800
ACCCCTGCACG	TGCCACGCGC	ATCCGCGCTT	CTGCCACGGT	ACGCAACAGC	GTGCTGAGTT	1860
CATCGGGCAC	CGTCGGTCTT	GTCTTCTGAG	ATAAAGGAGG	CTGAGCAAAT	CCTTCCTCGG	1920
TAAAGAAACA	ACTTGCGTAT	GCAGCACCGA	TGCGCGCGCA	CAGCCATTGA	TATCCTCATC	1980
CAGTTCACTG	ACCTGCGCTG	TGAACGCCGC	AACGCGCTTC	AGCGGCTTGG	CACCACAGTC	2040
AAGGGcGCGC	AGgCGgCGTC	GAgTGCTTCT	TGCTCATCCA	TAAGCTCcTG	GCTATGTTGA	2100
AGGTTGCTCG	CGTAAACGCC	GCGGTCGGAT	ATGAGCCGTG	CGTACGCGGC	ACTGAGTGCG	2160
GAGGAAAGCT	CGCCTGCGTG	ATACATGCGC	TCGACGTCCG	GATGCGCAAT	GACATCCGGG	2220
GTACAGAGCG	TAATAATCTT	TTGAATTTTT	GCTTCGAGCA	CGCGAATCCT	GCGCTGAACA	2280
ACCGCGCTCT	TCGCCTGGAG	GCCAACTCTT	TCAAGAATTG	AACCAAATGT	GCATGTTTCC	2340
AAGAGCTGGT	CACGCTTGGC	GCGTAAATCC	TGCAGAGTAG	ACTCAAGCTC	CGCCGTACGC	2400
GCATAGATCG	GTTGAGAGCG	AGGTAGGCCT	ACGTGCGCGT	AGGTGGCATA	GTACTIONGGCT	2460
ACAAAACTCC	TGAGTACATC	CCGCTCCTGA	CGAGCATGGC	GGTGCAATAC	TTTGCTCACC	2520
CGCTTTCCAA	GAGCGGCAAG	TTCTTCTTGT	CTTTGAAGTA	TCGACTTAAT	ATCAAGGATA	2580
GACTCAGCAA	CCTGATCGCG	CTGACGTTGA	AGCGCGTGGC	ATCGGCTGAT	GTCAGTGTCC	2640
TGTACGCCAA	GTCCGCTGAT	GTCACACGCA	GCACCGCCGC	GCACAATATG	TTCAACCGAGA	2700
CTGCAACAAT	GGCTCTGCAG	ATCCTGCTGC	GCACGCTGAC	ACGCGGCATT	CAGCGCGGAA	2760
AGACTCTTAT	CCGCGAACAT	GACCGCATTG	TAAACACTTC	CCCTGCGTAT	GTACAGGGCA	2820

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CCTCACTCCC TCTTTACCCA TGCAAGGACA GACGTCCTGC CTAACCTCTGG CGGGGTACTA 2880  
 CCTGCGCGCT CGTATTCGGG TACAGATTAT ACGCCCGATC CATTGCGTTA GGCAAcCTGC 2940  
 GCCAGGATTG CAAGCACTGC CATTGTCATC ACCTCTGGTT GGAAGCGCTG ATACCCGTAG 3000  
 CGGATCGCTA CGTCTcCTAA ACCTcCTcCC CCAATCGCCC TGCCATTGCT GAGTATCCAA 3060  
 TTAGATTAAT TACCATCAGT GCTACACCAG AAAnCACATG CAGGAGCAGC CTCAGGCAGC 3120  
 ATGATTTTTA GTAC 3134

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ATtnTTTAAT nATAGGATCC CGTCACGTCA TACACAACTT TCTCCGCATA AAGGCACTCA 60  
 TCTAAGTTAA GCTGAAGCCC CTCATACAGG ACATCAATAG AACGTGCTAG GTGATAAATA 120  
 TTGTCTTGAA ACACAAAATT CTGCACCACA GACCTCCCCA CACATACGTG ACCGACGCGG 180  
 GCACACAGGA AAGCGCACCT TCTGCGAACA GGTTCCTCAC CTCGTCTGCC GTAAGAGCAC 240  
 ACGCACGAAT GTACCCCTC AGACGACGCT GCGCCGTCGG CAGCATCGGA TAAAAGGACA 300  
 AAAGACTTGA TGCGGCACAC AGATTACGC TACGCTGGCG TCTCGCCGCG CGTTCTGCGC 360  
 ACGCTACTCC TCCTTGTCGG GTGAGTCTAG TGCAGCCTGA TAAGGTGAGC CGTCCATAGG 420  
 AGTTATTATG AGGACCTACG AGnTAATGGC CGTTTTcAGT GCACACGAGG ATCTCTTTCT 480  
 TCAGGGTTCC ACCGCCGTTC GTGCCCTCCT ACAGGAAAAC GACGCATCAT nCGCCCGCGA 540  
 AGACCATATT GGAGAnCGGG AACTTGCGTA TCCTCTGAAG AAGCAAAAGA GGGGCCGTTA 600  
 nCTGCTCTTC ATTGTTCAGT GTTGAGCCnG GGAAA 635

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CGGTACCTTC GGTTCCTGGG CAGGGCTTAC TGCAGCCGAG CAGCTCGTCT TATTCAGCCG	60
GTAACCTGGCA CCGCCACAGT TCATTGCTTG GCGTGCTAAG TGCAGTCCA AGGAGGTAGG	120
CGCCATACAC GAAGAGTCGG CGTATTAAAG GGGTCTGTCA GAACTATGCG GTGCCGGTGC	180
AGCTGGGGGT ACAGCACTAT TTTAGCGCGC ACTGGGGGAT AGACGCGACG GCTACCGTTT	240
CGTTTGGCAT TGACACCAAG CTGGCTAAGT TCCGCATCCC GTATACGTTG CGCTTTGGCC	300
CCGTCTTCCG CACCTAGGGG ACGGCGCTGG GArAAAgAG TCCTGCCGGA AGGccCTGCG	360
GCGGGTAGTA GCTACCAGGA GAGGGTGACG CCGCACACGA TGCGGCCGAT TCCCTGGGTG	420
AGGCACTCGG ACACCAGCAG GTACGGGACA TCAGAGAGCA TACCCTGTTC CCAATCAAGG	480
GAGAATACCG TCTTCTCTAT GAGACTGGCT GAAATACCAG CACGCAGCTG TGCACAGTAC	540
TCCTTGGTTA GATAGGTAGC TCCTACTGCT CCACCTGCAG CAGGGGCATT CAGGTGTGCA	600
CGGTGGTAG AGGCATGGAC CGTAACGCTT GGCTTCACCC AGCCGTAATC CTGCACCGGG	660
ATGCGATAGC TACACCACGC CTTCCCCACC ACCGGTGGAC GGATATACTC CTTTTCTGA	720
ATGCCACGCA CAGCCGTCCC CCCGTTATTT TTGTATAGCG CATAGGTGAG GGGGATGTAC	780
ACGCGTGTTC CAACGCCGGC GTCCAGGCCG GTGAGCAGGT GGGTGTAGGG GTCACCGCTC	840
TTAGTTTCGA GCTTAAGGAA TCCGGCAAAG TCGCCACAGC TTGCGATGGT GTTATCTAAC	900
ACCCTGGTGC CAAAAACGTT TGCCGGTGCT GTGGCAAAGT ATATGCCAGA AGACAGCCAC	960
TTCCACTGCG CCGTAAACAG CGCATCGAAG GCGACATTGT AGGTGTCAAG ATACAGACAC	1020
ACGGCGCTGA CTCCCATTAG AAAGGCACGC CATGCAGACG CACGCAGGTT CTGTATAGCC	1080
TGACGTATCT GCTGCCCCGC GTCCAACGCA TCCGTCTTCT TCTTCACTTC TTCGGTTACA	1140
AACGCTGTAC CCTCAGTGAA AAACTTTGTA GCCTCAGCCG TAAGCTTTGG AATAAGATCG	1200
GCGAGATCGT CCTTCAGTAA TTTTGTGTA TCCGGAAGGT TGAAGAGGCT CATCGGATTT	1260
CCCTTATGCG GTGCAAGCAA CGCATCAGCC ACGTCTTCTA TTGCCTTGGT AAGACCGTTG	1320
ATGAATGCCT GTGCTGCAGC CTTGCTCTGA GCCACAGCCG CTTGCACTTT CTGGTTAATT	1380
TCAGCAACGA TTTGCGTCTG TACCTGCTCA AACCCTTCA CCACCTGcTC CGCATCGTAC	1440
TGCAGCAAAA CCTGCCCCAT CAGGGAAAAT GCAGGAAGCG CGGGAAGCGG TGACGGTGTA	1500
GGAGGGTCGG TAATGAACAC CTTCAGGTTC GTCAAAAGCG TGGCAGCTAC CGGAGGGGTG	1560
ACTTTTACGT TTGACACTGC CGTTATGTAC GCGTTTCCCC TCGACTGAAG GGCGGTTTCs	1620
GTGGyksCgT TACGGCATCA AGCA	1644

(2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

CACGTACCGT CTCTGCAACC GTAGAAGCCT TCAGAGAAgG ACAACCCGAT CAAgTGTAAC	60
TGATCTAGAT ACGCAGCTTC TGCAAgGCAG TTTGCACCAA CGCTTCTGCA CGCGCATTCA	120
cTGAcTGCAT CCCATCCGCG TAACGCGCCG CAAtGCGCGC TTCACCACAC CCGGCAGAGA	180
ACCGGTATTC ACCCCAATAC GCAAAGCAGT GCCGGTTGCT CGAGCCTTTT CTACCACCGC	240
ACGCACGCGC TCACGCACAC CGATATTCCC CGGGTTAATA CGCACTTTTCG CTACCGGTCC	300
GTCCATACAC CGCAGCGCAA GCCGGTAATC AAAGTGAATG TCTGCAACAA GCGGCATACG	360
CGTGCGCGcG CAAAGCsCcA CAAAAAGCTC AGCCGATTCC CTGTCAGGAA CGGCAAAACG	420
CACAACGTCA CACCCTAATT GTTCAAGTTC CAAAAGACGG TCCACAATGG ATTGGAGATC	480
TGCACCAATG AGCGGTTCTT TCCACATTGT TTGGATAGGA ATCGGTGCGT CACCCCCAAG	540
AGGCAACGCA CGCACATGTT CCTTTCCTCC AATTACCAAT GATCGTGCAC GGTAGTGGGA	600
CGCACGCGGT CTTAATTTTA ATGGAACATC CAAAAGTCCA CTCCCATACG GACTATTGCA	660
GGGAGACACA CCGGCAGATG AATCCACCTT TTCTCTGgC tGCCGCGCag CACGCTCGTC	720
CCTCTGATTc ACCGGGCCAC CACTTGCGCA CGCACACTTT GCGCAACTTC CACTCCACAG	780
AGTGCTTCGA TAACTGCGAA AGAAAACtCT TCTGCCGCAC CTGCCGCACA CGCGGTCAAA	840
AGATTTCCAT CACGTACCAC CCGCGCGCGC TCAGGTTTAC GAAGCGCACG CGATTCTCTC	900
TCTTCCGTCC TTTTCCCAAC CCCATCGTCA TGTGCGGAGA ACACCGCCGG CTCCATACCC	960
GGATAGCAGG TATAGCGACG TGACCCAGG AGATTCCACG CAGAGAGCAC TCGCGCCGGG	1020
GCAGCACACA GCGCAGCGAC GAGTCCTCCG CGCAGGTGCA CGCGCATGAC AAAATCACGC	1080
ACCGCCGCAC AGGCGGCAAG CGTATGACAG TTTTCCAACC CCCCGGAAG AAGAACCGCA	1140
TCTGCGGCGC ACGCGGCATC CGCGATGCCC GGAGAAGCAC AAAGCGCCTC AAGACTGCAG	1200
TCGCAGCTCA CACGCAAGCC ACGCGTAGAA ACAACCTGCT CTGCCCCAAC ACCCAGGAGC	1260
GTTAACGCTA TCCCCGCACG TCTGAGATAA TCCAACGGGG TGATAGTCTC CACTTCCTCA	1320
AATCCGTGTG CAACAAAAAG GTATACCCGT ACGCTCACCG CAACACCCCC GTACCTGTTT	1380
TTACAGCAAC AGTGCAACCC CGCGCACACA GACTACGGAT AATCGTCCTC CGTTCAAAAG	1440

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CGACGTACTA GCCGTGCGCC CCGCGAGCGC AgCACTACCT TAGGATAGAA GAACTAAAAA	1500
CCACGCGGAG CCTGTGCCGG ATCTATTGGT TTATTTTTTT TATATACCAT AAAGTACAAT	1560
CGTGATCGCG CCGCTGCTGC GTCAAACCCC AAATTACCGA GCACGTCGCC GGCAGAAACA	1620
TAATCTCCTG ACTTTGGCAA AATACGCTCA AGTCCTCCAT ACACGTACAC GTGCTTTCCC	1680
GGCGACTCTA CAAAGAGCAC CTGACCATAA CCCCAGTGGG TCCCCCTGGA GATTACCTTA	1740
CCAGACATGA GTGCACGCAC GGCAGCATTT CTTTCCGAAT CAATAACAAC CCCGTAGgTC	1800
TTGCCCCGCA CGTACGCAAG CGAAGTCGGG CTCACCGGCC AGCGCGCATT CTTATCAACT	1860
TTCTTACTGA TATACTGACG CGGATCACGC AGAGAAATTT CTCTCCTCTC GGGGGCCGGC	1920
ACAGCAGCGG GGGGAGAAAC AGGAGTCTGT ACGGGATCGG CACGGGCACG CGCCCACTGA	1980
TCCCCATCGG GCAAAGAAGA CACAGATAAG ATGCGGTCCG CGCCCGCCAC GGTAGGAGGC	2040
GACTTTTCAC GCGGAGGAAT CACGAGCACA TCACCTGGGT GAATAGTGTG CGCAGCAGAG	2100
ATTCCGTTGG CTGCAAGAAG CGCGGCAAGT GAACAGTTTA GCATACGGGC AATCGAAAAG	2160
AGGGTGTAC CCCGGCGCAC CGTGTATCCT CGTGGAAC TAATGCGCTG CCCAGGCACA	2220
AGCTGGTGTA CGTTTGCCAG ATTATTTGCC TGCGCAACGC AGAAAGGGGC ACGCCATAGC	2280
GACGCGAAAG TGAAAAGAGG GTCTCGCCCT TAGCAATCAC GTGCACGTCT GCGCCGCGCC	2340
GTAGGCTGCT GCCAACAAAA AACACCCCGC AAGCGACAGA AAAAAACCGC CCATACCCGC	2400
CCCCTTCTCG GCAGATAAAA AAAAAGCATG AGCGTCACCT ATGCGCGCCC GTTCCCCCTG	2460
TCGTAAATAA CAAACGTTCA CCCGCAGCCG AGACACTCCA CAGCCGGCAG GAGCACGCAC	2520
TAACCCTACT TGTCG	2535

## (2) INFORMATION FOR SEQ ID NO: 176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

TGGTTCTTGC GCCGATTTGC TGACGTACTT GAGTCCAAAG ATGCGCAAGG AACTGGAAAA	60
TGGAAGTGAT TAAGGATTAA TGCTCATGGC AAGGAAGAGG CGTGCTCCGC GCGGGGCGGC	120
ACAAGGGTGG CTAACGACAT ACTCAGATAT GGTACAGCTT ATGCTCTGTT TTTTGTGCAT	180
GCTGTTTAAT CCAACTGAAG TTGATATCAC GGTGTTGCAG AGTATTGCTG CATCGATTGT	240



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AGGTGATCCT ACCGGTGGAG GGGTTTCTGC CTCCTCAGGG AGGCTCGCTG ACTTGGGAAA	300
CACCGTTAAC ACGCTGCCTT CACTGGAAAA GGGACAGAAG CTGGCGACTG CGCTGAAGAA	360
GGCGGTTTCG CTTTTCGCTC CTGAGATTAA AAGCAATAAG ATTGCGGTGA CCAGTGATGA	420
GCGCGGTTTA GTTATTTTCG TCACTTCGGA TTCGTTTTTT TATCCGGGGT CTTCCGATCT	480
GAATGTGGAG GAATCTCGGG AGGCGTTGTT GCGTGTTCG CAGTTTTTGT CTGATCATGC	540
GCTCGCCCGT CGACGGTTTC GCATTGAGGG ACACACCGAC TCAGTTGAGG TGCCCGAAGA	600
TGGGAGTACA GACAATTGGG AACTTTCTAC CCGTCGGGCG GTGCGCGTGT TGCATTATCT	660
TACTGATTTT GGTGCaCAGG AAAATCGCTT TTCCCTTGCa GGGTACGCAG ACACACGCGC	720
AAAATTTTCA AACGAAAGCc TGAAGGGAGG GCGTACAACC GGCGGGTTGA TATTGTCATC	780
CTGGACGAGG GTCACTTTGT ATGGTACACT TCCGCTTCCC CTTTCCCAGA GGTGAGTTTC	840
CGGTATCTGC ACAGCCTGAG TTTGAGCTGG TGGCgCGTCT GCACGCCGCT GTAGTACGTG	900
AGGAGGATGT ATGGCAGAAA AGGACTCCAT AGGAGATATC GCTGATGATT TTGAGGAACA	960
GCTTGTCGCT CCTGCTGCGG ACAGGGTGGG CTTTCTGCCA GGATTGCTCA GATGGGTTCG	1020
CATTGCAGTA GGGGCGGTCA TCTTCATTGT GACGGTGGTG ACAGCCACCG CGCTGGTGCT	1080
CGCAAAGCAG GGGAGTAGCC ACACGGCGTA TCCGGTTcAC AGGAGTTTCG GgAGTCTCGC	1140
GAGCTTTTGC AATAcTACGA GTmCATGGGC CTATCCGTAC CAATACTGCA GATGCGCTAC	1200
CGGGGACGTT GTAGTGAGCG TTGCGT	1226

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATCAAATATT CCGGGGATAT CGTCACATTT CCTGAAAATT CTACCTTTGC AAAAGAAGTT	60
GCCGGAACAA CAAAAAGATA AAATACAAAC TCCACACACA ACACGAGCAG CAATATAACA	120
ATTACCACCT TCAGTACTGC AACTCTCACC CGCATAGACA TATACCCTAC CAGAGGGTAC	180
TTGCACGCTT CAGTATTTCT ACACAAAAAC TGTTCCTTCA CGTCCCTCC tTATCTTCTC	240
ATCCCCTGAA ACATTGATGA TCAATCCACA TAAAGAAAGC GTTACCACAA TAGATGAACC	300
TCCTGAAGAA AAAAAGGGAA GAGGAATACC AGTGGCTGGA ACTAGACGTA CCACCACTGC	360

843

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AACATTCAAA ATTGACTGTA AAACAATTGC CGCCGACGCG CCGAAAGCCA AAAAAGTATT 420
AAAGCGATTA GCACATCTGA GTGCGATAGA AATGCCAGTG AGGGTAAACG CAAACAACAA 480
CATTAAATAT AAACACACAC CAATGAATCC CATCTCTTCT CCAATAACGA CAAAAATAAA 540
ATCCGAATAT ACTTCGGGCA CGCTCGCAAT TTTCCTCACC CCATTTCCAA TACCACGCCC 600
CCACAACCCT CCATCCATCA GTGCCTCGAG CGCCGCGTTT ACTTGGTATC CTGCGCCAAG 660
CGGGTCTCTA TCTGGATACA AAAATGAAAG CACTCGACGC AAACGATTGG TGGACGTGAC 720
GATCATAAGC ACTGCTATCG GCGCAAGAAC CATTATGCCT CTAAAAACC ACCACAGAGG 780
CGCACCTGcA ATGAAGAACA TAACCACTGT GATAAAAGC AAAACATAG CGGTAGAAAA 840
ATCGTTTTGA AAAAAACTA CTGACACAAA AATCACGCTC ACAACAAAGG GAGGAAAAAT 900
TGATCGTATA GGTGTATCGA AATGCTCCCG GTGCTTATCA AAAAAAGTTG CAAGAAAAAC 960
AATGAGTACC AGCTTCACAA ATTCAGATGG CTGAAAATTA ATATCAACA CCTTAATCCA 1020
ACGCGTCGCT CCATTGCGCG TTGAACCAAT ACCAGGGAAA AACGTGCACA CACAGAGCG 1079

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## (2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 556 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

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GnTTTGAAGC CGTAGGCATC TGTGCGCTTG CAGAATGTAT ACATGCAGGG AGTGCGCGTA 60
CGTGCCACGT GAGTnCTTGG GGAAGCAGC TTATGTTTAG ATCGCGGGGG GGGGGGGGGG 120
nGnACTTGTA GTGCTTGAAC GGGATGTGGA CCGAGTACTG GAGTACCTGG GAAAGACGGC 180
GCTTGTCCAT TTGCGTCTTT CCGCCGCGGC GCGTGCCAGT TCTTCCCACT GTGCGCAGAG 240
CAAAGAGTAT GTCGGCCGTC TTGAAGAAGC GTGTAAGTAC CTGGGTGTCT CTGGCGAGTG 300
CGCGTTTTCT CCAGGGGATT CTTTGCCTAC CGAAGAAGAC TACACGTTGG CACAGCAGAT 360
ACTTGCAGAA GTTGACGCTT TGCACGCACG CGAACGAGAG GGTGATGCTC CCTCAGTTCC 420
CCGTGGGAAG AGTTCTGTAG CCCATGATTC TGCCAACGAA GAGCAGTTTC AGGGTGAGAA 480
ATGTGCGCTC GGCTCGATGC GAnCCCCGGC ACTGTGTGCG CTGCTTAGGC GTTTTGCCT 540
GCAGGAAnGT GTGCAC 556

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## (2) INFORMATION FOR SEQ ID NO: 179:

844

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TnTGACTAAA GTACATGCTT GCAGCGATAC TCAATGAAAT TGGATTCAAC ACCGGGCTAT	60
ACGCTTCTCC TCACGTTATG GATCCGAGAG AGAGAATAAC ACGCGCGGGT GTGTTTTTTT	120
CACCTGCCGA GTATGCAAGC GCGTGCACAC ACGTATACCA CACGGTGAAA AAAACAGAGA	180
ATCTGCGCGA CTACGGCCAG GCGACGTGGT TTGAGCTTAT AACGCTACTG GCGTTCATGC	240
TATTTGCACA ACAACGCATG GAATGGTCCG TTTTGAAGT AGGACTTGGA GGAAGACTAG	300
ATGCAACAAA CATCATTTGT CCTAGTATCT GTCTCCTTCT CCCCATAGAA CAAGAACACA	360
CGCGCATATT AGGAACACGT ATAAAAAGTA TTGCAAAAGA AAAGGGCGGC ATTATCAAAC	420
CCTATACGCC TATTTTTGTT TTGATCAGCC	450

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TGGGATCTTG CAACTGACGC TCCCCCTGAG CGTGTGCGTA TGCTTTTTAn ACGCACGGTT	60
CCTACTGGnA TTGAACACGG CACTGTTACA ATTCTTTTCA nAGGGCATTc TATTGAGTGC	120
ACTACGTTCC GTGTGAGTC GGATTATTCC GATAGAGACA TCCGGATTCT GTTTGCTTTG	180
CCGCGCGCAT TGAGGACGAT TTGGCAAAGC GCGACTTCAC TGTCAATGCT TTCGCTGCCG	240
CGCTCCCCTC GGGGGAAATC ATCGACGTAT GTGGCGGTTA CGCGATTGc GTAACGGTCT	300
TATCTGTAGC GTTGGGGATG CACATGCTAG ATTTTCTGAA GATGCGTGCG TCCTTTGCGT	360
GGCTGTGCGT TTTGCAGCGC ATTATCTTTT TCCATCGAAG CGCGCACGnT GAAGCAATTA	420
TCGCGCTACG GCTTCATACT GCACGTAATT CTCGTGAnCG GGTGCGTGAT GAACTTTCTA	480
AGATGCTTTG TACTCCCCGT CCGATATTGC GCTCCGCTAA TGGAAGAGAn TGGGATGCTG	540
CAAACACTTT TTCTGCGCT GGCAGTGT GTGGGAGAAA CGAAnGGGAA GGAGAAGGAG	600

ACGCA

605

## (2) INFORMATION FOR SEQ ID NO: 181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGnCGTTTA AACGAAAAGG AGAGTTCGGT TTTTGCACGT ATTGAATAAA TGTTTTAAAC	60
CAAGTGGATG CATTGTCGTG TGTAAAAAAT AATTTTGGT AGCAGTCGAG CGGAAGCATG	120
GAAAATGAGC ACAGTACCGG GGGTGTGCGC GTACCGTGCG ACAAGTTGCG CATAGAATGT	180
TTCAGCGGGG GTGTCAATCG TCAGTTCGCG GTACGTAATG CAACAAGGCA TTTGCTGCTG	240
TCCTCAAGTA CTGCAGGTTT AGTAGCGGGC ATATCAGAGG CTTCAAGAG ACGGTAATCT	300
AGGAGACAGT ATTCCATTCC GGCCTTTACG AGTGAGGGAA TGAGCGCGGC GCTCCATGCA	360
GATGCTTCCA GAAAGCAGCC CCGTGGGCGT TTTATAACGT GTTCTCGCAA GGTAAGTG	420
AGTAGCTCAA TTTGACTAAT TACATCCGCC TGAGGGAGGA GGGGAAGATA CGGCTGGTAA	480
AAACCGCCGC TGAGTAATTC AAGCCGTTTG GAACCAAGCA GATTGTTGAT AAGATAAGGA	540
TAGGGAGAAT TCTTTTGTG TATAAATTGA AAAAAAGAAC CGGTCATGTG CACCGTCAGT	600
GGGAGTTGTT CGTGCCTGCA CAGACCTGAA AAAAATGCCT GGTACTGAGA AGGATCGTGC	660
TCTGCGTGCA GGGACTGAAC ACATGCTTCC GTTAACCTCG CAGCAAATGC GATACGTATT	720
TTGGTATTGT CTCCTTTTTT CATAATCGGG TTCTCATCCC CGCCGCGGGT ATCGGAAAAA	780
GCCACAGCTC GTCAGTACCG TACAGGCTCA GTGCAATAAA mCCCATACTT GCTAAGAGAA	840
GTGCAGCTGT TTTCTCCACT GcAGTGCCGT TTCCCTGCGT GATGCGCTGA TGTATCGCGC	900
GTAAGATGGT GGAGAAACAT AAAAAGCCGA CACAGCTCAC TCCCCACATA ACGAGCGCCT	960
CAAAAAGGTT AAGGGCAGTG TACGTAATGT AAAATACGAG TGCGTATAAA AGACCCCACT	1020
CGCTCTGAGC ACGGTGTGAT GTACACGTGC GCGACAGTTT TCCGCTGCAT GTACTCAGAC	1080
AAAAGGCACT TGCGCCACG CCAACGGTG TAAGAAAACG CAACGCAAGC GGGTCATATA	1140
CGTAATGTAT ACAGACCCAG TTACCGGTTA TCAATATTCC GCnTAGGAAA AGGAAGCGAC	1200
ATGTATGGAA GAGCGTGCAA CGTGGAGAGA GCGCAGCGAT GCACAGGCGA TCTAATACCG	1260
ATGCC	1265

## (2) INFORMATION FOR SEQ ID NO: 182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GCACCCGAT GACCGTTCnT GATCGAGCGG GTACGTCCAC CGTGCGCCCC ACACCGAATG	60
TnGAGCGTCC GCGCTCCCC CTGCATGCGG TACACAAAA ATCCGCTCnA CGCCGTCACT	120
GCCAGCACCA GCGCCACGCA GCACCCGTCC AGCAGCGTCA GCATTCCGCC GCGCGCGGCA	180
GCCGACCCGA TTCGGGGGAG AGGTGGAGGC ACGATCATTC TCGCCGCAGG CCACGCGTCC	240
CCCCGTTAGC GCTCAAAATA CGCACGCGCC TGCCGCGcCA GACGCCGCCG CCCGAGCATC	300
CCCCGCACCC CGCGGGCAAA AAATACGTCC AACACTGCAC GGGCGTGCTG CACCGCCGCA	360
TACCCACGCG CCACCAGCTC tGCGGaCGAG AAAAATCACT CTGGTCccGC CGCGTTTCTA	420
CCCGCACACA CGCGCTCGGG TAATTGCGCG CCTGCGTGCG AACC GCATGC GACGCACACG	480
AAAGACTGCG CACAACCACG TCAAACCCCG TCCGAAAGTC ACTGAGCCCC AGCTGCTCAA	540
ACCGGTCAAA CGTCACCGCC AGCACC GCGT cAAAACCCTG CGCGCGCGCA ATCCACACCG	600
GCGTGTGTGT CAATATACAG CCGTCCGCCA AATACACCCC CTCCTGCCGC ACCGGCGCAA	660
AAACACCCGG GTACGCACAC GAGGCGCGCA ATGCACGGGC AAGCACCCCA CTGGAGAGCA	720
CAACCTCCGC GCCCGTACAC AGATTGACCG CATTGCACAA AAACGGAATT TTACAATCGT	780
GAAAGGATTT CCCCCCGTC ACCCGCGTCA gsAGcGTGGC AAAC TTTTCT CCCGAATCAA	840
GCCCCAGCCC CCGCACGAGC GTGTTCAAAC TCACCCCCAG CTGCACCAGC TTGCCCAAGC	900
GTTGAAACGC AGCCCGCGCC CCCCACACCA TCCCCGCCTC AACGCACGCA GAGGGATCCC	960
GTGCATTAC ATAGTCTGAA ATAACAAAT CACGCTGAAA AAACGCCTCC ATCTCCCGCA	1020
CCGACATCCC CAGCGCATAG AGCGCCCCCA CCACCGCACC CATAGAACAT CCTACGACAC	1080
ATTGCGGCGG CGGAACCTGT AGCGCTTCAA GCGCCTTGAG CACCCCAATG TGGGsAATTC	1140
CCCGCGCACC ACCACCTGAA AGAACGAGCG AsCACTTCAC GTGCGGTCAT TATGAGCGTT	1200
TTCTCCCTG CTGTCCATTC TCCCCCAGT GTGATACCGT TCCAGTACGC AgTATGGAAT	1260
CGTTTGTACG CAGCGCACTT GCGGCGCGCA CACTCCCCA	1299

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

TTAACCGGGC GTTTCCTTGC AGGTTACGCA GGATTGCTTG CAGCAAGCGG GGCAGAGGGT      60
GCCTTTGATT GGCAGAGAGC GGACGCGATT GCAGCGTTAG ATCAGGCAGG AGCGCAACAT      120
GCGGTTTCTC CTATCGCTCA TCCTGCAGGg TGGATGGAAC TTAATCCGGC TGTGCTGTCT      180
GATGTGTATA GTGTGGCTGC AGGATATCCG AGTGCGGAGG GACTCCCTCA TGCGGGGGAT      240
AACCGGGCGG CGCTTGCAAT CGCATCGTTG AGAAATAGCC CGGTTATGAT TGGCAATCGA      300
CACACGTTTG ACGAGTTTTT TGcAGAAGTG ACAACAGCAA TCGGTCTTAA GGGAGAACAr      360
GCGGAgCGTT CGATGCAAAT GCACGCTGCA ATTCTCAAGG AGCTCACAGA TATGCGTGAT      420
GCGACGTCGG GAGTGAATAT TGATGAAGAG TTGGCGGACA TTATTAAGTT TCAGCACGGC      480
TATAATGCGT CTGCGCGTTT TATTGCGGCG GTGAATGAAA TGCTCGACAC CGTCATCAAT      540
CGTATGGGTG TTTAATTTTC AGATAGTGCA CGGTATGAGG AAGGGAGGAT GGGCGTGAAG      600
CGTATCAGCT CACACATGCA GGGCACAGAC AGTGCCTTTT TCTTAAGGGA GCAGGAAAGT      660
AGACTACGGA AGGTAAACAA TCAGCTTGCA ACGCAGCGTA GGATCCAGCA GtTCGCGATG      720
ATCCGCTCGC TGCAGGTCAT TCTGTGAGGT ACAAGTCGTC CCTGGCGCGT TTAGATCGCT      780
TTGAGAGAAA CACGAAACT TTACGTGACC AGTATCAAAT CGCCGAGGGG TTTATGACTT      840
CTGCGCTGAA CGTAtACAGC GTCTTCGGGA AATGgCTGTC GCAGGAGCGA ACGGAACCTA      900
TACTCCTGAC GATTTAAAAA AAATGGCGAG TGAAGCAGAT GAGCTTTTAC AGGAGCTGGT      960
GCACAATGCA AATGCAGTGA GCGCAGATGG GGTGCGGGTA TTTAGCGGTA CCAAAGTTTT      1020
CACAGAGCCC TTTGAAACGG TCATGGGGAA TGTTGAGGGA TTAGGGTCTG AAGTGATCAC      1080
TCAGGTACGC nTnTTTCCCA AACCGGGGGG TTTTTT      1115

```

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

CAGCCTTGGG CGACTTCCTC TGTGAATGTT CAGGCCTATA CTAGGCAAAG ATTTGAGAGG	60
TTATCTCGGC AGACCTCCGC AGCTCTCCCT CCACCGTAAC AATCTCCTCT CAGGACCATG	120
ACCCATCTTT TACCCTCTAA GCTCAGATCT CTCACACTTC ACAGATTCCC AGGCCCTGGC	180
TTGGTTCCTC CTCCCTGCAC GACAGCCTGG AAATGGGCTC TTATAAATCA GTGCAGTTGT	240
GGGCATCACC TTGGCCTTCC CCCATCTTAG GGATCATAGT GCTAAATTGC ATGTTGTCCA	300
AAATCTGAAA GCCATgTTTT ATGTATTTCC CCACTTTTCT CATGTTTAAG GTGATGCAGT	360
TAATCTaCCT CTGTTAcTCC GCCTgACTGA AATTGGAAGT CCCgTCTgTG CTTCTCTCCC	420
AGATTcATAC CAkGCTCAGT TAnCTGGTCA ATTTTGTCTG TTGA	464

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CGCAGGTTTT GCCGTGTAAT CTAATGCTTG AgCtctGCGG ctAACTTCTG TCCaGAaTCA	60
GCAaTTTCCC CAAAAACAC GCTACaTGcm TcAAaGGCAT AATCACGTAG AGCAAACAGC	120
GCATATACGA TAAAAAACCC AAATACAAAC TGCATATCAA GCGTAGAAAA ACGGTGCACC	180
CAAAATACCG ATATGTAACC TGCTGTACAT GAAAACCCCA CCGTGCATAA CACAAAACGC	240
GATAGCGCAA ACACCACTTC TTAAAGGAA ACAATTCCAG TAGACGCAA TGCCCACTGA	300
GAAATAAAA CTATAAATAC ACCTCCTAAG GGAAAAACA CAAACACCCA GGGAAAAACC	360
GcAAACAAGA ACAAGATAAT aACCCACGTG aTaAAACCCA AAGCCACTGc CCCCgGAGa	420
AACAGGAGTT GTTGCCGATA TGcAATACTT TTCATCATGA ATGCTTTTTT cACCAAAGTT	480
GCGAACGTAA aCAGGGAATG ATTAGAAAAA AAAGCGCCGC GTTATAACAC AnTACCCGAA	540
ACAGAAGAAA ACAAATAATT TTGGTAAAAAT TTAAAACTTC	580

## (2) INFORMATION FOR SEQ ID NO: 186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

AAACCGCGCT GCGCAGCCTG GGTAAACGT TCGCTTGAA ATAGAAAATC AGCAGGTTGT	60
CGGGsCGAGT ATGGGGGAAG AGAGTATTCG GCAGGGTACG CGCGCGCTGG TGTGGGGGCT	120
GTGCGCGGTG CTCTTATTTA TGCTGGTGTG GTATCAAGAA GCGGGCGTAA ACGCTTGTGT	180
cGCGCagCTT TTGAATCTGT ATATCATGTT CCGTGTGCTT TCAGCGTTTA ATTTGacCTT	240
ACGCTTTCGA GTATCGCGGG GATGATTCTC ACTATTGGTA TGGCAGTGGA TGCGAATGTC	300
GTTGTCTTTG AGCGTATACG GGAAGAACTT GCGCTGGGCA AAAGcCGCGG GGCTGCTGTG	360
TGTArCGGCT TtGagCGTGC GTTTTGGGCA ATTATGGATT CAAACGTGAC GACGTTTATA	420
GCAGCGCTTT tCCTTTCGgT GCTCGgTACC GGTCTATtA AGGGTTtCGC ATACAGTTTG	480
GCTATCGGGG TGGTGTCTC CGTATTACG GCATTGTTCG TTTCCCGTCT GATGTTTGAC	540
TACGGGACGG AGGTTTACa CAAAAGACC GTGCGCATTG GATGGAGGAT TGCTCGCGTA	600
TGAGACAGGT GGTGCGTTTC AGTTTGCTGT TCCTGCCATG CGCGATACTC AGTGTAGTTC	660
TCATTGGTGC GGGAGTGCTC CGTTGGGCAT TGTGGGGGAT GAGCTTTGGT ATCGACTTTC	720
AGTCTGGTTT GATTGAACGG CTGAGGATAG CACCTCCTGC TTTCTCTCTC GTGTACACCG	780
GAACGCATCG ATGCAGTTTT TTCAGGATGA ACAGAAGGTT GTGTTTACTG TCTCTTCGCC	840
TGGGGTGCTC GGTGagCGTT ATGAATTTTT GTATACGGAG TATCCAACCC TTCGTGCCTT	900
CTCCGagGGA GCAAAGAAGG TGGAGCACCT CAGTGTACG CTCCATGcCC CTGagACTGT	960
GtAcATGCGT GAwACATTCT CCGGGGCGGA GGGCTCCACG TTGTGAGTG CTTCGTGTTT	1020
TGTGCATTAC TTCTCGGAGG ACGTTCGTGC GCCAGGGGTG GAGGAGTTGC GCCGTGTGCT	1080
GAAGGATGTA CCGTCTGCGG TGGTACAGCA GGTAGGGGTG CGCGCTGAGC ATACCTTTCA	1140
AGTTCGCGTT GCAGCTGAAA CTGCCTTCCC GTCCTCCCTT TkGCCAGAGC AGGGAGGAAC	1200
TGCTCTGGCm CAGTCCGATG CTCCCATCT TGTTACCCCT CAAGGTGCGG TGGAAAGCGT	1260
GGTGTAaCGC GGCGCTCGTG CGCGCGTATG GAGCAGATCA tGTGGTCCGT TTAGCGATGG	1320
ATTTtGTCGG ATCTCGTTTT TCTCATCTGT TGGTGCCTC AGGCGTTGTT GTTGGTT	1377

## (2) INFORMATION FOR SEQ ID NO: 187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

CTGCTGACCA TGGCGGCGGG GTGTCTGCTG GTGTGTGCTA AGTGTTGAG AGTCCCTTGT      60
ATTGTTAGAT TCCACAACCTG CACATTGCGA TGTGCCTGTT CGATACAGTG AGCAATGTGT      120
GCGAAnATGT CTGTATTCCG TCGGAGTAC TCGGTGGTGC GCTGCAGGGT GCGCATGTGC      180
CTGACGAGTA AGGAGAAAAA AAGGGACACG GCGTGTGCT GTTTGTGAGC TTGGAAAAAA      240
TGCAGCGTAG AATCAAGTGA GGTAAGATCn AnTCCTGATA CTTGAGGTTG AGTACCTACC      300
GAAACCCAAG TATCAGGAAT GATGCGTCCG ATACACCTAG CGTGCTGGCA CACATACAGC      360
CAAAAGTACA TCACGGACGT TTGCACCTCT TCTAAAGAAA ACGACAAAAA CTGGATATAA      420
ATAGTGGCAA GAGTACACCC TGTGTGTTTT TTGCATCGGT CGGTCTGTCA TGAAATACGC      480
GTG                                          483

```

## (2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 846 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

TTTTCAGCAT TACATTGGGC GCTTTCGAGA ACTGTGGCAC CAAGGAGGTA ACGGACGCCT      60
ACTCTATCTA TGATACCACC GGCCAAGTGA TGTGGGATAA AAGCTATCTA TTTGGGATGC      120
AGGTGCCATT TCGTTATTAT GCAGAATGTG CACTTCGTTT TCATAAGACA CCTTTGTATG      180
TAGATGTGCA TGTGCCAATC ATTTCTGATC CCTTTTTTTC TACTGATTTT TTACAACGGA      240
tGAaGATCTC AACTGGTTTC ATCTTGACTT TAAGTCCTCG ATCGCTCAGA GAGCTTACGC      300
AAAGCACCAT AAGCAGCTAT GACTGGAAAA TCTCTGCTTC GCTGCGCCCT GTCTGGCTTG      360
TACTTCATCC TTGGTTGCGC GATTTTTTCG TCGATCCGAT TTCGTTACCC GTACATTTTA      420
ATTCGAAGTC TGATAGTAAA AAAACAACCT CTTCTCCAGA GCGTAACTTC TTCTACCCTC      480
ATTCGATGGA ATCTCGAGCA GGATTGTCGT TCTCTGGTAC GCTGTTCTCT CATGTGTGGG      540
AAAGACAAAA ATCTCAACAA AAAGAATCGT ACGCGCCAAA AGArATACGT AATCCACTTG      600
CATACACTCC TGCAGACGGG TTATCTAGGG AGGGWTCTCC TCCTGAACAG TCCCTGnCA      660
GTATCAAAGG AGAACAGCGA GACTGATTCT ACCTTCGATT TTTTATGCC AGAATTTCTG      720

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851

GAAGAAAATG AACGTCGTAC TGGTACTGAT CATGCGTATG TTTTACGCG ATACGCTTTA 780  
GATTACAAAG GTAAAGGTGA CATCGTGTAC GATGCACAGT TCAATCACGG TTCGTGGGGA 840  
TGACGC 846

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CTGnCACAGG nACAAACGGC GACCCCGGCA GTTTAACGGT GAACCCTAGG TTAGTAGCGG 60  
AAAGACCGAC GTACATGTTG GGTTCGTGAG AGCTAAAGAA CTTAGCAACG TTCCCCACCC 120  
ATTGCAGACC CACGTCGGTA CCCAGCGACA GGTGCGTTAG gCCCTGCGCG TCGCGGAACC 180  
CCGCCTTCAG GTTAGCCCCCT ATGGAAAGTC CCCCAAACCG ACGGGAGAAG TTCACAATCC 240  
CCAAGCCCCC CAGTTTMTTA ATTGGGTTGG AGGCAGGCGT GCACACGGGC CCCGTGGAGG 300  
GAGAAAAGTT AAACCCGGAT TCGGGGAAAA ACATACGCAT CGACGCGCCG TATCCCCAGT 360  
TGCCCGACTG GCCAACGTAG GAAAGCGTTT CGGCATGCGA ATTGTTAAAT CCGACGGTGT 420  
GGGCAAAGGT TAGCTCACTG TCGTCATGT TCGCACTCCC TGCTGGGTTT GCCTCAAAGA 480  
AGCTGGCATC GTTTGCCAAT GCGGTGAACG AACCGTCCAG AACACTCAGA CGCCcTCCGG 540  
AAnGGGAGGA AAcTGCGCGC CTCTTAACT CACTCATCTT TGAGCGAGTC TTCGCCGAG 600  
CTTCTGAAGA GGCAATCGCC ACGCTGGCTC CCGCGAGCAC GAAACCACAG ACGAGCGCTG 660  
CGCTCTTATA AAAACAGAT TTGTAATGT 689

## (2) INFORMATION FOR SEQ ID NO: 190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

TACTCCCCTC TCTGAACATG GGGAGCTGGG TGTTTGCGCA GACGCGGGGA CAGGTGGTGT 60  
GTCCGAAGGA GCGGCGCTGC CGTGCGCAG GAGGGGAACG CGTTCCTAAC TCCCTGCCGA 120

852

AACAGGTTGC CGGGTGC GCG GTGCCTTCTG CAAAGGACTC ATCAAAGGCT ACCTCAAGCG	180
GCTACGGCTC GGGGTCCGTG TTGCGCGTAG ATGCGAAACG CATCGATTAT CTTCTGAATT	240
TGGTAAGTGA GACGGTGATT ATCAAGGCCT CGCTCAATCA GAGTGCCTg AATT'TGGGGA	300
GGTGTACACC CTATTCCAAA ACGCTAATGG CGCGTACAAG GAGCGTTTGC GTAAGTTT'TT	360
TGATAGGGTT CCCGCTTACT TAGAAAAGGT AAAGAACGGT CAGGACGCAG ATGCGGTGCG	420
CAAGGGGATG ATAGCAGAGG CTGTCGGTGT CTTtGACATT TTTTCTTCGT TTGAGAATGG	480
ACTGAAACAG TCCGTCAC TA AGTTTCGGTC TTCTGCTCAG AATT'TGGGGC GTATT'TCTGG	540
TGAGCTTCAA GAAGGTGTGA TGAAAATCCG CATGGTGCCT ATTAGCCAGA TTTTCAGTCG	600
TTATCCCGCT GTGGTGC GCG ATCTCTCGCG GGACTTGCGT AAAGAGGTGC GGTGGTCAT	660
TGAAGGAGAG GAGACGGAGC TTGATAAGTC TGTGGTTGAA GATT'TGCTCG ATCCCATTAT	720
GCACTGCGTc GTAATTCTCT CGACCACGGC ATAGAAGCGC CTGAAGTTCG CGCGCGCTCT	780
GGAAAACCGG CGCAAGGTAC GCTTcTCCTG CGCGCAACAA CGAAGGAAAT ATGATCGTaT	840
TGAGGTTGCC GATGACGGGC GTGGcATCGA CGTGGAgGCA tGAAGACGAA AagCAGTTGA	900
GCGArGTGTG TTGCACCCAG GcAAGAACCT CACTGAGGTT GA	942

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CAAGTACAGC TACGCCGCGC ACAAGCTCAA ACAAGGACAG AGCCACTCAA TCCACAGTGC	60
ACACACAGCC GGACGCAACC GGCAACCTAT CTCACGCACG AACCTAACCG GGGTAAC'TCT	120
GCTGGCAGAG GTCAACAGGA CGGGGATTCT ACCTCCGATT TGCACAACGT TCAAGCACTC	180
ACGTACGCAA GATATACGCA CCGCTTTTTC CTCAAGTGCA CCCGGCGTAT TCCGATACCC	240
CTTACCAAGC ACGGGGTGCA ACGGCAGGGA TGCCAnGGCG GCTGGTCCGC TTGAAAGCAC	300
CAAAAGGAGT ATGCTTCATG ATTCATCATC ACAACATGAG CGTATGTTCT CTCCAAAGAA	360
CGCTCGGACA CAnAAATTGT CCGTCCAGAA GAACnTGGAA GTTGTCTTCA GGA	413

## (2) INFORMATION FOR SEQ ID NO: 192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

TACATACCTC GCTCTGCTAA TCCTGTTACC AGCCCCCTG GGCGCAGGAG TTGTCCAAGA	60
AGTATTGCTC TAAAACGGTC AATCTGTACT TCGTACATGG CAATATCCGT GACTTCCTCC	120
CCCATCGCGA TATTCAGGGC AGCTTCTCCT TCGTTGCGAT TAATGACTAC ATATCTGAGG	180
TTATCTTCGG TAACCGGGAT ATCATCGTCT TCTATGACAA ATCTGCAGGG CTCACATTTT	240
GTCTACAAGA AATGCTGAGC GCTTACTTAG AGCGTATGCA TGCCAGTAT CCTACTGAGG	300
CACTTGCTGA CTTTCTTTTCG CGTGATCCGG TGAAAGCTTT TCGGTACCTT GAGCGCTACT	360
TTATTATGAA CATGAAACAG AATAAGCGTA GGTCCATC ATCGACTATC TGAATCTCTC	420
GTTCCTCAG AAGATATGCA AACTAAGCGA AACAGATCGC TATGCTCGTC ACCCTCAATC	480
GCGGGCAAAT GATCCGGTGT TCA	503

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1038 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CAATTGCGTC GGTCGCCGT TCTTCTCAGT GCCTTGTTTCG TGCTGCTTCC GTTTGCGCTG	60
CCGCGCTGCT TGCGCACAAG AACCTAGCGC GCGCGGCGGG TTGCAATCCT TTTTTCGCT	120
CTGGGCCTCA TGCTGTGTGG TACGCTCTTA GACGGGCGTT CGTGGCGTAA CGAGCTTCCC	180
TTTACCTGT GCCCCGCAGC GCTCATTTGA GGGTCGCTGT ATTTATCAC CCGCCGACCT	240
ATCTTTTCA ATCTGCTGTA CTTTGGCAT TTTGGCTCTT TCGTTGCGGT ACTCTATCCG	300
GATCTCACTC GGGCGCACAC CATCTTGTA GCGTACTTGT TCATGCTCAC CCATTGCCTT	360
GAGCCTGCGA TGGTCGTGTT CAGCCTGCTC CACTTGCGCG AsGCATTAGC AAGCGTGGCC	420
TGCAATGCGC ATGCTTGGCT TTCTTCTGCT TGCAGCAAAC GCACTCTTTT GGAATCGGAG	480
ACTCGGCGCC AATTACCTTT TCATTAGCAA ATACCCGCTT GAGATCCTTC GGGTAATCCG	540
TCCTTTTTTT GTGTATCAGC TGCTGTTTGT CAGTGCACTG TGCCTGTTAA TGCTGGTACT	600

854

CTACCTACCC TTCCGGCCAA GCCAACACGG AAGAAACCAG CTCTTCGTCA TTTAGCTGCT	660
CGCTGTGGTT CCATCGGACC CTTCTGCCAA GGCAGAGGGC ACGCGTGCCg TTGGGaCATC	720
GTGGTGGAgT TGCAGCGCGC TtGcGTCaMa mGGCCTtAmT CCGCGGTCAA cGCGAACGTA	780
TAATGGTGCg CtGTGACTTC TGTAmCAAAA mCGCTTATCA TCcAAGCAGA CCGCTCCATT	840
TTACTTGATG TGCACGCTCC TGAGGCGGTA GAGCACGCAA GCGCTCGTT TCCTTTGCAG	900
AACTGGAAAA ATCTCCAGAG CATCTACACA GCTACCGACT CACTCCTCTT TCTCTGTGGA	960
ACGCCGCGAG CGCAGGGATT CAGCCCCCAG AATGGATTGC ACAAACACTG ACGCGTTTCT	1020
CACGGTTCA nTCCCCCG	1038

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TTGTCGATAC GnGATATATC nTATCTGCTG GGCAAAATGA CCAAAATGTG GCAGTCCAGT	60
TGCAAAAGGG GGACCGTCAA AGAAAACATA AGACTTCCCC TGCGCACGCT GCGCCACAGA	120
CTGCTCAAAC ACCCGGCGTT CCCGCCAAAA GCGGAGAATA CGCCGCTCCT GCGCGACAAA	180
ATCAACCTTT GGGTCCACAG GCGTATACAT ACAACCTCCG TTGCTCAGAA TCGCATAAGG	240
AGCGTAAGGC ATTATATCAT TTTCGTCTT CCTTTTCCCC ATACGTCTTA TGACCGGCGC	300
CACACCTTTC CCCACCTGCA CCAGATACCC CACGTGTGGC GTAATCGCAG TGGCTCTGCC	360
ATTACTGCAT GAGTATTACT ATGCAATAAT GCCCCACATT ACACCTTCTG CAATCGAATA	420
CGAAAAAGGC ATCATCAGAA C	441

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CAAACAGCGT TTTGACGC ACATGATGCA ACAAATATTC ACTGACTGCC TGCCTATGG	60
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855

ATAAACCGTC TTCAGTTGCC GTTCCCCGTC CTA CTCTTCGTC CATGATAACA AGGCTGTCGC 120  
GGGTTGCTGC ACGCAGGATG TGTGCTGTTT CACTCATTTT TACCAAGAAG GTAGATTCCC 180  
CGCGCGCAAG GTTATCGGCC GCTCCTACCC GACAAAAAAT ACGATCGACG GGGGTGAGCT 240  
CTGCCTTTTC TGCAGGGACA AAGGAGCCAA CCTGCGCAAT CAGGCAAATG AGCGCATCTG 300  
ACGCAAAAAA GTACTTTTTTC TGCCATATTC GGTCGGTGA TGAGCGCAA A<sub>n</sub>CGGGCAAC 360  
AACGCATGTT CAATTGAAGA AAGTGTGAGA TCATTGGGTA CAAACTCCCG GAGGAGATGA 420  
AATCCACCA CGGATTCTGC CCCCGTATAC GATGCACGTC TTGATAAGAC GGTGATCAGC 480  
AGTGACGCA<sub>n</sub> GGCGAAAGTG GGACTCA<sub>n</sub>TT GCAC 514

## (2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 407 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TTTGTGACAA nTGGTACCGG CAACTGG<sub>n</sub>AA GGCTTTTCGAG TAGAATCCAA ATTTACAAAA 60  
CATTTCCCATT AAAAGCACAG AAGGAAGAAA AATAAGGCAG GCGTTTCAAG CTACTGTTGG 120  
GCATGAGTTA ATTTCCGGCAG ACTATACACA AATAGAGCTG GTCGTGTTGG CCCATCTATC 180  
TCAAGATAGA AATCTTCTCA ATGCATTTTCG ACAGCACATT GATATTCATG CATTGACTGC 240  
TGCATATATT TTCAATGTGT CTATAGACGA TGTACAACCT GCAATGAGAA GAATCGCAAA 300  
AACTATTAAC TTTGGAATCG TGTATGGAAT GAGCGCTTTA GATTGAGTGA CGAACTTAAA 360  
ATTCTCAGAA GGAAGCGCAG AGCTTCCATT ACCGTTATTT TGAAACG 407

## (2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 410 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GGGTGG<sub>n</sub>GTT GGTCGGTCCC CCAGGA<sub>n</sub>GGT AAGACGTTGC TTGCACGCGC ATGGCCAGGT 60  
GAGGCGTCAT GCCCTTTTTT CGCATCAGTG GCTCAGACTT CATCGAAATG TTTGTGGGGA 120

856

TTGGCGCCTC GCGTGTGCGC GATTTTATTC AAACAAGCGC GGGAGAAGGC GCCAGGGATT 180  
 ATTTTATCG ATGAGCTTGA CGCAATTGGA AAAAGCCGCC TGAACGCTAT CCATTCCAAC 240  
 GATGAGCGGG AACAAACGCT TAACCAGCTT CTGGTAGAAA TGGATGGGTT TGATAACACC 300  
 ACCGGTCTCA TTTTGCTTGC TGCTACCAAT CGCCCCGATG TGTTAGATCC TCGCTCCTA 360  
 CGCCCCGGTC GTTTGACCG ACAGTTTGC TAGATCGGCC CGATCTTAAG 410

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

nGACGCAACA CTGACAACTG ATGGnTTTCG TCATCTCTCT CGGTTCCCTG AGTTCTTTTA 60  
 CATACGGTCT CTTTGCCACG GCGCGTATAG CAATGGGCGT GCATGCCAAC GACACGGCAC 120  
 TTGTATCGCA CTATGTGGCG GATTTGTATT TCGAATCAGC TGCAATGATC GTAACGCTCG 180  
 TCACGGTGGG TAAATACCTG TCCGCCTTGT CTAAAGGGCG CACTTCTCGC GCACTCACAC 240  
 AACTGCTAGA CATAAAACCT AAAACGCTCG CGTTATCGTC AGTATCTGTT CCGCGCGGAG 300  
 ATCCCTTCTT CCCCACAAT GCAACGCTGC ATCAGCCCAT GAGACCCATG AATTGAGATA 360  
 GAAATCTGCA CAGGACGTAA TTGTTCCGAG AnACGTAATT GTAAAAGCCA GGTGAGTAAG 420  
 TTCCGGTAn 429

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

CGCTATCGTA nGGAGGATCG CTGGGCTAAT TCGGTAAAGG CGGTCATTCT CTCCTTCATG 60  
 GATGGTGGGT ATCACCTGAC GGGGTGAAC TGCACTATCC TTTCTCAGAT TCCTCCTGAT 120  
 GCGGGGCTGG GTACTCCCAA TCGCTGAAG TTGCCATGGC CCTTGTGCTT GGAAGTTGTT 180  
 TGCCGCTACG CTGCCAAAGG AAAGTGTGTG TTCGATCGTG GAACACGCAA ATGAGCGCTA 240

857

TCTCAAGACC CACGCACATC GCGCGGATAT TCTGTGCGTG TTGTTTGCAA AGCAGGGTAA	300
CTGCGTGCGC ACTGATnACC GCAAGAAGCA nCGGAACTG TGTCAATTCC CTCGGAGGGA	360
AACGTATGTG CTAC	374

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

TGCAGCAGGC GTCTGGATGT GCAGGAGCTT GCGCAGTTAC GGTGTGATCT GTCTCGAGTA	60
CAGGAGCAGG TATATGCGCA GAATGAAAAA AACCGAGCCC TCCTCCGTGC GCAGTCAGCG	120
ATTTGCGCCA CAGnCTCGAT GAATTTCTGTG CGGCGCGTGG GCTGGTGAGC TATGAGGACG	180
GGGAGGACTC AGGGACGGTA ATTGATCTGA GTTTATAAGC GCTTTTGCCA GACCATCTCA	240
GGGAGGAGG TGCGGCAAGC TGGATTTTTTC CAGTCGGTTG TGTGACAATG CGCTGTGGAA	300
CCCCTGTGTA TTTTGCGTCC CCTTTTGGA AAAGGTGAGT TAAAGCAGAT GTGGAGCGTG	360
CGCAACGCCG CGGnTATGTG CT	382

## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GGGGCCAAAT AATTCCGnTC CCAAATGGCC AAGnGGTTAA GCCAAAAAA AAAAAGGCCC	60
CGGATTTTGG GTTCTTAAGG AGGAAGGGAG GCCCCAAAAA GGCCAAAACC CACCCCCCCC	120
ATTATTCGGA CTTCAAGGAG GACCATTAGG TCGGGCTTTC AGGCCATTAG AGGCCGCAGT	180
AAGCAGCTGG CAGGCGTACC GAGCCTCCCG TTTCGGTACC GAGTGCAAAC GGTGCCTGGA	240
CCGCCTGCGA CGGCGGGCAG nCAAACCGCC GGAAC'TTCCC CCGCTGGTGC GGCTCCGATC	300
CCGAGGATTA CGCGTCGGCC CATAAACAGA ATACTCGGTG GAAGAGCCCA TAGCAAAC'TC	360
ATCCATGTTC GTTCTCCCGA GCGGGATAGC ACCTGCGGGC GCGCAGnCGG CAAACAACGG	420



858

TGGGCATCGT ACGGGAGCCC TATAGTCTGC AAAGAGTTTA CTGCCACACG TGGCAGTGCT 480  
 TTCCTTTTCA CTGAAATATT GTCCTTGACA GCCAAAGGGT AGACCTAACA AAGGCTTACC 540  
 T 541

## (2) INFORMATION FOR SEQ ID NO: 202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

CAGTAACAAC GCCAACCGGT CTCATCAGCA ACACGGTCCC AGATGnACCA CCTTCnGAGA 60  
 CGCTTCGGCT ACGGTCACCA ACTAGCACTT TGAAAAACAA GAACAACAAA AGAAAGAAAA 120  
 TGACGTtCAA ACTGACCAAC CGAACGGCAT TTAACCCACG AgCAGCCTCC TAAAGAGAAC 180  
 TCTCAATGAG TACATTGTAA CCTcCACCTc ATGTGTGTTA TGCCTCGTCT ACTCCCGGCA 240  
 GGCCATCTTT TCAGGAAATA CCAAATGTTT CTGAAAGAAG ACTGGCACAT TCCCAGCAGC 300  
 ATATTGCTTG CGATAGTCAC GCATAGATAC AACGCCACCG GaTGcAGTGT CACGATAGCA 360  
 ATCAGGTTGA TGACCGTCAT aAATACCATA AAAAGATCCG CAACACCCCA AACAAAATGA 420  
 AAACTCGCAT GCGCACCGAC AAATACCGCA CTGACACAGG TAACTCTGAA AACACTCAA 480  
 ACCATTTTAT GGTcCTTAAT GAAACGTACG TTTGACTCCG CGTAgtAATA GTTACCCATC 540  
 AGTGAACTGA ATGCAAACAG AAAGATCGCA AGCGTCACCA AGTGCACCCC CACGGGGCCA 600  
 ACTTGCTTGG ACAGCGCTTG CTGCACGAAC TGCATTCCGC TCACATCCAC TGATCCTGn 660  
 AACATCAGAG AGCAGCAACA CAAAAGCGTC AACTACAAA TTAGCATCGT GTCTATAAAC 720  
 AC 722

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

ATCnCTCCGA GAGTTTGGTC GAAGGAGGCA TGGCTGTGTT CAGCATTCTA GAAAAGAAAC 60

859

AATTTTCTCC GCAGTGT TTTT ACTTGAAGGT GCATGCACCT GATATTGCAA AAAATCGTGC 120  
 TGCAGGACAG TTTGTGCTTG TTCAACTTGa TGACGAATAC GCTGAGCGCA TACCGCTAAC 180  
 GATTGCGGAC GCGCATGsGA TgAAGGGTGG ATTGCGCTAG TGATCCAGAC TGTGCGGCC 240  
 ACTACTATGA GGCTGTGCGA AAAGGAAGTG GCGGATTCCA TCTCTGTAGT TCTCGGTCCG 300  
 TTGGGAAATC CAACTCTCAT TGAAAATGTA GGAAGTGTG CCTGCGTTGC AGgGGTGTG 360  
 GGGCAGCTCC GctGkATCCT ATTGCCCAGG CGCATAAAAG GGCTGGAAAT CACGTCATTG 420  
 TAATCCTTGG GCGCGCAAT CGGGATTTAA TTATTTTGA AGAGGAGATG CGCGCGCTTG 480  
 CAGAcGAGCT GGTcATTGTC ACAGACGACG GCTCATATGG ACGCAAGGGC TTAGTGA CTG 540  
 AGCCCCTGCG TGAnTGTGCG AGCGCGCGTC CTGTCCACAG GAGGTGGTTG CTATCGGTCC 600  
 GCCGATTATG ATGAAGTTTT GTGCGGAAAC GAnGCGnCCC TTTGGGAT 648

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

TGCACTGTAC TACACAGTGT ACGAATGCGT GAAGGTGATG TCTTCTGAGG TCGGTGCGTC 60  
 TTTGTACGTG CACATCCCCT TCTGTGCGCA ACGCTGTGCT TACTGCGATT TTTACTCCCT 120  
 GGTGCGTTCA ACCTATTTTA GGCCTCATCA GCCTTGTCG CATTTTATCG ATCGGCTGCT 180  
 ACAGGATGTG GCATTGCAGC GGGAGTGCTT TGGGGTCCAG GGGTGGCAGA CAGTGTATAT 240  
 GGGTGGAGGT ACCCCTTCGC TATTGGCACC GCAGGACATT CGTCATTTTT GCGTACGTTA 300  
 CGCGCCGCGC AGGnATTCCG ATTCAGGAGT TCACTCTTGA GGTGAnTCCT GAGGATGTGA 360  
 CCGAAG 366

## (2) INFORMATION FOR SEQ ID NO: 205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

860

CATAGATGAC TTTGACGGTG CCTCCGAGGA TCAGGGTCTC GCCTGGCGTG CTGCGGGGAG 60  
 CAAGTTCATC ACAAAGGGCT TCCCTATCCT CAAGTATTTT GAGGGCATGC CACAGGCGGT 120  
 GCGCATGGCG GGCTCGTGGC AAGGGAAGGA CAAGGAAGCC CGGTTTCATCG GAGTAGAGTG 180  
 CAAGTTCAAT CGACAGGGGA ATAAGTGGCT GGACCTAATT CCGACTAAGG GTGGTAGCGA 240  
 TTACGAGATC CCCCTGCGTG GGGTGGTCAG TGGGTTCGAC GTGTGGGTGT GGGGTGCAGG 300  
 TTATCAGTAC TCGCTCGAGG CTTTGGTTAG GGACTGCACG GGACGAGTCC ACACCTCCT 360  
 AATAgGCaAC CTCgAcTTCC aAGGGTGGAA rAAcCTTAGt GTTTCGGTTC CCACACACAT 420  
 CCCACAGACG TCGCGCTATT TGGGGAGCGC GCAACAnCTG AATTTTGTCTG GTTTCAGGAT 480  
 CCGTACTAAC CCATCAGAnC GGGTGGATGA TTTCTACGTG TnCTTTGACC AGTTCAAGGC 540  
 GCTTGCTAAC ATGCATATCG ACTTTT 566

## (2) INFORMATION FOR SEQ ID NO: 206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CAAAAGGCAG TTGACAGATG CAGAGGCGGA TTTTATCCAG AATTGTGTGA AAAATGATGA 60  
 CCTTATCATG GCGCTGAATA TTTTCTCTAA CCGGGTGCAG TTGTCTCCTT GGACGTACGA 120  
 CGACCTCATG TTCGTTGCTG GTGGGGGAAG TGAGTnAGTA CCGAGAAGTA GCTCTCTTTT 180  
 CATAAAAATC TTTTCGGGAA GAGTGCCCTA TCAAGCCAAA GACGAATGCT TGTTGTTTAC 240  
 CGCAGCGTTG AGGGTACTCA CTCCCGCGAA TATCTTTTTT AGGGGTGCG TGGTCTTTCT 300  
 GGTATGCTC ACCCTCACCA TATCaAGCAT GGTCTTTTTG GTTATTGAGT ATCTGaGCGT 360  
 GCGCCGATTC CaGTGCGcAC AGGGGGACGC GCGCCCTCGT CtGCTGGACC TCAAGGTAnG 420  
 CGCGCTCTCG GACAGAnGAG GnCCCAGGTn TCGCCTGGTA CACCGCCTGA GTGTCCAGTG 480  
 TCCGTCTTTT GAAACTCATG GGCAGGACCT TGCTTCTAAG GAGAGCGTGA GCGACCTCGn 540  
 AAGGTTTACA TTTGTACAAC CATTCTGACG AGGAGCTTTT TTCCATACAT GACTCGGTGT 600  
 TCCAGGAACA TACAGGGSgG GAGGGCCGGA TGTCTTCCTC TTCCGGTGAG GAAGGGTGCG 660  
 GGCAGACGCT GCTTCCCGTT CATGAAAAAA AGAGCACCTA TGGTCTTTTC AATCCCTTr 720  
 CCGGrGTCGG TTGGCGGGCC TATCTGGAGG AAAGGCTTGA GGCAGAATTA GGACGCGCCA 780

861

CCGCTTCCGA ACAAGACCKa AsGCTAATGA TAGTACAGGT GGAGCACCCC GCGCACCAGA 840  
 CAGCCGTTGC GGACGCAGCG AAAAAGCTCG TGGAGTTCTT CAAATTTTCGG GATATGCTCT 900  
 TTGAATTTCGA GGGTAGTTGC TGCTTCGCGG GTATCGTACA AGACGCAAGC CTCGAAGAGg 960  
 AnTGGTaCTC GCGAGGGaTA TACACAAGKa GCTGTGCGGC GCCATTGAGA GCGCACGCgT 1020  
 CCTTATCGGC ATCGCGAaCG cKTACGTCCA GACTAACTAC CGcGGcCCAC TTaATTGAGG 1080  
 ArGCGCACGC GTcGGTGAAG AGGGCGCGAG AAGACCCCGC ACACCCCATc ATCGcTTTCG 1140  
 AGGCCCCCCA CCAGTGTGGG CGCCCGTATC GGTCTTCAGC TTATAGGGAT GTCCCGGACC 1200  
 GGTCTACCTG CTAATAATGG CTTCTTCTC GCCGCGCCGC GCACTCTGCA GAAGCGCAGC 1260  
 ACCCAACCTC CTGAAACTCT GGGAAGAAAC AGTTGCACCG GTGACCACAT CCACCATCTC 1320  
 GGGATTACCC TTTTCAAGCA AAGCATCGGC GAGCTCTCTG AAGGCCTTTT CAGGACCTAT 1380  
 GCCCGAGGAT GCATACATGA CCCGATGGTA GTCAGCGTCC TGGGACTTAA ACCGCCCTTC 1440  
 TTTATGCTGA TAATCGTAAA CCACCTGCAC CATCTTGCCA CCATCAAAAG TAACCTCGAG 1500  
 AAAGTCCTTC CAACCATCTT CATCAAAATC CTGATACGTC GCCCGGTACG TGCCATTCGG 1560  
 GATAGAACTA AATGAACACG CCCCAAGCAA CACCGCAAGA C 1601

## (2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GTTGTnTCCT GTGCGACGCG nAAATACCTT CCCACACCTG CTGGTTAAAG GACTTGTCAT 60  
 CGATGTCCCC TGAATCGGTT ACCATTCCAA CGACGAATCA CCACCTTCTG CGCCCCCTGC 120  
 GTTTCCCATC TCGGGCCTGT CGCTCTTAGA GCAGCCGATG AGCAGCATGG CGCAAAAAAn 180  
 GCCCGCAAAn GCGCGTACCC ATTCTCTCTC ACAAGAATCC TCCCCCTTT ATCGACAAAC 240  
 ATGCGnAAAA TAAnGGGTCA CAGTGTAACC CAAGGGACAA nGAGGTnCAA AGAGTGGTGA 300  
 GTTTTTGCGT GTGTGCAAGT GGCAAGGTGA AGGGGTACTA GACAGGCCCG GGGGGGGGT 359

## (2) INFORMATION FOR SEQ ID NO: 208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TCTTGCAGAA AGTGAGGCGG ACTTCCGTGC AGGAACCGAA ACACTGCAGG ACCTTTGTCT	60
GTGAGTCTTT CCGGGCATAC GCACACAAA GAGGAGGTGC AGGCTGAGGT GGAGGCAGGA	120
GAGGTTCACT GCCCAGCGCT TTGCCATCAG CCGGTACTCG TGCAGGAATG CCTGACGTTG	180
TTGGAACCTG CAATTGTGGG TATCTCGCGA GGTGCAGACA GCACGAGAGA TGGGGCGGGG	240
GCGTTTTTTA TTGACGGGAC ACTGGGGGAT GGGGGACACA CACAGGCGTT TTTGCACGCG	300
TACCTTGcGC TCCGTGCGCT CCGTGTGAA ATAGATCCGT CAATGCTCGC ACGGGCGCGA	360
GCGCGCTTGA CGCCGTTTGG CAAGCGGCTT cGCTATGTCC TGGGGTGGTC TGATGTCTTT	420
TTGCCTCCG CATATGCATC AGCTCCTGCC TCTCCTGCAA CGGGAAGGAC TGCAGCTGGC	480
GCCGCACTGT GCCGGGTGCG TATCCGGCGC CGCAGA	516

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCACAnAnAG GACCAAAAAG GACCAATGGC CCGGGGCCGG CCCCACCGG CCACCTTCCA	60
GGAACCGGCG GTGGCGGGTT GGCCCCCGC GGTTTTTTTAA AAAAAAACC GGCCGGCCCT	120
TTTTTTAAAA AACCTTACCA AAACCGGCGG TTTTCCAACC CAGGCCAACC CGGGGGGGGA	180
AACTTGCCCC TTTACGGGGG AGAGGGTGT AACACCCGGG CTTATTGGGC GCGATGGAGG	240
TACGCACACG TGCAGCGTTT TACTCCCGAC GGCTGGCTCC GTACAGGGGA CGCTTTGGGA	300
CAAAGACAGA AACCGGTAAT CTCCTCCCCT GGCAGCAGCT CGTGCCATAT GCAACTCGGT	360
GCGCGCGGAG AAGCGGTGTA CGCAGAnGAT CTTGTTTGTG TGCTTATGCA AnATCCGTGG	420
CGTGGTGGCA GCACACGTGC GCGTTAGAC ACGCAAnGGG CAAGCGCACT GCGCCGTATG	480
GGTAAACAA GGAGCCGAAC GAATACGGGC ACCCTTCAGA TAGTGTGCTT TTTGCGCACC	540
C	541

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

GGTGACCGTC ACCTACCGCA CCGTACATGG CGCATGCTCT TTTTGCCGCA ACTACATCAT      60
GGCTAGAGTG ACTACCCGGA CCGGTCATAA CCCCgATGTG ATAATCCTCC ACCGCTTTCG      120
TGCCCCCGGT ATTTTGTGGA GCACGCGCGC CCCCACAGCG ACACAACAGT GCACCGACAC      180
ATACCACCCA TACCTTCAAT AGAAACTGAC TTTTCATAGT CTCCCCTTAA CGATCTGCAC      240
ACACCATCTC TCCAAAACGC TTAGGCGTAT GGTCCACCCC CCCCCACGGT GGGAGGAnAA      300
nAATTTTCCC AAAATTTTGT GGTGGGTT                                     329

```

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

TCGTTTGTAT CGTTGAGCGT GTTATCGCTT CAAGGGACAA AGGTGCCATA CTCATTTTTC      60
TGCCAGGGGA GCGTTCtATT AAAAATTGTA TTACCCGTCT TTCCCATGAA CGTTGGTTCC      120
GCAAGCTCTT TCTTTTGCCC CTCTATGGAA GATTGAGTAA AGAAGAACAA GAGCAAGTTT      180
TTAACCGCGC GCCATTTGGA AAAAGAAAAG TCGTCATCGC AACGAATATT GCAGAAACAT      240
CCATCACCAT TGACGATGTA ACTACCGTCA TTGACTCTGG TTTTGGGGGG TTTnGGGAAAA      300
AGGGTTTTTn AAAAAAAATT TTTCCCGGTT nAAATTTAAA AAACCCCCC GGGGCCTTTT      360
TTTTCCCCC TTAAATnAA ACCTTGGGCC CAAAAGGTT TTTTTTGGGG GGAAAAACCG      420
GGAAAAAAA AnCTTTCCCC CnTTTAAATT TTTTTTCCT TCCCAAGGGG GGCCTTTTTT      480
CCCGG                                     485

```

## (2) INFORMATION FOR SEQ ID NO: 212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

TTGCATCGCG CGTCTGCAAG CGCGTGnACC AGCTTAnCCA TTGAAAAAGT ACACAAACCA	60
AAAACAGGAG GGATTACGCC GAGCACCATA GAGCACGTat TGGCGGAGAG GCATACACCG	120
TGGTGCTCGA CCGCTCGTGG ACGTATGAAA AGGGCTGGAC CATTGCGCTG TTCCCCGATG	180
ATAAGGCGGA TGAGGCTGGA GCGTATGTAA AAyCCCTTTC GGTtTCAAAA AACAAAGAGG	240
GAAACTGGAT GGTtGCCATT CCCAACGCGG CGCTCAAAAC CGGGTCGTAC ACGCTGCGCG	300
CAATAACGCC GCGGAATATT TACGCAGAGG TCGGGGGGAT ACTGCATGTA GTGCTCTGGC	360
GCAGGCCCAT CTTTTTCTAT TATGACCTGA GCGTGGGATA CGCGCCGGTG TATCGGCCGC	420
AGaCCACGCC GCGACAATCA ACGGTGTTTC TGACTTTTTTC AAAATCTGTT CTCCTATCGG	480
GTTTGTCGGC ACGTTTGAGA TGTGCTTTTT TAAGCGCAAC AGCAGCACCA TCAGCGCTGG	540
CTTTAACGCG CAAATGCACT CCGATTCAAA ACAAGTGGAC GTGAAGCTCG ATGGAAACTT	600
TGCGTATCTA TACGAACTTT ACCCGCGCAT CGAGGTAGGC GGCATGCTTG GGTtGGGGTA	660
CTCGCTGCCA TTCGGACAGC GCAAGGAAGA CGACAGCATG TACTCCTACG TGACAGGAAC	720
GATGAAGTAT TTTTACTAA TAGCATTACC TCGCGTTCA ACAGCAGCAC ATGTTGACCG	780
TAAAGCCGAG TTTCACAGGA GTGAGCCT	808

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

CTGCGCCCGC AGGnAAAAAA GTGTGTGCAG CAATCCAGTC TCTTCATTA GGCGGAnGCA	60
ATACTCGGAC GGGGAGTACA AGCTCTTAGA AAGTTCTCAC GCACCCGCTC AGAGAATACG	120
TGCGTATGAG CGCGnAnATA AATTGCTTCA CGCGTGCGCG CTTGATGGA AAAAGAnAAC	180
TGCGCTGCAA AACGCACAGC ACGCAAAGGA CGCAACGCAT CTTcAGAAAA TCTTGcCTGT	240
GCATCCCCCA ACGCTTAAGA TAAGAACCGT TACGCAAATC GGAGTAnCCG CCACATTACG	300
TCGATGATTT CC	312

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

CTGCTCTATG TAGCGTTTTG CCTTTCGCCC TGTTCATT TCCACGATTT TGCCGTGGTG	60
GAGGACGAnG GAACCGAGGA TCTGCACGTC ATAGGGACGC TCGCCTAAAA CACGACGAGC	120
TGCCTCGCGC GCAAnCATAT ATTGCCTGAG GnAAAAAAGC GTCAAGCGCT TTCTTCCTGC	180
AGCGGCACGC GCTCTTTAAA CTCAGCTGTT TTTTGTGTTG AACTCAGACT CCTGGAGAGG	240
AAGTTACCCA GGACTTCCTG GGTGCTTGT ACGGTCATTT CAAAAGAGGC AGGTAGATTT	300
TTTTCAGAnC GCGCTCGTGT CTGGGTAGCC AAAGnAGTAG CCTGTAGTGT CAGTGTCTGA	360
CGTAGTCATG GTAGTTACTG TTAGCGGTC TGTAACCAAn AAAACAAGGG TAGACCGTCA	420
CGGTCACCCC CT	432

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGTGGGAATA AGAGAGGGAG GAGACATACA GTTCAGCACA TGCTCACTCG ATCTTACTCC	60
TAATGATAGA GCTAGAAACG TGCCATGGGA CTCCAAATCC CCTTAAATTG GCAAGTACCA	120
ATGCCATCTT AACTACTTAA ACTGATCAGT TTCAGTTCAT AATTGATCAA AAAGATAGGA	180
TTAAGTGTC AAGGATCAC ATGAATAAAA CCAGTGTCTT CTAATAATAA CTGATAGAAT	240
TAAAAAGGAG AGAATGACTC AACATGGGAA GTGGGATACA CAGCAGACTC AGAATGACAA	300
ATGTCCTAAA CAGCACTCTG GCCACACAAT CAGCTCTTAA GGCATTGCGA TCTGGCTAAA	360
AAGCCAATGA AAGTTTCTCA GGCATGGAAA GCCAAGAACT GTGGCAAAAA ATGGCCTAAA	420
TGAAACATCT GTGTGAGTGA GATCCCAGCA GAAAGAACGG GCCATCAAGG AAAGAGGTAC	480
CTTTCCCTGA AGGGAGGAGA GAACTCCAC ATTGACTATG GCCTTGCTTA AATAAGGAGT	540



866

TGGCGAACTC AAGAGGCTTC CATAAGCTTG GCAACTCATG ACAAGAGCCT TGGGTGATTA 600  
CTGATGCCAT AAACAAGAGT GTCAATTGT T 631

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

ACATAGTACA ACACATTAAG GACAGAGATC CTACATGGGG AGTAAGTGCA CAGTGACTCC 60  
CTTGTGTGATT TAACAACCTGA CACTCTTATT TATGACGTCA GTAATCACCT GAGGCTCTTG 120  
TCATGAGCCA AGGCTATGGA ATTCTCTTGA GTTCACAAAC TCTGACCTTA TTTAGACAAG 180  
GTCATAGTCA AAGTGGAAGT TCTCTCCTCC CTTGAGAGAA AGGTACTGCC TTCTTTGATG 240  
GCCCATTCTT TCCACTGGGA TCTCACTCAC AGAGATCTTT CATTTAGGTC ATTTTTTGCC 300  
ACAGTGTCTT GGCTTTCCGT GCCTGAGAAA TTTTCATGGT TTTTTTTTTT GCCAGATCCG 360  
AATGCCTTAA GGGCTGATTC TGAGGCCAAA GTGCTATTTA GGGCATCTGC CATTCTATGA 420  
GTCTGGCTGT ATATCCTGGC TTCCCATGTT GGATTGTTCT CTCCTTTTTA ATTCTATCAG 480  
TTATTATTAG CAGACACTGG TCTTATTTAC ATGA 514

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

ATCCCTGTTA AATATAAGAG TGGGAATAAG AGAGGGAGGA GACGTACAGT TCAGCACATC 60  
TTCAATTGGA CTTAGCCATA ATGGTAGAGT TAGAAATGGG CCAGGGGATT CCAATTCAAT 120  
CCCATCAAGG TGGCATGTAC CAATGCCATC TCACTAGTCA AAGTGATCAG TTTCAGTTCA 180  
TAATTGATCA TAATGATAGG ATTAAGTGTC AAAGGGATCA CATAAACAAG ACTAGTGTCT 240  
GCTAATACTA ACTGACAGAA TTAAAAAGGA GAAAATGATC CAACATGGGA GTTGAGATAC 300  
ATAGCAGACT CATAGAATGG CAGATGTGCT AAACAGCACT CTGGGCCTCA GAATCATCCC 360

867

TTAAGGCATG CGGATCAGGC TAAAAAGCCC ATGAGAGTAT TTTAGGCnGG AAAGCCAAGA 420  
CACTCTGGCA AAAAACAAAA AAACAAAAAA AAAACAAAAC AAAACACAC ACACACACAC 480  
ACA 483

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

ATTTTCATTT AGGGTGGTGT TTTTTTTTTT TTTTTTTGCC ACAGTGTCTT GGCTTTCCAT 60  
GCCTGCAAAA CTCTCATGGG CTTTTTAGCC AGATCTGAAT GCCTTCAGGG CTGATTCTGA 120  
GGCCAGAATG CTGTTTGGGG CATTGGCCAT TCTATGAGTT TGCTGTGTAT GCTGCTTCCC 180  
ATGTAGGATC ATTCTCTCTT TTTTAATTTT ATCAACTGTT ATTTGCAGAC ACTGGTCTTA 240  
TTTATGTAAT CCCTTTGACA CTTAATCCTA TCTTTTTGAT CAATTATGAA CTTAAACTGA 300  
TCACTTTAAC AAGTAAGATG GCATTGGTAC ATGCCACCTT AATGGGATTG AATTGGGATC 360  
CCCTGGCACA TTTCTAGCTC TACCATTAGG GGTGAGTCCG AGTGAGCATT TTCTGAACTG 420  
TACATCTCTT CCTTCTCTTA TTCCCACTCT TATATTAACA GGGATCACTT TTCAGTTAAA 480  
TTTAAATGAC TAAGAATAAT TGTGTGTTAA TTAAAGAGTT CAACCAA 527

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CTGAGAAGGG AGAAGCAGCT TCTACACAGC TGCCTCCAGT TCAACCAATA AACTGTAGGA 60  
CCTGCTCCTG ATTGGAGGAG AGCAGCGTAC TCGGCGTGTG GGTAACAGAG TTGGGATTGG 120  
TGGAAGAGGA CTATAAGGA GGAGAGAGAC AATATGCACC AGGAACATCT AAGGGGAACA 180  
TCTGGGGGAA CACCTGTGCA GCCCCGAGA GAGCCGGCCG GCGGTGTGCC GCTTCCCCCG 240  
CGGAAGTGGG GAAAGTGGCT AGGGGGAACC GCCCTTCCAC GGAGGTGGAA GGTTGGTAG 300

868

CCAACCCGGG AAGAACCAGC AGCAAACCCG GGGAGGGCCG AGCAGACGAA AGAACAACGC 360  
 AGGTCTCTGTG TTGTTCTCTC ACGAAGACGG GGAGCGACAC AGTATTCTGT GATAGAGGAC 420  
 TTTGTAGCAC CATCAGTTAT TGAATTCAAG TCACTTCCAG 460

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

CCGTCTTCGT GGAGGAACGA CACAGGACCC TGCGCTGTTC TTTCTTCTGC TCGGCCCTCC 60  
 CCGGGTTTGC TGCTGGTTCT TCCTGGGTTG GCTGCTGGTC CTTCCACCT CCGTGAAGG 120  
 GCGGTTCCCC CTGGCCACTT TCCCCACTTC CGCAAGGGAG CGGCACACCG CCGGCCGGCT 180  
 CTCTCGGGGG CTGCACAGGT GTTCCTTCAG ATAGATGTTC CCCTTAGATG TTCCTCGTGC 240  
 ATGCCGTCTC TCTCCTCCTT TATAGTCCTC CTCCGCCAAT CCTAACTCGG CTGCCCACAC 300  
 GCCGAGTATG CTGCTCTCCT CCAATCA 327

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

nGGAAATTTT TCCAAAAAAA GGCCCTTGGG TTAACCCCTTA ACCCGGAAAT TCCnTTTTTC 60  
 CCCGGCCAAC CCGGCCGGG AAACCGGTTA AATTTTGGGG GCCGGCCAnG TTTCCAAAAA 120  
 AACCAAGGTT TTAACCTTCC GGAAnAAAACn TTAACCCCAA CATTCCGnGG GGCTGGGGAA 180  
 CCAACGGCTT CnAnAGGGGG AnCCACTGTG GATTTCATGGG TTCGGCAGGC AACGTGTCT 240  
 TGnATAGGAT TGCGCACAAT TGGGCTGCCA AnGCATCGAG CATACTGCTT GCGTTTTTGC 300  
 TCGTGCAATT TTACAGCGGC AGTCTGCTGG AACGGCGCGC CATTTCTGTT CCGTTAGTTG 360  
 TGAGAAATGA AGGGCGCACT AACTCCTGCG CTTCGCTTTC CTCAAAGGT GACGGTGCTG 420  
 GATGCGCGCT TTCACGTGAT ACGCTCGGCG CACTGCCGGG ATCTGACATT GTCC 474

## (2) INFORMATION FOR SEQ ID NO: 222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

GCGTCAGTCG CGTCAGATCC CCACGCGTCC GTGCCCCGTTG CACGCGTGGA CACTGCCAAA	60
GCGCAGTGGG CTGCTGGATA CCGCTGCTGC GGGGCTATAT CCGCGTAACA GTGTAAGCCA	120
ACGGTGTAGG AAAGTGGCGC ATTTTGCGTG TATGCTACGG TGTCCGAGAA ATTACCAAAA	180
CGGTGGAGGT GTATTATGAT TATCCTCAGC CTAAACTGCG GCAGTTCATC TGTAATAATAC	240
CAGGTGTATA ACTGGACAGA GCGTGCGGTG ATTGCCGTTC GTGGCCCCGn TTTGGGGGGT	300
TTAAAGGnAA AGnCCGnTT GGGTTTTTAA ACCTTTCCCA AGGGGGCCCA AGGGGGAATT	360
TCCTTGGGnT TTTTAATTTC CCAACCGGGC CCAATTGGnn AAGGGGGTTG GGCCnAACC	420
GGGGGGCCCC CGGGnAAAGG nnAGGGnAAA AAACCCCCAA ACCGGGTTTT TTCCCGGGGG	480
GGGGGGGAAA AAAAAAAGG GTTTTCCCCC CCCCTTTGGG GnCCCCCCCC CCCTTTTAAA	540
ACCCCCCCCC CAAATTTTAA AACCCCCCGG GAAAAAGAn	580

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AnTAnGCTTG GTCCTAAGGG TCGCAATGTC TTGCTTGAAA AAGGGTACGG GGCTCCCACA	60
GTCACGAAGG ATGGGGTTTC CGTTGCGAAA GAGGTTGAGC TCGAAGATCC GTTCGAGAAT	120
ATGGGTGCAC AGCTTTTAAA AGAGGTGGCT ACGAAGACGA ACGACGTAGC TGGGGATGGC	180
ACAACTACTG CGACGGTATT GCGTATTTCG ATGGTGCGTG AGGGTCTGAA GGCGGTTGCT	240
GCCGGTATGA CGCCCCCTGA GTTGAAGCGT GGTATGGATA AGGCAGTTGC GATTGCAGTC	300
GATGACATTA AGCAAAATTC CAAGGGTATA AAGAGCAATG AAGAAGTCGC TCATGTAGCG	360
TCAGTATCTG CGAATAACGA CAAAGAGATT GGAAGGATTC TGGCAAGCGC AATCGAGAAG	420

870

GTGGGGAATG ACGGGGTCAT TGACGTTGAC GAAGCCCAGA CAATGGAAAC GGTGACGGAA	480
TTCGTTGAAG GGATGCAGTT TGATCGTGGG TACATCTCGT CCTACTTCGT CACTGACCGA	540
GATAGGATGG AAACGGTGTA TTGAAATCC TTACATCCTT ATCCTACGAT AAGTCCATCT	600
CGACTATGAA GGATTTGCTT CCGCTACTCG AGAAAATTGC GCAAACAGGT CGACCGCTGC	660
TTCATCATAG CTGAnGATGT CGnAAGGCGA AA	692

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

AGCGGAGACT TACCAACGAG CCGATATGAG CCGCGTATGA CTTGCCATTT ATCGTATGCT	60
TTTGCGTATT CGCTTTTCT GCAGCGACGG TTTGCTGGTT GAACACAAGA ACTTGCTGGA	120
TTGCAACCGC GGTGCGACTGC GCAACCCGGG CCTGTACCTG CTGGGTGATA ACGTTCCTGCA	180
CCACGCCAGT AATCTGCCCG ATAATGGGCC TCGCGGCGGC CGCCCCGCA CTAAGGAAGA	240
AGAGCTTGGT TACATTGGC AATTGCGCTG CGATTGCGGT AAGTGAAGGC AAGTCAGGTT	300
GCCGAACAGG ACTTTGCCGG ACGTTCACCG GAACGTCACG TcAATATTCA CTACTTGTGT	360
TCCATTGGTG CGTTTAATCT GATCGTGTGC CTGCTTCACC GCTCCTTCAG CGATCTGAGT	420
AATAACTGAT CTTGCCACCT GCACCGAGTT ATCTATGGTG CTACCAACCG TATCAGCCGC	480
CTGTTTAGCC TGTTCTGCG CAcGTGcGTA AAAATTGCCA GTGCAACCTC CTGTGCACGC	540
TCGCGTGTC TTTGCGTCCT CATCGCCGCG GTAGCCTCAC TCTGGTGTTG GTTACCGGCG	600
TCGAGGGCGA AGGAGAAGCG GAAGCCGGCG CCTGGTTCGA GGGTGAGTCG GCCCCCTACA	660
TTCCACAGCA GTTTATCCTT GTTCTGATTG TTTGCGTCCT TCTGTGCACC GATGAGGTAT	720
CCGTCTTCTA GCGTAACATT GCTGGCAAGC TCTACCGTGC ACAGAGGGTG TCCTGCACGC	780
GCATACATTA GCTTCAAGTC TGCCCCAAAG CCATACTTAC TGTGCGTGGG GTCAGTACTA	840
TCCCAGGCAC CGTTAGAGGC AAAGGAGAGA AACCCACAT CAAGGCTGAC CCCACTGCCC	900
CCAATGTCCT GTGCCCATA ACCAACCTTG nCGGCTAAAA CCCC AAAACC CGGGGCATAC	960
TGTAACGCAT CCTCCTGGTA ATGCGGTGGT CAAnCCAAGG	1000

## (2) INFORMATION FOR SEQ ID NO: 225:

871

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TCAAAAATCT GAATATCCTA CCATATGACC CAACCATCCC ACCCCTGGGA ATTTACCTAA	60
GGGAAATTAA ATCAATAAAT AAAAGAGTTA TCTGAACCCC CAGGTTTATT GCAGCTCAAT	120
TCACATAGCT AAGACATGGA ATCAACCTAA ATGCCCATCA ACCAATGACT GGATAAAGAA	180
ACTATGGGGT AAGTACACTA TGGAATACTA CATGGGCAGT AAAAAAAAAA ATTGAAATCT	240
GGTCATTGGA CAACAAAATG GATGAATCTG GAAAACAGCA TAATTAGTGA ATTAAACCAG	300
TCCCAAAGGG ACAAATACCA TATGTTCTCC TTGATCTGTG AGAACTAATG GAGTACCTAA	360
AAGGAAATCT GTAGAAGTGA AATTGACACT TTGAGAAGGG ATGACTTGAG CTGCCCTTGT	420
CTTGACTTTC AAGGAACAGT TTTTCTTTTT TCATTTTTTT TCTTCAGCT ATTTGCTGAA	480
CTCTTTAGTT AACATAGAGT TAATCATATA AAGTCATGA GGATGGATCT CAGTAAAAAA	540
TAAGAGTGGG AATAAGAAAG GGAGGAGGAA GTTTTGTAAC TGTAAAGCTA TATAGTTATA	600
CATACATTCC TATGTACTTA CTCTAAGGC ACAGTTTAAA AACTTGTCAT GAGATCCCAA	660
ATCTCATTAA GCTGGGTGGA AAAATGCCAT CTTAAGTGTT AAAGTGATCA TATTAGTGTT	720
AAAGTGAACA TATAGATACG TTTAAGTGTT AAAGTAAACA TATAAATAGG TTTAAGTGTC	780
TGGTAATAAT AATAGATATA ATTAAAAAGG AGAGAATTTT CCAACTTGGG AAATAGTCCA	840
CA	842

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TACAAATTGA GTGTCAGTGT GATTTTCAGG TTAATTCATT CAGAATTCCA CAGGCAGTCA	60
GCTGGAGGGG TGGATGAATC CGGGAACAGC CGGTTTCCTT GCGACTAAAT AAAGCCTTAT	120
ATCATAATGG ATTCTTGCAT TTCTTTGGCT TTTTCTCCG TTTTCTTATT TATCATGGTT	180

872

TATAATGAAT TTTCTGATGT GAGCTTTTGT TTTGTGGCAG GCATATTGAG TTCAGGGCAT	240
AAGAGGAAAT TTCTTTTCC ATCAGGGCAC AGCTGTTGGC TTGCTCCAAT TCTGGTTTGC	300
TGTCATTGTT TTCGGTGCCT CAGCCGATTG TGGTTTCTTG ATCAAAAATT TCCTAAATGT	360
TTTCTGGGTC TGAGTTGGTT TTGCCTTCTT CCTTCCCAA TTTTGTATTC GGATGCAATA	420
CAACAAGTG TTTGGACAGA GTATGCATTA CGAAATAGAA ACACAACATT AAGGCGTTTG	480
AAGCTTAGAC ATCTACAGGT AGCACGAGCA AGGTGAGTTT TTGTGTTTTG GAAAATCAAA	540
TGGAACACTT TAGCTGAGGT	560

## (2) INFORMATION FOR SEQ ID NO: 227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

TGnAACTTC AGTTTGGGAG GCAATTAATA TCTGTCACCT CAGCCAAAGT GTTCCATTTG	60
ATTTTCAAAA ACAAAAAAAC TCACCTTGGC TCGTGTTACC TGTAGATGTA TAAGCTTCAA	120
ACGCATATTT GCTGTGTTTT TTATTTTATA ATGTCTACTC TGTCTCACT CTTATTTGTA	180
TCACATCAGA ATACAAAATT TGGGAAGGAA GAAGGCAAAA CCAACTCAGA TCCAGAAAAT	240
TTTTAGGAAA ACACCACTCA AGAATCCACA AATCGCCTGA GGCACCCAAA CCAATGAAAG	300
CAAGCCAAA TTGGAGCAAG CCAACAGCTG TGCCCTGAAT GnAAAAAAA CTCCTCTTG	360
TGCCCTGnAC TCAATATGCC AGCCACAAA CAAAAGTTCA CAGCCG	406

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GAACTTGCAA AAAGCGTGGT AACnGTATT GCACGGGTTA AGGATGATAT GTGTnAACTG	60
CTTGATAGAG GCTTCGTGCG CATTCTTGGC CAAGCAGCAG GCAGAGTCGC CACTCCGGGG	120
AAAAAGCTTT TGCTTCTCAG GCTCCCTGCA GAAATGGAGA TCGCGCGnCT ATACACCGTA	180

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TACGCGCGCT CGGnGGCGTT nTGAGAACGT CGGGGATCCT CTAkAGTCGA CCTGCAGGCA	240
TGCAAkCTTG kCACTGGCCG tCGTTTTACA ACGTCGTGAC TGGGAAAACC CTGGCGTTAC	300
CCAACTTAAT CGCCTTGcAG CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC	360
CCGCACCGAT CGCskTCCC AACAGTTGCG CAcCTGAATG GCGAATGGCG CCTGATGCGG	420
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATGGTGcAC TCTCAGTACA	480
ATCTGCTCTG ATGCCGCATA GTTAAGCCAG CCCCgACACC CGCCAACACC CGCTGACGCG	540
CCCTGACGGG CTTGTCTGCT CCCGGCATCC GCTTACAGAC AAGCTGTGAC CGTCTCCGGG	600
AGCTGCATGT GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGACG AAAGGGCCTC	660
GTGATACGCC TATTTTTATA GGTTAATGTC ATGATAATAA TGGTTTCTTA GACGTCAGGT	720
GGCACTTTTC GGGGAAATGT GCGCGGAACC CCTATTTGTT TATTTTTCTA AATACATTCA	780
AATATGTATC CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA TTGAAAAAGG	840
AAGAGTATGA GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC	900
CTTCCTGTTT TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG	960
GGTGCACGAG TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT	1020
CGCCCCGAAG AACGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA	1080
TTATCCCGTA TTGACGCCG GCAAGAGCAA CTCGGTCGCC GCATACACTA TTCTCAGAAT	1140
GACTTGGTTG AGTACTCACC AGTCACAGAA AAGCATCTTA CGGATGGCAT GACAGTAAGA	1200
GAATTATGCA GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT ACTTCTGACA	1260
ACGATCGGAG GACCGAAGGA GCTAACCGCT TTTTGCACA ACATGGGGGA TCATGTAAC	1320
CGCCTTGATC GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC	1380
ACGATGCCTG TAGCAATGGC AACAACGTTG CGCAAACAT TAACT	1425

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GGGGCTTTTT AACCATATCT GAATGCCTTA AGGGCTGATT CTGAGGCCAG AGTGCTATCT	60
AGGATATCTG CCATTCTGTA AGTCTGCTGT GTATCCTGCT TCCCATGTTG GATCATCTCT	120



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TCCTTTTAA TTCTATCAGT TAGTATTAGC AGACACTAGT CTTGTTTATG TGATCTCTTT 180  
GACACTTAAT CCTATCATTA TGATCAATTA TGAAGTGCAA CTGATCACTT TAACTAGTGA 240  
GATGGCATTG GTGCATGCTC AATTGGACTT ACCCCTAATG ATAGAGTTAG AAATGTGCCA 300  
GGGAATTCCA ATTCAATCCC ATCAAGGATT TTATTTAATT TAATTTAATT TTATTTACTT 360  
AT 362

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CGGATCCCCG GTCAATTGTG GAGACATAT TATCAATTTA CCAAGAGAAA GCCGAGGTGG 60  
AAAGAGTTCA GAATTGAATT TGCCCACGGC nAATATnGTT AAAAAGTCTA GATTAAAGGC 120  
CAACCAACCA AAGTTAAATA TAGGCATTAG GATCTGGCTG AAGAGCCCAT GAAATTATTT 180  
TAGGCATGGA AAGTCAAGAC ACTCTCAAAA AAAAAAAAAA AAACtanATG AAAGATCTCT 240  
GTGATTGAGA TCCCACTGGA AAnAATGGGC CATCAAAGAA nGGTACTTTT CTCTTAAGGG 300  
nGGAGAGAAC TTCCACTTTG ACTATGACAT TGTCTAAATA AGATTGnAGT CAACAAACTC 360  
AAAAGGTTTC CATAGCCTTG GCAACTCATG ACnAGAGCCT AGGGAGATTT CTGACGCCAT 420  
AAACAAGAGT GTCAnTTTGT TAAGTCAACA ACAGGAGTCG CTGTGGCACT TACTCCTCAT 480  
GTAGGATCTC TATTCnTAAT GTGTTGTACA AGGnGAATTA ATGCTATAAC TAGTACTCAA 540  
ACAGTATTTT TCAC 554

## (2) INFORMATION FOR SEQ ID NO: 231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

ACCCAACCTC AGCACTAACC TTGACGAGTC ATTTCTTTGA TTTGGTCATT GGTAAAATAC 60  
TGACCAACCG TTTGAGCTTG AGTAAGCATT TGGCGCATAA TCTCGGAAAC CTGTCTGTTG 120

875

CTTGAAAGA TTGGTGT TTTT CCATAATAGA CGCAACGCGA GCAGTAGACT CCTTCTGTG	180
ATAAGCAAGC ATCTCATTTT GTGCATATAC CTGGTCTTTC GTATTCTGGC GTGAAGTCGC	240
C GACTGAATG CCAGCAATCT CTTT TTAGAGT CTCATTTTGC ATCTCGGCAA TCTCTTTCTG	300
ATTGTCCAGT TGCATTTTAG TAAGCTCTTT nTGATTCTCA AATCCGGCGT CGTCAAAAAC	360
AGGAAGCCTG GGTAACCCAG GTAGTGCAAC AGGCGACGCA GACAGTAACG GCTGGAGTTC	420
GAAGCGCGCT GGAATCTCGG GGGACTACGT ACATAAACGC GCTAGAGGCA GTTCAGCCTA	480
ATCCTGCTAA ACCTACCGGT AAGGnTGTC AAAATCTTCA CACCCCGCAG GAAGTCCGCC	540
G	541

## (2) INFORMATION FOR SEQ ID NO: 232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AAATAAAAAG AATCATCAGG AATTCCTACA AAGATCTATA TGCCAACAAA TTGGGAAACC	60
TATAAGAAAT GGATAGATTT CTGAACACAT ATAATCTACC CAAGCTGAAT CATGAAGACA	120
TAGAAAGTCT AAACAGATCA ATAACCAAGA CAGAGTAATA TCAGTAAGAA AAACCCTCCC	180
GCTTCCCATG TTGGATCGTT CTCTCCCTTT TTAATTCTAC AGTTAGTATT AGCAGACACT	240
AGTCTTGTTT ATGTGATCCC TTTGACTCTT AGACCTATCA TTACGATCCA ACATGGGAAG	300
CAAGATACAC AGCAGACTCA TAGAATGGCA GATGTCTTAA ACAGCACTCT GGCCTCAGAA	360
TCAGCCCTTA AGGCATTCAG ATCTGGCTCA AGAGCCTATG AGAGTATTTT AGGCATGGAA	420
AGCCAAGACA CTCTGGCAAA AAAAAAGGG GGGGGGGCAA ATGAAAGATC TCTGTGAGTG	480
AGATCCCAGT GGAAAGAAAA AGAACGGGCC ATCAAAGAAG GAGGTACCTT TCTCCGAAGG	540
AGGAGAGAAC TTCCACTTTG ACTATGGCCT TGTCGAAATA AGATTAGAAT CGGCAAACTC	600
AAAAGGCTTC CATAGTCTTG GCAACTCA	628

## (2) INFORMATION FOR SEQ ID NO: 233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

TAATGGAAGT AGAGAATGGG AGGGAAGTGG TAGGAAGGGA GAGGTGTGTG AGGCTGGGAA	60
ACCACTACAA ACTTAATAAA AAATCAAATG CTGAGGTAGG ATGTCAACTA CGTAAAAGAA	120
AATAGACCAT AGAATAATAA ATGAAAATAT ACCAAAAGCA CTTAAACATT TTCCTACTGT	180
TGGGTAAATA GGTGAATTAC AGTTTTTAGC TTCAGGCAAT AAAAGAAAAT CTTGTGGTA	240
AGATTTCAAG TTTTAAAGA AGTTTATCTT CACAATTGAT CACACTGATA GGTCAAAGAG	300
TCAAAGGGAT CACACAAACA AGACTAGTGT CTGCTAATAC TAACTGATAG AATCAAAAAG	360
GGAGAGAACA ATCCAACATG GGAAGTGGGA TACACAGCAG ACTCATAGAA TGGCAGATGT	420
CCTAAACAGC ACTCTGGCCT CAGAATCAGC CCTTAAGGCA CTCGGATCTG GCTGAAGAGC	480
CCATGAGAGT ATTTTAGGCA TGGAAAGCCA AGACACTCTG GCAAAAAAAA GGCCTAAAT	540
GAAAGTTCTT CTCTGTGAGA TCCCAGTGAG TGAGATCCCA GTGGAAAGAA CAGGTCTTCC	600
AAAAAGGAGG TACC	614

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

GCCnGCCAAC CCAAGGnTTT TTTACCCGGT TTTTGGCCA CCAAATTTCC CTCCCCGGC	60
CACCTCCAAG GGCCAAGGAA ACCATTCCCC CGGCACCCCA ACCGGACCAC TGCACTGGCA	120
AGTnAAGnCG GCATGGGCAG CAGTCGGTGC AGGACCTGCA GGATCGCTCA TTCCTGGCGC	180
TCCTCTCAGT GCGGGAGTCG GCTCTCGCGG CGnTGGGGAG CGTTGCCTGC GCCAGTAGAG	240
CCGCTGCTCC GCCAGGCGGG ATGACGCATT GGGTGCGCTT GCAAGACTGT GGCAGCGTG	300
C	301

## (2) INFORMATION FOR SEQ ID NO: 235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AACGTGGCAG	ACGTGGTAAC	TACGTCATCG	ATAAnCAAGG	CATCACGCGG	CACACGAGCG	60
TGCGCCCCGA	GCTCTATACT	CCCTGCAAGA	TTCTCAACAC	GCGCAGCGCG	ATCTAAAGTT	120
TTGCTGCGCG	AAACGACCCT	CTTACTCGCA	CCAACGCACG	ATTAACGGTA	AAACCAGCCA	180
ATTCTAGTCG	ACGCGACACG	TCCGCAAnCG	GGTCCCATCC	TCTTCTCAGC	CATCATGCAn	240

## (2) INFORMATION FOR SEQ ID NO: 236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AAAAAAAAGG	GnGGGGGGAA	CCCAAAATTC	CCCCCAAAA	nGGGTTTAAC	CCAAAAAAGG	60
GAAAAAAAC	CCAACCCAAA	TTTAAATTTA	AAAACCCTTC	CCCCCTTTAA	AAATTTTTTG	120
GnAACCCAAT	TTGGGAAnTT	CCAAAGGGAA	AAAAATTGGG	AAAAACCCTT	TTAAAAACC	180
CCCAACCAAA	AACCCAACCC	AAAATTTAAT	TTAAGGTTTC	CAAAAAAACC	TTTTTTTGGG	240
AGGGCCAATT	TTTAAAAAAA	CCCCCTTAAA	AAAAAGGAAA	AAAAGGAATT	CCCCTTAAAA	300
AAAATTTTTG	GGCCAATGGG	AnGAAAGAAA	CCTGGCCTAG	GnATTTAACC	CCTnCCCAAA	360
AnGGGATTC	TCCCCAAATG	GAAGAACCTG	GGGCCAnGCC	TGGAATTTTC	CTCCATCCnG	420
ACCACCTnC	CCnGAnCTAG	GGGGGAAGAA	ATGGAAAACC	AnCATGGTTT	AAAAAAAAAA	480
TCCCTTGTC	AATCCCAGAA	ATACCGGTAA	CCCCAGTTAG	AnGCCTCCTC	CATTTAATTA	540
AAATGGAAGG	GTGGAAATTT	AAAAAAA				567

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

CTCCATCCAG	TCTATTAnTT	GTTGCCGGGA	AGCTAnAGTA	AGTAGTTCGC	CAGTTAATAG	60
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TTTGCACAAC GTTGTGCA TGTCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT 120  
GGCTTCATTT CAGCTCCGGT TCCCAACGAT CAAGGCGATT ACATGnTCCC CCAGTTGnGT 180  
TGAAATAGTA ATCAGCAGGT TTTCGGGGCG AGTAT 215

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ACTGACTTTG CTAATAATCA GACCTACATT TAACTCAGAT TAATAATGCT TGCTTAAGTG 60  
TCGCTCCCCC TCTTCGTGGA GGAACGACAC TAAATCCTGC CTAGGCTTCA TATCCGAGTC 120  
ACGGCACCAT TATGTCGCTC CCCCTCTTCG TGGAGGAACG ACACAGGACC CTGCGCTGTT 180  
CTTTCGTCTG CTCGGCCCTC CCCGGGTTTG CTGCTGGTTC TTCCCGGGTT GGCTGCTATC 240  
CCTTCCACCT CCGTGAAAG GGCAGTTCCC CTTGGCCGCA TCCCCATTTC CGCAGGGAGC 300  
GGCAAACCGC GGCCGGCTCT TCTCGGGGCT GCACAnATGT TTCCCTTAAA AGTCCCCCAA 360  
AAAnGTTTCT GG 372

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GCATGCCTGC AGGTCGACTC TAGAGGATCC CGGGCATATA AACAACGCTG CCCCCGTTCC 60  
TGAAGCAGGA AGCGTACGAT AGTGAGCCAG CGGAAAGAGA AGTGCTGCAA GGCGGACCGC 120  
AAGCTCTGCA GGCACCCGAT CGCAGCAGC 150

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

GCATGCCTGC AGGTCGACTC TAGAGGATCC CGGGGAGACG CTGAGCGCTC TCCTCGCCCA	60
CGAAAGACAC CGTGnGnGCC CGGTCCCTAG AACGGACGGT CCGCAAGGTA CTTGTACTCT	120
TGCCACTGTC TCCGCGCCTT CTCTTCTGCG	150

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GAGGGAGGGG AGGAGGGAGA GAGAGAGAGA AAGAGAGAGA GGTCCCTCTGT CCACTGCTTC	60
GTTCCCCAGA TGGCCACAAC GGGCCAGAGC TGAGTCGATC CGAAGTCAGG CGCCAGGAGC	120
TTCTTCCGGG TTTCACACTT GGGTGCAGGG TCCAAGGAT CTGGGACATC TTCTGCTGCC	180
CTCCCAGGCC ATAGCAGAGA GCTATnAGAA GCAGCCAGGT ACTAGAACTG GTGCTCATAT	240
GGTATGCTGG CACTGCAGAC CnAGCTTTA ACCCACTCTG CnACAGTGCC AGCCCTGAAT	300
GTTTTTGAAT A	311

## (2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCTCTG GGGTAGAAGG TTTTGGCTAT	60
GACCCGATTT TCCTGTTGCC ACACCTGGGC AGGACGTTCTG CTCAGCTCAG CATTGAGGAG	120
AAGAACCGCG TCTCTCACCG GGCATTGCG	150

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GAAAATATCG GAGAGAGAGA CTAGCAAACA GCCTAGGGAA AAGCCGACG AAAAAGGAGC	60
CGGAAGAAGC TATTGAAAGC CTAGGCATAG ACTTGATAC GGAAGTTGG	120
GAGAAATCTC TAAGGTCGAA AGCGAAAGTG AAAGCTAGAA CAAACAGATT CGGACGCGGA	180
CTGTGGGGAG AGGCCAGGAG AAATGAGGGA GGAATATCGT TGGAGATAGC TTGGGGAAAC	240
ATACCGGGTA GAGAAAACG TTAGGGAAAT TGAAGCCGCG GGGGCAGGC CAAGGCGGAA	300
ACGAAAGCCA CTTTGGGGTT CTCAGGTTAG CCCGGAATA GGGGCAAAA AGTTGAAACC	360
AGAAGCTGAG ACGTAAGCCA GATTGGGATC CGTCTGATTA GCCCGGGAG CAAAGGACGG	420
GAAGCCAAAT CGTGGGGCGG AGACGTACGC TGGGTTGAAT TCGCCAGGCT AGCCCGGGGA	480
ACTTGATTG AATGCTAGTG GTGGAGACGC AAGCTACGCT GTGTTACTCG CGGAAGCCGC	540
CGCGTGCAGA GAGAGCACGG GCGTGAGTA GATAGGGAAC GGGGCTGGCG TAnGCC	596

## (2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

ATGChTnGCA TGCCTGCCGG TCGACTCTAG AGGATCCCCG TCACTTGCCC CCAGCTCCAA	60
ACATTGCATC GTGACCCGTG CACCTTCTTT TGCAATGCTA GAGAGAATGA TTACTGGAAT	120
ATCAATGCGT AGACGTTTCC GCTGTTCAAG	150

## (2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

TGTTCTGGGC AGGGTTTTCT GAGTAAGAGC CCCAAAACAC AGGCAGAGAT ATTCAAAGTT	60
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881

TCACATTGG GTTAACTGGA TCATATTTT GCACGTTTCAT GGCTGAAACA AGGTCTTAAC	120
AAAAC TCAAA ATTGACAAAT GAAATCATGT CACATTAAAA TGCTTCTGTA CAAAAGACAA	180
GGTTTTATTT GTTTGTATGT TTTTATATAC CTGACTCTGA AAACCTTATG CnGGGGCTGG	240
TGCTGTGGTG TAGCAGGTAA AGCCGCTGCC TGCnGTGCCG GCATCCCATA TGGGGGCCGA	300
TTTGAATCCG GCTGTTCCAC TTCTGATCCA GCTCTCTGTT ATGGCCGGGA AAGCAGTAGA	360
AGAGGGCCCA AGCCCTGGGT CCCTGCATCC ACTTGGCAAG ACCCGGAAGA AGCTCCTGGC	420
TCCTGCCTTG GACAGGCGCA CTCCTGCTAA GCGGCCAACT AnGGAGTGAA CCAACAGATG	480
GAAGACCTC	489

## (2) INFORMATION FOR SEQ ID NO: 246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTAAAGTnC CCCGGGGGCT AAGCCCTTGG CCGAAATnC AACCCAGCG TACGTCTCCC	60
GCCCCACGG TTTGGCTTTC CCGTCCTTG CTCCCCGGGC TAATCAGACG GATCCCAACC	120
TGGCTTGCCT CTCAGCTTCT AGTTTCAACT TTTGCCCCC TATTCCCGG GC	172

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

ATCAGAAGTG GAGCAGCCGG GTCTGGAACC GGCACCCATA TGGGATGCCG GCACTTCAGG	60
CCAGGGCGTT ACGCnTGGCA CCACAGCGCC TGCCCTGAAA CCTTTTCTTT TACACAAAAT	120
GCAGATGGCT AATACTTCCA CTAACAATGT CCAGTATCAG GTTCAGCTAT GGTTTCTCTA	180
GCTGGGTGTG ATACTTCCTT ATTTTACTT GAAAAGCACA GTGACAAAGA GAGAGGGAAA	240
GACACACATG GCTGGGCCAA GAGGAAGCCA GGAACCAAGA ACTCCACCCA GGTCTCTAAC	300
GTGGATGGCA GGGCCCCAAG TATTTGGGCC ATCCTGCACT GCTTTCCCAG GAACATTAAC	360



882

AGAGAGCTGG ATTGGAAGCA GAGCAGTCAG GATTCTGAACC TGCACTCTGA TATGGAAGGC 420  
TGGCATCGCA GGTGGCAACT TAGCCTGATG GACAACAATG CTGGCCTTGT GATGTTTATT 480  
TTTATGATTT TCTACAGCAG AACAGCAGT TCCCAAATGC AGATATTTCC AAGCCTGCAT 540  
AGACTCATAC TTCTTTTCAG GTAGCAGTGA CTGAGAATAG AATCTGCAAT CCCAGTGTTA 600  
TCAACATTAC ATTCTAG 617

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CCCCGGGCCC AATTTTAAACC GGGCCCCnTT CCTTTCCCCC AAAAAAATTT GGCCAAACCC 60  
CGGGAAGGnT TAAAACCCCTT TTAAATTTTG GTTGGGCCTT TTTTGGGGGn CCAnTTAAAA 120  
AACCTTTCCC CAAACCGGGG GAACCTTCCA AACCTTTTC CTCCCCCTT 170

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GAGCATTTTG AGAGGCAGCA AGTGATGGCT CATGTAACAG GTTCTGGCC ACCTGTGTGG 60  
AGGAGCTGGA TTGAGTTTAT GGCTGCTGGT TTTGATCAGG GCCAGCCCTC ACCATTCTGA 120  
CCATCAGCAA AATGAACCTG TAGCTGAATG CTTCTCTCTC TCTCTCTCTC TCTCTCTCTC 180  
CCCCCAACCC CATCTCTCTC TCCCCGGTCT CTTCTCTGT CTCTACCTTT CAGATGAATT 240  
TTTTTTAAAA AAATTAGTAT TTTGATGCAA AATTGTTTGA CATCTCTGAC CTTTTCATAA 300  
TACACCTTCT CCATTATCTT TTTGAGGACT GCTTTAAGCA TAGATTTGTA TGTAGATATA 360  
GATGTCTTTC GTCTTTTTTA AAAAAGATTT ATTTATTTGT TTTGAAAGTC AAAGTAACAG 420  
AAAGAGAGAG AGAGAGAGAG CTCTTCCGTT AGCTTGGTCA CTCCCAGAT GGCCTAACAG 480  
CCAGCACTGG GCCAGGCGCC GGGTCTCCA CACAGATGGC AGGGACCCAA ACACTGTGTGT 540

CAACTTCTGA TGCTTTCCCA GGCCATTAGC AAGGAGGTGT ATTAG

585

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

AACCAGGACA GAATCCGGCG CCCCGACTGG GACTAGAACC CGGTGTGCCG GCGCCGCAGT	60
GGAGGATTAG CCTAGTGAGC CGCAGCGCCG GCCAGGAATA AAGTTAATTA AGTAGGTGAA	120
AGACTTGTAC ACTGAAAATA CAAAACAAAT TAGAGAGTAC AAAAATAAGT GGAAAGACAT	180
TCCAGGTTCA TGGATTAGAA GGTTTAACAT TATTAAAATG TAGTTTAAGG GGACAGCATT	240
GTGGCACAGC AAGTTAAGTC ACCGCTTCCA ATGCCAGCAT CTCATATCAG AGTGCTGGTT	300
TGAGTCCCAG CTGCTCCTCT TATGAACCAA CTTCTTGCCA ATGCACTGGA AAAGCAGCAT	360
ATGATGGGCC CTACCACCCA TGTGGGAAAC CCAGTTGAAG CTCCTGGCTT TTGGTCTGGG	420
CCTGGCCCAG CCCTGGCAGT TGAGACCATC TGGGGAGTGA ACCCATGGAA GATCTGTGTG	480
TGTGTGTGTG TGTGTGTGCG TGACTGTGCA TGAAGATCT GTGTGTGTGT GTGTGTGACT	540
CTGCCTTCAA AATAAATTAA GAACCG	566

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

AGGAGGTAA GACCTAGTGA ATGCGTGGAG CTTATGAACT GGAAGTGTGA AAAAAAAAAA	60
AAAGTGAAG ATGTGTGGGA GAACTCAGGG TGTGCCTGAG AAGTGAGTAC TCTCCGTGGG	120
AGACACCACA AACTTGGTAC CCTTGGCTAC CCAGTGAGAG CCATTGCAGG GGAATCTGAG	180
CTTACACTGA GGAAGTGAACA GATCCTTTGT GTGGTCCTTG GGACAGAGCA GAGGAATATT	240
ATACACACTG GGGCTAGCGC CCAGGCACTG ATTGCCATCA AGGAGAAAAG CTCAGCTGAG	300
CAAAATTACT TCCCTTCTGA ACACAAAAAG AGAGAGAGAA GTTTACTATG CCTAACCTGG	360

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GTGTGTCACC TTTGGGCACA CCCTTAACCC TGAAGAACTG AGCCGAGCTC TCTGGnCCAA 420

ACCCGTCAAA AGCCTCTAGn G 441

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

ATGCCCAAGT CCTTGGGTCC CCGCACCTGC GTGGGAGACT GGAAAGAAGC TCCTGGCTCC 60

TGCCTTCGGA TCAGCGCACT CCTTCTGTTG CGGCCATTGC GGGAGTGAAC CAACGGATGA 120

AAGACCTCTC TCTCTTTCTC TGCCCTCTGC CTCTGGnCC TGCCCCTGCC CCTTCCCCTT 180

nCCnTACCCC TACCTCTATC TCTACTTCTC TGTAAGACTC TTCATTTCAA ATACATAAAT 240

AAGTCTTAAA AAAAAAAAAAG CCAAAGTTTT CTACAGTTTC ATTGGTTCCT GGGAAAAGAT 300

GCCACCACAG TGATTTCCTT CCCAGCTGTG AGCATTCCTC CTTACCCTTA TCGGACCCAT 360

CAGGATGCCT GGTCCAAGTC GCCCACCGTG CATAGGCATA CAGTGGATCT TGGGTGCCTG 420

CTTCTGTGCA CATCCAATCT ATCTTCCTGA CCTCTGGCCC AGAATTATGG TCCTTGATCC 480

TCCATG 486

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

nGGAACCCnT GATAAGCAAG TGGCCAGGTG AAGGTGGAAA AATCAAAAAA ATATGGCATG 60

ATATTATAGA AGCCAAGTAA AGAACATGGT TATATAGAAG GAAGTGACCA GCTATCTCAG 120

AAACTGCTAG CTAAGTCATG TACAATGAGA ACTGAGGGAT AATACTTATA AAATGAGAAG 180

GTAAGAAGAA TATGAAAATT GTCTACCAAC CTCTACCCAA AGCTATACCA CTTTCCAGGC 240

ACCCTTGAGA GATCTTCCAC CATGTCTATA CACACAGATT TACTTGTAAT GTTAGTAGTA 300

GTTAAGTCAT TTGCATTTTG GAGCTTTATA TGCCCATGGT TTATAAACAG AAACAGAAGT 360

885

TATTAAAATT TTAGAAAGCA TAGGAATACT GAGGATCAGT CTCCCAGTAC TACTATTTTA 420  
AGATTTTATT TATTTATTTG GAAAGAGTTA CACAGAGAGA GGAGAGGCAG AGAGAGAG 478

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AATGCTGGAG AGGATGTGGT GAAAAAGGTA CCCTAATCCA CTATTGGTGG GAATGTTAAC 60  
TGGTAAAACC ACTATGGAAA TCAGTTTGGG GATACCTCAG AAATCTGAAT ATAGACCTAC 120  
CACATGATCC AGCCATGCA CTCCTGGGAA TTTACCCAAA GGAAATAAAT CAGCAAAGTA 180  
AGGAGCTATC TGCACCCCCG TGTGTATTGC AGCTCAATTC ACGATAGCTA AGACATGGAA 240  
TCAACCTAAA TGCTCATCAA CTAAGACTGG ATAACGAAAT TATGGGATAT GTACTCTATG 300  
GAACACTACA CAGTGGTAAA AAAATGAAAT CCAGTCATTT GCAACAAAAT GGATGAATTT 360  
GTAAAACATC ATACTTAGTA CGATAAGCCA GTCCCAAAGG GACAAGTACC ACCTGTTCTT 420  
CCTGATCTGT GATAAGTAAT AGAGCACCTA AAAGAAAATC TGTA 464

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CCTTTTACT TGTGAACTC TTTATTTAGT GGAGCGTTAA GCCTGTGATG CTAAAATAAA 60  
TTAAAAATAT GTTATTGCCA AAATTAAAGG GAGAAGGGAG ACTGGGAnGG TGAGAAGAGT 120  
GGAAC TAAGT ATCAAATTCT TAGGACTGTA TATATGAACT ACTTGAAAAC TGTTCTCTTT 180  
ATATTAATAA AAATTTAACA TAAAGCACT GAAAAAATA GTATATTTAA ATCCTCTACA 240  
AAATCAATTG CTATGTATTT CTACCTTCAA ACCCATAAAT ACTTGCTTTG TGTGTGTGTG 300  
CAGTGTGTGT GCATGTACAT ACCTAGACAC AAAAAAATG TATGTGGGGC TGGCGCnTGG 360  
CACGCTGGGT TAATCCTCTA CCTGCGGCAC CGGCATCCTC TATGGGCTCC GAnTCTAGTC 420

CCGGnTGCTC CTCTTCCATC CAGCTCTCTG CGTGGGCCCA GAAAGG

466

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CAAAGTCACT ACTTATCAAT AGTCATTTTG AATATAAATG GCCTCAACTC TCCAATTAAA	60
AGACGCAGAC TGGCTGAATG GATTAAAAA CAAACCCATC TACTTGCTGC TAACAAGAAC	120
ACATCTTTCA ACAAAGGTGC ATGCAGACTG AAAGTGAAAG GTTGGAGAAA GATATTCCAT	180
GCCAACAGAA ACCAAAAAAG AACTGnCATA GCCATCTTAA TATCAGACAA AATAGACATT	240
AACACAAAAA CTGTTAAGAG AGACAAAGAG GGGCACTATA TAATGATTAA GCGATCAATT	300
CAATAGGAAG ATGTAATAT TATAACATA TATGCAACCA ATTACAGGGT ACCGGCAGTG	360
CAAAATAAAT GTTAATGGAC CTGAAAGGAA ACAAACCTCC AATACAATAG TAAAGAGGGA	420
CTTCAATAGT CCACTTTCAG CAnGGACAGA T	451

## (2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CAGAACCATG GGAAACCACT ATGAAAGAAG GTGAAGGCAG AATATTTCCC AGTAAAAGTA	60
CAAAGGAAAC TCAAAGTAAA CTATAGGAAT ATCTGTGGGA AAATGGTAGG GCCAAGTTGT	120
TACTTATCAA TAATCACCTT GAATGTAAAT GGCCTCAATT CTCCAATTAA TAGATACAGA	180
CTTGCTGAAT GGATTAAAAA ACAAAGCTCA TCTATTTTCT GCCTTCAAGA AACGAATCTC	240
ACCAACAAAG GTACATGCAA ACTGAAAGCG AAAAGATGGA AAAAGATATT CCATGCCAAC	300
AGAAACCAAA AAAGAGCTAG TGTAGCTATC CTAACAGCAA AACAAAATAG ACTTTAACAC	360
AAAACTGTT TGAAGAGATA AAGAAAGGCT TATGCAATGA TTAACGGATC AGnTTACCGG	420
GAGATGTGAC TATnTAAnGT ATAnGCACAC nTTACAGTAT ACTGAAAAC TCTCCTGATG	480

887

AnCATGGTTC ATAGAGAnAT CAnAAGAGAA ATAAGAAATA AAAAActGTT GAGGGACTTT 540  
AACAAAATAA GAAGTATGAC TCTGTGGATT ACTGTTATnA CTATTATGAT CATAAACCTG 600  
CTCTGATAAG CGCTTnCAT ATATCACTTC TATCTTTA 638

(2) INFORMATION FOR SEQ ID NO: 258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCTCTnTC TCTCTCACTG TCCACTCTGC CTGTCAAAAA ATAAAAATAA AAACAAAAAA 60  
TAAAAAAGT ATCTCTGTG ATTGAAATTT GTGTTTTTTT TTATTAACT CATTTGCATA 120  
TCTTTATCAA CATTTTGGCC ATCTGTTTTA TTCTCTGAAA TATCTTTTTG TGAAGTCTAT 180  
TTAATTTTTT TCTGAAGATT TACTTGTTTA TTTGAAAGGC AGAGTTACAG AGAGGGAGGG 240  
TGAGACAGAA AGAGCTGAGA GAGAGAGTGT GAGAGAGAGA TGGATCTTCC ATCTACTAGC 300  
TCCTTCCCTA AATGGCTATA ATGGCAAGGA CTGGGGCAAG TTTAAGCTAG GAGCCAGAAA 360  
CTCCATGCAA GTCTCCCATG TGGGTGGCnG GGnCCATGTA CTGGGG 406

(2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGAGAGCTGG ATCAGAAGTG GTGCAGTTGG GACTTGAACC AGTGCTCATA TGGGATGCCT 60  
GTGTCTCAGG GTTAACCTGT ACCACAATGC CTACCCTCAT TATACCACTA ATAATCTGGA 120  
ATCAGATTCA TTATTGCTTC AACTCCTGGT AAGGAGTATA GATCAGTAAA GGTTCTTAGA 180  
GTAGATTAAG ACAAGCTGCC TAAAAAAGCA AAGGTTTGAA GTAATAAGCT CTTGGAGAAA 240  
ATAGATGTTG TCGAAGGGAA TGCTCGAGTG ATTCTAATAA ACCGTCATTC CCTGTGATTG 300  
CTTTACATGG CGTGCAGTGC ATTTGGAACA AGACAGACGC CAAGTCAAAT CCTATTCCTG 360  
GCTATATGAT GTTGACTGGA GATAGTTCCC ATCTCTGAGA CCCAGTTCTT ACTGGGTAGA 420

CTGTGACACT GGCTGTCTCC AAG

443

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGGCTCTTAA TCCATGCTGA GTGGATTTTT GTGTAAGGTG CAAGGTAGGG GTCTTGCTTC	60
ATGCTTCTGC ACGTGGAAAT CCAGTTTTCC CAGCACATGG AACCCCAAAC CCCCTTAAGA	120
TGGTATTTTT ACCACCCAGC CTAAGTGTTA AAGTGATCAT ATGGATAGGA TTGAGTGTCT	180
GGTAATAATA ATAGATAGAA TTTAAAAGGA GTGAATGCTT CAACATGGGA AGCAGTCCAC	240
ACAGCAGACT CATAATTGCT TTAAAAAGCA CTCTGACCTC AGAATCAGCC CTTAAGGCAT	300
TCTGGTCTGG CTGAAAAGTC CACGAGAGCA TTCAGACATG GAAAGCCAAG ATATTGTGAC	360
AAAAATGTCC TACACGAAGG ACTTAGATGG TGGAAAGAAG TGTCCATTAA AGAAGGAGGC	420
ATTTTCTCTA AAGAGAGGAG AGAACTTCAA CTTTGCTTAT GACCTTGTCT AACTACGGAA	480
TGAGTTGTG GATTCAGAAG GCTTCCATAA CCTTGGTACC TCATGTCAAG AGCCTCAGAT	540
GATCACTGAC ATCATACTTA AGAATGTTAA TTGTTGGGGC TGGTGCTGTG GGCACAGCAG	600
GTTAAAGCCC TGGCCTGAAG AACTGGGCAT CCCCATATTG GGCACCAGTT CTAGTT	656

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

ATCAGTGCCT TGTAATTAGG TGCATATACA TCTATAATAG TTACATCTTC CTGTTGACTT	60
GATCCCTTAG TCATTATATA GTATTCCTCT CTGTCTCCCT TAACTGTTTT TGTGTTAAAG	120
TTTATTTTAT CTGATATTAA ATGGCTATGC CTGCTCTTTT TTCATTTCTG TTTGCATGTA	180
ATATCTTTTT CCAAACCTTC ACTTTCAGTC TGCATGCATC TTTGTTGGAA AGATGCATTT	240
CTTGTAAGCA GCAAATAGAT GGGTTTGTGTT CCTTAATCTA CTCAGCCATT CTGTGTCTTT	300

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TAAGTGGACA GTTGAGGCCA TTAACATTCG ATATGACTGT TGATAAGTAG TGACTTGCCC	360
TGCCCTTTCC CAAAGATATT CTAATATATG CTTGAAGTCC GTGATCTTTA CGTGAGGTTT	420
TCTCCTTACC TCTTCATATG AGGCCAGTTT CGTGTGTAAC ACATATTATG CATTTTGTGA	480

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CnAAATTCAA AAACCTGGA GGATGACATA TATTAACCAC TTATTCCAGT AGTAGCACAT	60
GTACGGCTAT TATAAATATA GATGTATTGG GGTAGCTATT GCTTACTTAA CTATTTAAAT	120
AGTCATTGGC TTAGCTTGTA TAGGTCAGGC TCAGCCGAGT AGTCCTGGCT TTCACTGGGC	180
TACCTGGTGA ATCTTGAACC CGTGATATAC CAGGGAGGTG TCTCTGCTTC AGAGTATGGC	240
TGGTTGTTGC CTGGGACAGT GGAACCAATG GCCCAAATGT CTCCTCATCTC CAAAAATAGC	300
CCAAGCTTTT TCACATAGTG TTTCCAACGA TCCAACAGGA AGAAAAGCAG GCAAGGCCTG	360
GAGACTTAGG CTCAGAACCA GCTTACCTTC ATTTCTGCTG TGTTCATTTC ACAAAGCAA	420
ATCACAAAGC CAGCCCACAT TGAAGGGGTG AGAAATAATT TTTTTTTTGA CAGGCAGAGT	480
TAGATAGTGA GAGAAAGAGA CAGAGAGAAA GGTCTTCCTT TTCCAATGTT TCACCCCC	538

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

GCnCTTCCAG AAAAATCTTA TTTACTACTT TGGCCCTAGA AATCATAAAT GACTATGATA	60
GAATGTAACT TTTAACAGAG GTGAGGAAGG CATGGTTTAA TATCCAGTTT TGAGAATACA	120
ATTTTCATTT GTATTTTATT GATGTTTATA GTTCTTTTAA GATTATTGA TTTATTTGGA	180
AGTCAGAGTT ACAGAGAAGG AGAGGCACAC ACACAGAGAG AGAGAGGTGT TTTCCATCTG	240
CTGGTTCACT CCCCAATTGG CAGCAGCACC ACAGACCGA CCCCTTATAG TTCTTTTCAA	300



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ATCATTTTAC ACTGTCTTTT TATTCATCTA GTACAGAGAC AGAAGAATGG ACACAGAGCT 360  
AACATAGCTG AGTATTCAAG GAGACAGGTT AAGGGGTAA ATGCCTCATA TCATATTATT 420  
TATACCTTAG ATTAATTCTG GGGACAGTAT TATCTGGAGT TTACAAAGTA GAAACTGAAT 480  
GGAAAGAGCT TAGAAAAATA CCGTGTTTTT TAATATCATT AAAAAGGCCA ATCAAGGGGC 540  
CAGCACTGTG AAATAGCAGG TAAAGCTACT GCCAGCATGG ACATTCCATA TGGGTGGAGG 600  
TTGAGCCCGG CTAGTCTGCT TTCAATCCAA CTCTCTGCTA TGGCCAGGGA AAGCAGTGGA 660  
AGATGGCCCA AGTCCTGGGC A 681

## (2) INFORMATION FOR SEQ ID NO: 264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TGGCTTCTAG CTTGGGATTG GCTCAGCTCC AACTGTGGCA GCCATCTGGG GAGTGAACCA 60  
GTGGATGGAA GACCTCTCTT TCTCTCTGCC TTTGCCTTTC TGTAACTTT GCCTTTCAAA 120  
AATAAATAAA TAAAAAGAAT TGAATTAGAG AACATCTAGC TAGTGTCCAC TATAGAACTG 180  
AATATTCATT TAAAAAATGG TTAGAGAGTG TATAGGGCAA AAGAAAGGGC TGCTTTCTCA 240  
AGTACATCGT CAATTCCCAG GGAGGCTGGG ATCAGCTTGC CTTGGGGTTG GTCAGGAGAA 300  
TGTCAGGAT TACAGCAGCT CTTAGAGCCT GGTGTGAAG GGAAGTAATG GTGATCAAAT 360  
GAGAATTGTA CCAAGTGAAG TCAGCAGAAA GGACCAGCTC TGCTGCTGAT GGTGGGGATG 420  
TAAGAGGAGC TTGGAAGCTA CTGCAGTGAA TGTGAGCTTT GGAGATTTAT GTATTTGAGC 480  
TGTACAATA TGGGAAGAC TTTTTTTTTT TATCnTGTA GCTTCAATTT TTCAAAGTGT 540  
GAAATGGGGC GAATAATTAT AGACATAAAT ACAGAGCAAC AGTTTGTAAA TACCATAAAC 600  
CTCATGTCCT TCAACAGTG nTATTCATAC CnTATAGGGG TATTGTGAGT TCC 653

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTGTTCAA AAGAGGAAAT CCAAATGGCC AACAGGCACA TGAAAAAATG TTCAGGATCA	60
CTAGCAATCA GGGAAATGCA AATCAAAATC ACAATGAGCT TTTACCTCAC CCCGTTAGA	120
ATGGCTCACA TTCAGAAATC TACCAGCAAT AGATGCTGGC GAGGATGTGG GGGAAAAGAG	180
ACACTAACCC ACTGTTGGTG GGAATGCAAA CTCGTCAAGC CACTGTGGAA GTCAGTCTGG	240
AGATTCCCTCA GAAACCTGAA GATAACCCCTA CCATTCAACC CAGCCATCCC ACTCCTTGGA	300
ATTTACCCAA AGGAAATGAA ATTGGCAAAC AAACAAGCTA TCTGCACATT AATGTTTATT	360
GCAGCTCAAT TCACAATAGC TAAGACCTGG AACCAACCCA AATGGCCCAT CAACAGTAGA	420
CTGGGATAAA AGAAATTATG GGACATGTAC TCTATAAAA	459

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GGAGTCTAAA AATATTATTT CATAGAAGTT AACAATATAA TGATGGAGAC CAGAGTTGTG	60
GCACAGTGGG CAAAGCTGCC ACCTGTGACA CCAGCACCCC ATGTGGGCGC CAGTTCATGT	120
CCCAGCTGCT GCACTTGACAG TCCAGCTCCC TGCCAATGGT TTGGGAAAGC AACAGAAGAT	180
GGCCCAAGTG TTTGGGTCCC TGCCACCCAC GTGGGAGACC TGGGTCAAGC TCCTGGTTCC	240
TGACTTTGGC CTGGCTCAGC ATTGGCCATT GCAGGTGTCT AGGAAGTGAA TCAGCAGATA	300
GAAGATCTCT CTCTCTCTCT CTCTAACTCT TTCAAATAA GTAAATAAAT ATTTTAAAA	360
TATATATGGT GGATATCAGA CGCTGGGGAG GGAAGTAGAG AGGGAGAGAT AGTGAAAGGT	420
CTATGGTGGG TACAGCTGAA GAAAAGTGAG AAATTCTGAG GTTGTATTGC ACCATGTGAC	480
AACAGATAAT GTGTGCCAAC AGATAATGTA CCATACAGTT CTACATTTAA GAAAAGAAAA	540
CTAGAAGATA CAATTTTGGA TATTTTCACT ACAAAGAAA ATGTTAACAA TTAAAGGAGA	600
TAGATATATG TACCCCACTA GACATTTAAC AAGATAGACA TGTATCAAAA TGTCAAATGC	660
TACCCAATAA ATATTTATAA ATTGTAAATG TCTGTAAAT TTAAAA	707

## (2) INFORMATION FOR SEQ ID NO: 267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

TTGAGAGGCAA AATGTAGAAA GAGAACAGAG AGAGAGAGAG AGAGAGAGAG AGAGCGAGCT	60
TTCATCTGCT GGTTCACTCC CAATTGCAGA ACCAGCCAGA GACAGTATAG GCAGAATCCA	120
GGAGCTGGGA ACTCTGTCAG GGTCTCTCAT GTGGGTGGTA AGGGCCCAGA TACTTGGGCC	180
ATCTTCAGTT GCCTTCCCAC ACGCATTAGC AAGGAGCTGG ATCAGGACTT GAACCAGCAT	240
TCTGATATGG GATTCTGACA TTACACACAG CAGCTTAACC CACTATGCCA CAGTGGCGGC	300
CCTTGCCCTC ATCCTTAATA ACCTATATAC TACATCTGCC TGACTIONAT CAAAGTGGCA	360
GAACCTGGGA GCATCTCAAG ACATAGGAAT GGTGTAAGAA TTTTACTAGT GGGGCTGGTG	420
TTGTTGCACA GTGAGTTAAG CCGCTGCCTG CAATGCCGGA CTTCCCATAC GGGTGCCAGT	480
TCAAGTCCTG GCTGGCTCCA CTTCTGATCC AGCTCCCTAC TAATGCACCT GGGAAAGCAG	540
CAAAGACAG TGCAAGTGCT TGGGCCGCTG TCACTCATGT AGGAGACCTG GGTGAAGCTn	600
CCTGGGCTCC TGGGGCnTTC AGCCTGGCCC AGTTCCTGG	639

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 550 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TGCCTTTCAA ATAAATAAAA TAAACCTTGA AAAGAAAAAC TAATAGATTA TTAAAGGACG	60
AAAGAAGCTT GAATACAATT GCTTTTTAGC AAGTGTTAGT TATTTTGTG AGGACACGAT	120
CCACCTCGGT GTCCTTGAGT GCAGCCTCTC AGGGCAGTCA CAAGTCTTCA GAATTGGTCT	180
TAAAAGTCCT TTAGGAAGCT GCAGCGTTGG AGGGGGTCCA AAATCTGACA CCTCCAGGTT	240
CTCCTCACTG ATGGGGAGAT CATGGCTTCT CAGCACAGCA CCAACTGGGG TTAGTGTTTT	300
ATTTTGTGTT TAGATTTATG TACTTGACAG GCAGAGGGAG AGAGAGAGAG GAGAGAGAGA	360
GAGAAAGAGA GGAAACCTTC ATCTGTTGAT TCACTCCCTA AATGTCCATA ACAACTGGGG	420
CTGGACCAGT CCCAACCCAG GAGCCAGAAA CTCTCTCTGG ATCTCCCATG TGGACTGTAG	480

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GGACCCAAGC ACTTGGGCCA TCAACTCCTG CCTTCCAGAT ACATCAGCAG GAAGCTGAAT 540  
CAAAAGTGCA 550

## (2) INFORMATION FOR SEQ ID NO: 269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GTTGGGGGAT CTGGGATGGA GCTCAAGAGT TCCTGGCTTC TGCTTGATTG AGCTCTGGCC 60  
ATTTTGGGAA CGAATCAGCA GATGGAAGAT CTCTTGCTCA CTC'TTTTATT TTTTCAAAGC 120  
TTTATTTTAT TTATTTAAAT GGAAGAGTTA GAACGCTCTT CCATCCACTG GATTCACTCC 180  
CCAAATGGCA GCAATGGCCA GCGCTGGGTC AGGCTGAAGC CAGGAATTTC TTCTGGATTT 240  
CCCACATGGC TGCAGAGGTC CAAGGACTTG GGCCATTCTC CACTGCTTTC TTGGGCACAT 300  
TAGCAGGGAG CTGGATCAGA ACTGGAGCAG CTGGGACTTG AACCAGTGCC ATATGGGATG 360  
CGGGCACTGT AGGCAGCAGC TTTACCTGCT ATGCCACTGC GCTGGCCCCA TTCTCTCTTT 420  
CTCTGTCTCT TTCATCTCTCT CTCCCCATCC ACCATCTCTC TGTCAC'TTG CCTTTGAATA 480  
TATGAAAGTG ATTTT'TAAAA ATnAAAGTAA TTCTTAATAA TATCAGGAAA TGAATTCTAT 540  
A 541

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CGGTTTATTT AAAAGATATG TTAAGGGACT TAAAGGGAGA CTTAGACTCC AATACAATAG 60  
TACTGGGGGA CTTCAATACT CCACTCTCAG AAATAGACAG ATCAACTGGA CAGAAGATCA 120  
ACAAGGAGAC AGTAGATTTA AATGACACTA TAGCCCAAAT GGACCTAACA GATATCTACA 180  
GAAC'TTTTCA TCTGACATTT AAAGATTTTA CATTC'TTCTC AGCAGTGCAT GGAACCTTCT 240  
CTAGGATTGA CCACATCCTA GGCCATAAAG CAAGTCTCAG CAAATTCAA AGAATTAGAA 300

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TCATACGATG CAGCTGCTCA GACCATAGCG GAATTAAGTT GGAAATTATC AACTCAGGGA	360
ATCCCTAAAG TACACAGAAA CACATGGAGA CTGGAACAAC ATGGCTCCTG GAATGAACAG	420
TGGGTCATAG GAAGAAATCA AAAGAGAAAT CAAAACTTT CTGGAAGTAA AGGAGGGT	478

## (2) INFORMATION FOR SEQ ID NO: 271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GAATTGAGCn CGAAACAGGT GTAnCCATAA GTTTTGATAT GTTGTCATGT CACATCATTA	60
GTTTCCAGAA AATTTTGTGAT TTCTATTTTG ATTTCTTCTA TTACCCAGTG TTCATTCAGG	120
AACTTGTTAT TCATGTGTTT GCATATGCTC TAGATATTCC CGAGTTGCTG ATTTCCAGCT	180
TTTTTCCACC ATGGTATGAG AAGCTGCATG GTATGATTCC AATTCTTTTG ACATTGTGA	240
GACTTGCTTT ATGGCCTAGT ATGTGGTCAA TCCTAGAAAA AGTTCCATGT ACTGCTGAGA	300
AGAATCTGTA TTCTTCAAGT GTAGGAATAA AAGTTCTGTA GATATTAGAT CCATTGGGCT	360
ACAGTGnTGA TTAAATCCCT GnTTCCTGnT GGATTTGTC GGGGACCGTC CATGCT	416

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

TTGTTCTTAC TGAAGTGCAT CAGTGGCCTC TACCCTGCTT CTGCTGCCTT CCGCCCTCCC	60
TGGCCAACAA GCACTTGGA GAGGAGCCCT GGATGAACGT TGTAACAGA CCTCAAGACT	120
CCCTTGGGAT GCTGGCATCC CAGTTCCTAG CGCTGGGTT CCAGTCCTCT GCTTTCCTGT	180
CCCTGCCGGC TAAGTGGGAG AACTGGATTG GGAGCAGGTG CAAGCATCTG GGGAGTGAAC	240
CAGCAGAGAG GGGACCACGT TTAATCCTTT TCTCTCTGCC TCTCAGATAC ATGCAGATAT	300
ATACAAGTTT AAAAGGAATG CTCGGTTTTT TGGCAAATTA TTTGTTAATA AAAATTAAA	360
TATTTCTGTC ACTTTTTAAA CATTTATTTA TTATTTGAGA GAGTTACGAG AGGGAGAGAC	420

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AGAGAGAGGT CTCTATCTGC GGTTCACCTCC CCAGGTGGGC TGCAAGGGCC AGGG

474

## (2) INFORMATION FOR SEQ ID NO: 273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CGGACTGTGC CTGCATGGCC TGCATGTGAA CAGACTTGCC ATTGGCTGGG AGCGTCCTGC	60
TAGGGGAACC TAGGGTATAT AATGGGGATA GGATTGTGTA GGGGGATGAG GGCTTGGCTT	120
CTTTTCTTTC GCCTTGCATC TGGATGAATA AAGTTCCATG AGAACCGAGT AAGCAGCGAT	180
CGTGTCTGTTA CTATGCTGGA CTCTCGCGGG CAAGCGTCCG GCAGCCCCTA GACTCAAATG	240
TTGTCAGAAG TTTGAGAACT GCCATCCTAA AGAATTTCTG ATGGGGCCAG TACGGTGGCA	300
TAGCAGGTTA ACACAGTGTC TGCAGTGCTG GCATTCCATA TAGGCGCTGG TTCGAGTCCT	360
GGCTGCTCCA CTTCCAATCC AGCTCTCTGG CTAATGGCCT GGGAAAGCAG CAGAGGGATG	420
GCCCAGG	427

## (2) INFORMATION FOR SEQ ID NO: 274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CATCACCACC ACAAATGAAA ACTTAAGCAT GCACTGGTGA TCCACAGGAG AATGGAATTC	60
CTCTCTCCTA TAGGCCTGAG CACCACCCTG CAGGAGGGGC TTTAAAAGGC AGATGCAGCA	120
CATCTTTGAA TACCTTGTTC CTACTTGTGG TTGTGTGATT TTCTTTTTTT TTAAGATTTT	180
CTTTATTTTA CTTGGGAGGT AGAGTTTGAG ACAGTAAGAG GGAGAGACGG AGAGAAATGT	240
CTTCCCTATG TTGGTTCATT CCACAAATGG CTGCAATAGC TAGAGCTGCA CCAATCTGAA	300
GCCAGGAGAC AGGCACCTCT TTCTGGTCTT CCAAATGAGG GCAGAGGCCC AAGGATCCAG	360
GCCATCCTCC ACTGCTTTCC CAGGCCATAG CAGAGAGCTG GATTGGAAGT GGAGCAGCCG	420
GGGCTAGAAT CAGCACCCAT ATGTGAACCT GTGCTGCAGG CAGAGGATTA ACCTACTGCA	480

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CCACTGTGCT GGGCCTGGCT GTGTGATTTT CAGCATTTAG CATTGGAGCA TGGGTGTGTC	540
ATGGTTGGCC ATTCCCTAAC ACCATGGCTG ATCTCTACTC AGGTTTGCAG TTTTAGGCAA	600
CATTTTGAGC TGCACA	616

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

TGTGATAnTC TGnACTTTCA AATAAATAAA TAAATGAATC TTTTTTTTAA AAAAAGTGGA	60
TTAGGGTACC TTTTCCCCAC AGCCTTGCCA TCATTTATTG TTTTTTTGAT TTATATATGA	120
TAGCCATTCT AACTAGGGGG AGGTGAAACC TCATTGTGGA TTTTATTGTC ATTTATTGAT	180
GGCTAGTGAT CCTGAGCAGA TTTTAAATTT CACCCTTTGA AAAATGCCTG CTCATGTCCT	240
TTTTCTTTG CCTATTTCTT AACTGGATCG TTTGTTGCTG CTGAGTTTCT TGACTCTTTA	300
TAGATTCTTG ACATCAATCC TTTATCAGTT GCATAGTTTG AAAACATTTT CTTTGTATT	360
GTCAGTTGCC TCTTCAGTTT GTTGGGTGAT CCTTTACAGT GCAGAATCTT CTTAACTTGA	420
TGTAATTCCA TGGTCTATTT TTGCCTTTAn TGCCAGTGTT ATGGGGTnTT TCCAAGAAGT	480
CTTT	484

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTGTGCC TTTCAACTTT CCATCTTGTC CGTGTGAGGG GGTCCCTCAC AGGGGACGGT	60
GGGCCCAGCC TGTCGTGTGC TCACTTGCTGT GTGACATCAC GGATGGGAAC TGnGTGAAAT	120
TTCAGCTCCC CAGATCTGAA ATTTACAGAG GCAGCCTTTG TCACCTTGTT AGAGAATGTT	180
TTTCCATCTC AACTCAGCGG TAAACGGATC ATTTATACGC ACCTGTTTTT ATCTGGATGG	240
TGAATTTACC TGGTGGGTGG AAATTGGATG TGAGATTCAC ACAGCCTCAG AGCGTCTGGT	300

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CAGAGGTACT TACTGAGGCT GCGCCATGG TGCAGTGGGC TAAGGCACCG CCTGTGACAC	360
CGGCATGGCT GCTCCATTTG CAGTCCAGCT CCCTGCATAA AGCTCCTGGC TCCTGGCTTC	420
AGCCTGGCCC AGCCTTGGTC ACTGTGGCTA TTTGGGAAT GAACCAGCAA ATGGAAAGAG	480
TCAGTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTGTA ATTCTGCCTT	540
TCAAAAAAAAA TTTAGGATGT ATGTATGTAT GTATTTATnT ATnTAT	586

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

TCACTTTAAC ACTTAAAATG CTATTTTCCC TCTTAGCACA AGAGGACTTG GGGTGTCTATG	60
TCAAATTTT AAAC TATAACC CTTAGAAATA AATCTGTGGT AATGTATACA GAATTATGCA	120
GCTTTGCAGT TACAACTTC ATACACTTCA TAATTATGAC TTTAGGAACA TGGTGATTCT	180
TTCCACTCTG CCTGTCTG CACCCACATC CCCACCCCTC TTCCTCCTCC CTCTCTTATT	240
CCCTCTTTTA TTTT TGA CTA GGATATATTT TAATTTAACT TTATACATAT ATGATTAAC	300
CTATGTTAAG AGAAGAGTTC AGCAAAT	327

## (2) INFORMATION FOR SEQ ID NO: 278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TTCTAAAAAG ATTTTCTACT TCTACTTATA TACAAAAAAA TAAAATATTT CTTTATCTAA	60
TTGACACAAC CCTCTGTCCT GCTTTTTTGT TTAAAAGATT TATTTATTTA TTTGAAAGAG	120
AGTTAGAGAA AGGTAGACAG AGAGAGAGAG AGAATCACCA GGAAC TTTT CCAGGTCTCC	180
TGCTAGAGAG TAGGGGTCCA AGGACTTGGG CCATCTTACA CTGCTTTCCC AGACCAAAG	240
GAGACAGATG GGCTGGAAGT AGAGCAGCCA GATCTTGAAC TGGCACCCAT ATGAGATGCT	300
GGCACTGCAG GCTGTGGCTT TGCCCGCTAA GCCACAGTTC AAGCCCAAT ATGTCCGGCT	360



898

TTTTCGGATC ATATCAGTCT ATGACGTGCC ACTTATATTA CTATTAATCA ATGGCACCTC 420  
TTACTCTGAA ATGTGATTAT CTGTATGAT AAATTATACA TAAGTTCTTA AAATAAGTGT 480  
C 481

## (2) INFORMATION FOR SEQ ID NO: 279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GCGTGAGGAG CAAGATCAGC CTGGAAAACG TGTGACAGCG TACCACTTTG AAACAGCTGA 60  
GTATAAAGCA ATAGAATTTT CTGGAGCTA CACATGCCAA AACTAAAAA AGCAAGTTCC 120  
CCAGGCCAAC TGTTCCTTC TTCTTCTTCA TTTT TTTT TAAAGATTTA TTTATTGGA 180  
AGGCAGAGTT ACGAGAGAGA CGGAAAATA GAAAGAGATC TTCCATCTGC TGGTTCATC 240  
CTCAAATGGC CATTAACAGC CAGAGCTGGG CCAGGTTGAA GCTGGGAGCC AAGAGGTCCA 300  
TCCCAGTCTC CCCCATGGGT GCAGGGGCCA AACACTTGGG CTATCCTCCT CTGCTTTTCC 360  
CAGGCCCTTT AGCAGGGAGC TGGATCAGAA TTGGGGCAnC CGGGAnTTAA ACCCAGGCCC 420  
ATGTGGGATG CCGGTGCTGT AGGTGGATGG CTAAC TCACT GCACCACAAT GCCAGCCCCA 480  
A 481

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AACAGACATT CTTCGAGAT CTAGAAAAA TGATGCTGAA ATTCATATGG AGGCACAAGA 60  
GACCTCGAAT AGCTAAAGCA ATCTTG TACA AAAAAACAA AGCCGGAGnA TCACAATACC 120  
AGACTTCAGG ACGTACTACA GGCAGTTGT AATCAAAACA GCATGGTACT GGTACAGAAA 180  
CAGATGGATA GACCAATGGA ACAGAATTGA AACACCAGAA ATCAACCCAA ACATCTACAG 240  
CCAACTTATA TTTGATCAAG GATCTAAAAC TAATTCCTGG AGCAAGGACA GTCTATTCAA 300

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TAAATGGTGC TGGGAAACT GGATTTCAC GTGCAGAATC ATGAAGCAAG ACCCCTACCT 360  
TACACCTTAC AAAAAATCC ACTCAACGTG GATTAAAGAC CTAAATCTTC GTCCTGACAC 420  
CATTAAAGTT ATTAGAGGAA CATTGGGnGA AAnCC 455

## (2) INFORMATION FOR SEQ ID NO: 281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

GGCACTGGGG AGTGAAATAG CACGTGGGCA CTGTCTTTCT GTCTCTCAAA CATGTGAACA 60  
CATTTTTTTA AAGAAGATGA CAAAAATAG GTAAAGTCCT CTGTCCGACG TGTTCACACC 120  
ATTTAATTCA GTCTCTCGAT TGTTTTTACA AAAATAAAAG CCTTTTTTGT TTTACAACAG 180  
TTTTTTTTTT TAAGGATGTA TTTATTTGAA AGACAATTAG AGGGAGGTCT TCCATCTGCT 240  
GGTTCAGTCC CTAGATGGCC ACAGCGGCCA GGGCTGGGCC AGGCCAAAGC CAGGAACCGG 300  
GAGCTTCTTT TGGGTCTCTC AAATGTGTGG CAGGGCCAAG CAGTTGGGCC GTCTCCACTG 360  
CTCTCCCAGG CCGCTAGCAG GGAGCTGGGT CGGAAGCGGA CTGACGTTGC TGGCCTCGGC 420  
CTACCTGCTG GCACCGTAAG CTGGCTCCAG GACAGTTTGA TGGAGGTGCA GTCCAGCACA 480  
CTGTGTGTGT GTAAAAGTCA CACTTCCAGC ATACA 515

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GGAATGCCAG CCCGCCACTG CCGTCCGTCC TGGGTTGTTT CATACCCTAG CTCTTCTCCA 60  
CGTCGTGAAA GCCCAGGCGA GGAGACCTGG TGA CTGTCCC GGGCACAGCA CTCGGTGAGG 120  
CGTTCCAAGG GCATCCCAGG GTGCAGGCGT GGGCTGCCAC GTTCTCGCCC CACTCCACGT 180  
GACCCTTTT GGCCCTCAGG GACAGGGCGA GGATGTTGGC TGGCCCTGGC CGCCCTTCAT 240  
AGGGGTGCTC CTCAGAACCT GAGGGAGAAA TTCTTTTTCT CTGAGATTTA TTTATTTATT 300

900

TGAAAGAGAC AGAGATCTTT CATCTACTGG TTTACTCCCC AAATGGCCTC AACAGTCAGG 360  
 GCTGGGCCAG GCCAAAGTCA GGAGCCAGGA ACTCCATCCA GGTCTCCCAC ACAGATGGCA 420  
 GGGACCAAAG TACTTGGGCC ATCCTCTGCT GCCTTCCCAG GCGCATTAGC GTGGAGCTGG 480  
 ATCAGAAGCA GGAAAGCCGG GATTTCAGCTG GCCTCCAACG TGGGATGTGG GACAGAGCCC 540  
 ACCCCTGGCA GGTTTTTTTT TTTnnGnnTT TTTTTATAT TnnAT 585

## (2) INFORMATION FOR SEQ ID NO: 283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

ACTCTGCCTG TCAAAAAAAA AAAAAATCT TAAGGGGGCT CAGCTCAGCT GTGACTCCGT 60  
 GATCCGCTAA TATGAGGTCT ATTTCCAGTC CCTCCTCCTC CATTTCCAAT CCAGCTCCTT 120  
 GCTAATTAC CTGGAAAGCC ACGGGAAGAT TGACCCACTA CTTGGACCAG CTGGGAGATG 180  
 TGGAACAGAT GAAGCTCCCG GCACCTGCCT CCTGGATTG CCCTGGCCAC CCAGAGCCCA 240  
 TCCAGCAGAT GGAAGATCTC TCTTCCTCTC CCAACTCTCA GCCAGTCACC CCACAACTCT 300  
 TTCACATAAA TAAGAGTACA TTAAATTTAA AAGAGAATTG GCCAACTAAG TCTCTGAAGG 360  
 TGGGGGGGTT GGGCTGACCC TGGGGCATAG TAGGTTAAGC ATCTATCTGT GGCTCCAGTT 420  
 TGAGATGGAA GGACTCTCTG TAACTCTGAC TCTCCAGAAA AAAAAAAAAA GATAAAAAATC 480  
 TTAAAAAGAA TTATTATTAT TATTATTATT ATTATTATTA TGGGGCCTGT GCTGTGGTGT 540  
 AGCAGGTAAA ACTGCCACAA GCAGTGCCGG CATCCCATAT GGGCTCCCAT TCGGAATCCC 600  
 ATCCCCAGCT GGGCTGCTCT CTGCTAnGGT CTGGCA 636

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TAGAGATTTA GTAATCTTCT GAACTCTTTG CTTTCAACCA TTTTCAGTTG CCAAAGATCT 60